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COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF OVARIAN CANCER

Technical Field

The present invention relates generally to ovarian cancer therapy. The invention is more specifically related to polypeptides comprising at least a portion of an ovarian carcinoma protein, and to polynucleotides encoding such polypeptides, as well as antibodies and immune system cells that specifically recognize such polypeptides. Such polypeptides, polynucleotides, antibodies and cells may be used in vaccines and pharmaceutical compositions for treatment of ovarian cancer.

10 Background of the Invention

Ovarian cancer is a significant health problem for women in the United States and throughout the world. Although advances have been made in detection and therapy of this cancer, no vaccine or other universally successful method for prevention or treatment is currently available. Management of the disease currently relies on a combination of early diagnosis and aggressive treatment, which may include one or more of a variety of treatments such as surgery, radiotherapy, chemotherapy and hormone therapy. The course of treatment for a particular cancer is often selected based on a variety of prognostic parameters, including an analysis of specific tumor markers. However, the use of established markers often leads to a result that is difficult to interpret, and high mortality continues to be observed in many cancer patients.

Immunotherapies have the potential to substantially improve cancer treatment and survival. Such therapies may involve the generation or enhancement of an immune response to an ovarian carcinoma antigen. However, to date, relatively few ovarian carcinoma antigens are known and the generation of an immune response against such antigens has not been shown to be therapeutically beneficial.

Accordingly, there is a need in the art for improved methods for identifying ovarian tumor antigens and for using such antigens in the therapy of ovarian cancer. The present invention fulfills these needs and further provides other related advantages.

SUMMARY OF THE INVENTION

Briefly stated, this invention provides compositions and methods for the therapy of cancer, such as ovarian cancer. In one aspect, the present invention provides polypeptides comprising an immunogenic portion of an ovarian carcinoma protein, or a
5 variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with ovarian carcinoma protein-specific antisera is not substantially diminished. Within certain embodiments, the ovarian carcinoma protein comprises a sequence that is encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NO:456-457, 460-477 and 512-
10 570 and complements of such polynucleotides.

The present invention further provides polynucleotides that encode a polypeptide as described above or a portion thereof, expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

The present invention further provides polypeptide compositions
15 comprising an amino acid sequence selected from the group consisting of sequences recited in SEQ ID Nos:394-455, 458-459, 478-511, and 571-596.

Within other aspects, the present invention provides pharmaceutical compositions and vaccines. Pharmaceutical compositions may comprise a physiologically acceptable carrier or excipient in combination with one or more of: (i) a
20 polypeptide comprising an immunogenic portion of an ovarian carcinoma protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with ovarian carcinoma protein-specific antisera is not substantially diminished, wherein the ovarian carcinoma protein comprises an amino acid sequence encoded by a polynucleotide that comprises a
25 sequence recited in any one of SEQ ID NO: 456-457, 460-477 and 512-570 or (ii) a polynucleotide encoding such a polypeptide; (iii) an antibody that specifically binds to such a polypeptide; (iv) an antigen-presenting cell that expresses such a polypeptide and/or (v) a T cell that specifically reacts with such a polypeptide. Vaccines may
30 comprise a non-specific immune response enhancer in combination with one or more of: (i) a polypeptide comprising an immunogenic portion of an ovarian carcinoma protein, or a variant thereof that differs in one or more substitutions, deletions, additions

and/or insertions such that the ability of the variant to react with ovarian carcinoma protein-specific antisera is not substantially diminished, wherein the ovarian carcinoma protein comprises an amino acid sequence set forth in SEQ ID Nos:394-455, 458-459, 478-511, and 571-596 or an amino acid sequence encoded by a polynucleotide that
5 comprises a sequence recited in any one of SEQ ID NO: 456-457, 460-477 and 512-570 or (ii) a polynucleotide encoding such a polypeptide; (iii) an anti-idiotypic antibody that is specifically bound by an antibody that specifically binds to such a polypeptide; (iv) an antigen-presenting cell that expresses such a polypeptide and/or (v) a T cell that specifically reacts with such a polypeptide.

10 The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins.

Within related aspects, pharmaceutical compositions comprising a fusion protein or polynucleotide encoding a fusion protein in combination with a
15 physiologically acceptable carrier are provided.

Vaccines are further provided, within other aspects, comprising a fusion protein or polynucleotide encoding a fusion protein in combination with a non-specific immune response enhancer.

Within further aspects, the present invention provides methods for
20 inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as recited above.

The present invention further provides, within other aspects, methods for stimulating and/or expanding T cells, comprising contacting T cells with (a) a polypeptide comprising an immunogenic portion of an ovarian carcinoma protein, or a
25 variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with ovarian carcinoma protein-specific antisera is not substantially diminished, wherein the ovarian carcinoma protein comprises an amino acid sequence set forth in SEQ ID Nos:394-455, 458-459, 478-511, and 571-596 or an amino acid sequence encoded by a polynucleotide that comprises a
30 sequence recited in any one of SEQ ID NO: 456-457, 460-477 and 512-570; (b) a polynucleotide encoding such a polypeptide and/or (c) an antigen presenting cell that

expresses such a polypeptide under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Such polypeptide, polynucleotide and/or antigen presenting cell(s) may be present within a pharmaceutical composition or vaccine, for use in stimulating and/or expanding T cells in a mammal.

5 Within other aspects, the present invention provides methods for inhibiting the development of ovarian cancer in a patient, comprising administering to a patient T cells prepared as described above.

 Within further aspects, the present invention provides methods for inhibiting the development of ovarian cancer in a patient, comprising the steps of: (a)
10 incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with one or more of: (i) a polypeptide comprising an immunogenic portion of an ovarian carcinoma protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with ovarian carcinoma protein-specific antisera is not substantially diminished, wherein the ovarian carcinoma protein
15 comprises an amino acid sequence encoded by a polynucleotide that comprises a sequence recited in any one of SEQ ID NO: 456-457, 460-477 and 512-570; (ii) a polynucleotide encoding such a polypeptide; or (iii) an antigen-presenting cell that expresses such a polypeptide; such that T cells proliferate; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the
20 development of ovarian cancer in the patient. The proliferated cells may be cloned prior to administration to the patient.

 The present invention also provides, within other aspects, methods for identifying secreted tumor antigens. Such methods comprise the steps of: (a)
25 implanting tumor cells in an immunodeficient mammal; (b) obtaining serum from the immunodeficient mammal after a time sufficient to permit secretion of tumor antigens into the serum; (c) immunizing an immunocompetent mammal with the serum; (d) obtaining antiserum from the immunocompetent mammal; and (e) screening a tumor expression library with the antiserum, and therefrom identifying a secreted tumor antigen. A preferred method for identifying a secreted ovarian carcinoma antigen
30 comprises the steps of: (a) implanting ovarian carcinoma cells in a SCID mouse; (b) obtaining serum from the SCID mouse after a time sufficient to permit secretion of

ovarian carcinoma antigens into the serum; (c) immunizing an immunocompetent mouse with the serum; (d) obtaining antiserum from the immunocompetent mouse; and (e) screening an ovarian carcinoma expression library with the antiserum, and therefrom identifying a secreted ovarian carcinoma antigen.

5 The present invention also discloses antibody epitopes recognized by the O8E polyclonal anti-sera which epitopes are presented herein as SEQ ID NO: 394-415.

Further disclosed by the present invention are 10-mer and 9-mer peptides predicted to bind HLA-0201 which peptides are disclosed herein as SEQ ID NO:416-435 and SEQ ID NO:436-455, respectively.

10 These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

In another aspect of the present invention, the applicants have
15 unexpectedly identified a series of novel repeating sequence elements in the 5' end of the gene encoding O772P. Therefore, the present invention provides O772P polypeptides having structures represented by X_n -Y, wherein X comprises a sequence having at least 50% identity, preferably at least 70% identity, and more preferably at least 90% identity with an O772P repeat sequence set forth in SEQ ID NO: 596. Y will
20 typically comprise a sequence having at least 80% identity, preferably at least 90% identity and more preferably at least 95% identity with the O772P constant region sequence set forth in SEQ ID NO: 594. According to this embodiment, n will generally be an integer from 1 to 35, preferably an integer from 15 to 25, and X can be the same or different.

25 In one preferred embodiment, X comprises a sequence selected from the group consisting of any one of SEQ ID NOs: 574-593 and Y comprises the sequence set forth in SEQ ID NO: 594.

In another preferred embodiment, an illustrative O772P polypeptide comprises the sequence set forth in SEQ ID NO: 595, containing 20 repeating sequence
30 elements (i.e., X_{20}) wherein the X elements are arranged in the following order (moving from N-terminal to C-terminal in the O772P repeat region): SEQ ID NO: 574 - SEQ ID

NO: 575 - SEQ ID NO: 576 - SEQ ID NO: 577 - SEQ ID NO: 578 - SEQ ID NO: 579 -
SEQ ID NO: 580 - SEQ ID NO: 581 - SEQ ID NO: 582 - SEQ ID NO: 583 - SEQ ID
NO: 584 - SEQ ID NO: 585 - SEQ ID NO: 586 - SEQ ID NO: 587 - SEQ ID NO: 588 -
SEQ ID NO: 589 - SEQ ID NO: 590 - SEQ ID NO: 591 - SEQ ID NO: 592 - SEQ ID
5 NO: 593.

According to another aspect of the present invention, an O772P
polynucleotide is provided having the structure X_n -Y, wherein X comprises an O772P
repeat sequence element selected from the group consisting of any one of SEQ ID NOs:
512-540, 542-546 and 548-567. Y will generally comprise a sequence having at least
10 80% identity, preferably at least 90% identity, and more preferably at least 95% identity
with the O772P constant region sequence set forth in SEQ ID NO: 568. In this
embodiment, n is typically an integer from 1 to 35, preferably from 15 to 25 and X can
be the same or different.

In another embodiment, an illustrative O772P polynucleotide comprises
15 the sequence set forth in SEQ ID NO: 569, containing 20 repeating sequence elements
(i.e., X_{20}).

According to another aspect of the present invention, O772 polypeptides
are provided comprising at least an antibody epitope sequence set forth in any one of
SEQ ID NOs: 490-511.

20 According to another aspect of the present invention, O8E polypeptides
are provided comprising at least an antibody epitope sequence set forth in any one of
SEQ ID NOs: 394-415.

BRIEF DESCRIPTION OF THE SEQUENCE IDENTIFIERS AND DRAWINGS

SEQ ID NO:1-71 are ovarian carcinoma antigen polynucleotides shown
25 in Figures 1A-1S.

SEQ ID NO:72-74 are ovarian carcinoma antigen polynucleotides shown
in Figures 2A-2C.

SEQ ID NO:75 is the ovarian carcinoma polynucleotide 3g (Figure 4).

SEQ ID NO:76 is the ovarian carcinoma polynucleotide 3f (Figure 5).

30 SEQ ID NO:77 is the ovarian carcinoma polynucleotide 6b (Figure 6).

SEQ ID NO:78 is the ovarian carcinoma polynucleotide 8e (Figure 7A).

SEQ ID NO:79 is the ovarian carcinoma polynucleotide 8h (Figure 7B).

SEQ ID NO:80 is the ovarian carcinoma polynucleotide 12e (Figure 8).

SEQ ID NO:81 is the ovarian carcinoma polynucleotide 12h (Figure 9).

5 SEQ ID NO:82-310 are ovarian carcinoma antigen polynucleotides shown in Figures 15A-15EEE.

SEQ ID NO:311 is a full length sequence of ovarian carcinoma polynucleotide O772P.

SEQ ID NO:312 is the O772P amino acid sequence.

10 SEQ ID NO:313-384 are ovarian carcinoma antigen polynucleotides.

SEQ ID NO:385 represents the cDNA sequence of a form of the clone O772P, designated 21013.

SEQ ID NO:386 represents the cDNA sequence of a form of the clone O772P, designated 21003.

15 SEQ ID NO:387 represents the cDNA sequence of a form of the clone O772P, designated 21008.

SEQ ID NOs:388 is the amino acid sequence corresponding to SEQ ID NO:385.

20 SEQ ID NOs:389 is the amino acid sequence corresponding to SEQ ID NO:386. SEQ ID NOs:390 is the amino acid sequence corresponding to SEQ ID NO:387.

SEQ ID NO:391 is a full length sequence of ovarian carcinoma polynucleotide O8E.

SEQ ID NO:392-393 are protein sequences encoded by O8E.

25 SEQ ID NO:394-415 are peptide sequences corresponding to the OE8 antibody epitopes.

SEQ ID NO:416-435 are potential HLA-A2 10-mer binding peptides predicted using the full length open-reading frame from OE8.

30 SEQ ID NO:436-455 are potential HLA-A2 9-mer binding peptides predicted using the full length open-reading frame from OE8.

SEQ ID NO:456 is a truncated nucleotide sequence of the full length Genbank sequence showing homology to O772P

SEQ ID NO:457 is the full length Genbank sequence showing significant homology to O772P

5 SEQ ID NO:458 is a protein encoding a truncated version of the full length Genbank sequence showing homology to O772P

SEQ ID NO:459 is the full length protein sequence from Genbank showing significant homology to the protein sequence for O772P

10 SEQ ID NO:460 encodes a unique N-terminal portion of O772P contained in residues 1-70.

SEQ ID NO:461 contains unique sequence and encodes residues 1-313 of SEQ ID NO: 456.

SEQ ID NO:462 is the hypothetical sequence for clone O772P.

SEQ ID NO:463 is the cDNA sequence for clone FLJ14303.

15 SEQ ID NO:464 is a partial cDNA sequence for clone O772P.

SEQ ID NO:465 is a partial cDNA sequence for clone O772P.

SEQ ID NO:466 is a partial cDNA sequence for clone O772P.

SEQ ID NO:467 is a partial cDNA sequence for clone O772P.

SEQ ID NO:468 is a partial cDNA sequence for clone O772P.

20 SEQ ID NO:469 is a partial cDNA sequence for clone O772P.

SEQ ID NO:470 is a partial cDNA sequence for clone O772P.

SEQ ID NO:471 is a partial cDNA sequence for clone O772P.

SEQ ID NO:472 is a partial cDNA sequence for clone O772P.

SEQ ID NO:473 is a partial cDNA sequence for clone O772P.

25 SEQ ID NO:474 is a partial cDNA sequence for clone O772P.

SEQ ID NO:475 is a partial cDNA sequence for clone O772P.

SEQ ID NO:476 is a partial cDNA sequence for clone O772P.

SEQ ID NO:477 represents the novel 5'-end of the ovarian tumor antigen

O772P.

30 SEQ ID NO:478 is the amino acid sequence encoded by SEQ ID NO:462.

SEQ ID NO:479 is the amino acid sequence encoded by SEQ ID NO:463.

SEQ ID NO:480 is a partial amino acid sequence encoded by SEQ ID NO:472.

5 SEQ ID NO:481 is a partial amino acid sequence encoded by a possible open reading frame of SEQ ID NO:471.

SEQ ID NO:482 is a partial amino acid sequence encoded by a second possible open reading frame of SEQ ID NO:471.

10 SEQ ID NO:483 is a partial amino acid sequence encoded by SEQ ID NO:467.

SEQ ID NO:484 is a partial amino acid sequence encoded by a possible open reading frame of SEQ ID NO:466.

SEQ ID NO:485 is a partial amino acid sequence encoded by a second possible open reading frame of SEQ ID NO:466.

15 SEQ ID NO:486 is a partial amino acid sequence encoded by SEQ ID NO:465.

SEQ ID NO:487 is a partial amino acid sequence encoded by SEQ ID NO:464.

20 SEQ ID NO:488 represents the extracellular, transmembrane and cytoplasmic regions of O772P.

SEQ ID NO:489 represents the predicted extracellular domain of O772P.

SEQ ID NO:490 represents the amino acid sequence of peptide #2 which corresponds to an O772P specific antibody epitope.

25 SEQ ID NO:491 represents the amino acid sequence of peptide #6 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:492 represents the amino acid sequence of peptide #7 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:493 represents the amino acid sequence of peptide #8 which corresponds to an O772P specific antibody epitope.

30 SEQ ID NO:494 represents the amino acid sequence of peptide #9 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:495 represents the amino acid sequence of peptide #11, which corresponds to an O772P specific antibody epitope.

SEQ ID NO:496 represents the amino acid sequence of peptide #13 which corresponds to an O772P specific antibody epitope.

5 SEQ ID NO:497 represents the amino acid sequence of peptide #22 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:498 represents the amino acid sequence of peptide #24 which corresponds to an O772P specific antibody epitope.

10 SEQ ID NO:499 represents the amino acid sequence of peptide #27 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:500 represents the amino acid sequence of peptide #40 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:501 represents the amino acid sequence of peptide #41 which corresponds to an O772P specific antibody epitope.

15 SEQ ID NO:502 represents the amino acid sequence of peptide #47 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:503 represents the amino acid sequence of peptide #50 which corresponds to an O772P specific antibody epitope.

20 SEQ ID NO:504 represents the amino acid sequence of peptide #51 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:505 represents the amino acid sequence of peptide #52 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:506 represents the amino acid sequence of peptide #53 which corresponds to an O772P specific antibody epitope.

25 SEQ ID NO:507 represents the amino acid sequence of peptide #58 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:508 represents the amino acid sequence of peptide #59 which corresponds to an O772P specific antibody epitope.

30 SEQ ID NO:509 represents the amino acid sequence of peptide #60 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:510 represents the amino acid sequence of peptide #61 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:511 represents the amino acid sequence of peptide #71 which corresponds to an O772P specific antibody epitope.

5 SEQ ID NO:512 (O772P repeat1) represents an example of a cDNA sequence corresponding to repeat number 21 from the 5' variable region of O772P.

SEQ ID NO:513 (O772P repeat2) represents an example of a cDNA sequence corresponding to repeat number 20 from the 5' variable region of O772P.

10 SEQ ID NO:514 (O772P repeat3) represents an example of a cDNA sequence corresponding to repeat number 19 from the 5' variable region of O772P.

SEQ ID NO:515 (O772P repeat4) represents an example of a cDNA sequence corresponding to repeat number 18 from the 5' variable region of O772P.

SEQ ID NO:516 (O772P repeat5) represents an example of a cDNA sequence corresponding to repeat number 17 from the 5' variable region of O772P.

15 SEQ ID NO:517 (HB repeat1) represents an example of a cDNA sequence corresponding to repeat number 21 from the 5' variable region of O772P.

SEQ ID NO:518 (HB repeat2) represents an example of a cDNA sequence corresponding to repeat number 20 from the 5' variable region of O772P.

20 SEQ ID NO:519 (HB repeat3) represents an example of a cDNA sequence corresponding to repeat number 19 from the 5' variable region of O772P.

SEQ ID NO:520 (HB repeat4) represents an example of a cDNA sequence corresponding to repeat number 18 from the 5' variable region of O772P.

SEQ ID NO:521 (HB repeat5) represents an example of a cDNA sequence corresponding to repeat number 17 from the 5' variable region of O772P.

25 SEQ ID NO:522 (HB repeat6 5'-end) represents an example of a cDNA sequence corresponding to repeat number 16 from the 5' variable region of O772P.

SEQ ID NO:523 (1043400.1 repeat1) represents an example of a cDNA sequence corresponding to repeat number 9 from the 5' variable region of O772P.

30 SEQ ID NO:524 (1043400.1 repeat2) represents an example of a cDNA sequence corresponding to repeat number 10 from the 5' variable region of O772P.

SEQ ID NO:525 (1043400.1 repeat3) represents an example of a cDNA sequence corresponding to repeat number 10/11 from the 5' variable region of O772P.

SEQ ID NO:526 (1043400.1 repeat4) represents an example of a cDNA sequence corresponding to repeat number 11 from the 5' variable region of O772P.

5 SEQ ID NO:527 (1043400.1 repeat5) represents an example of a cDNA sequence corresponding to repeat number 14 from the 5' variable region of O772P.

SEQ ID NO:528 (1043400.1 repeat6) represents an example of a cDNA sequence corresponding to repeat number 17 from the 5' variable region of O772P.

10 SEQ ID NO:529 (1043400.3 repeat1) represents an example of a cDNA sequence corresponding to repeat number 20 from the 5' variable region of O772P.

SEQ ID NO:530 (1043400.3 repeat2) represents an example of a cDNA sequence corresponding to repeat number 21 from the 5' variable region of O772P.

SEQ ID NO:531 (1043400.5 repeat1) represents an example of a cDNA sequence corresponding to repeat number 8 from the 5' variable region of O772P.

15 SEQ ID NO:532 (1043400.5 repeat2) represents an example of a cDNA sequence corresponding to repeat number 9 from the 5' variable region of O772P, in addition containing intron sequence.

SEQ ID NO:533 (1043400.5 repeat2) represents an example of a cDNA sequence corresponding to repeat number 9 from the 5' variable region of O772P.

20 SEQ ID NO:534 (1043400.8 repeat1) represents an example of a cDNA sequence corresponding to repeat number 17 from the 5' variable region of O772P.

SEQ ID NO:535 (1043400.8 repeat2) represents an example of a cDNA sequence corresponding to repeat number 18 from the 5' variable region of O772P.

25 SEQ ID NO:536 (1043400.8 repeat3) represents an example of a cDNA sequence corresponding to repeat number 19 from the 5' variable region of O772P.

SEQ ID NO:537 (1043400.9 repeat1) represents an example of a cDNA sequence corresponding to repeat number 4 from the 5' variable region of O772P.

SEQ ID NO:538 (1043400.9 repeat2) represents an example of a cDNA sequence corresponding to repeat number 5 from the 5' variable region of O772P.

30 SEQ ID NO:539 (1043400.9 repeat3) represents an example of a cDNA sequence corresponding to repeat number 7 from the 5' variable region of O772P.

SEQ ID NO:540 (1043400.9 repeat4) represents an example of a cDNA sequence corresponding to repeat number 8 from the 5' variable region of O772P.

SEQ ID NO:541 (1043400.11 repeat1) represents an example of a cDNA sequence corresponding to repeat number 1 from the 5' variable region of O772P.

5 SEQ ID NO:542 (1043400.11 repeat2) represents an example of a cDNA sequence corresponding to repeat number 2 from the 5' variable region of O772P.

SEQ ID NO:543 (1043400.11 repeat3) represents an example of a cDNA sequence corresponding to repeat number 3 from the 5' variable region of O772P.

10 SEQ ID NO:544 (1043400.11 repeat4) represents an example of a cDNA sequence corresponding to repeat number 11 from the 5' variable region of O772P.

SEQ ID NO:545 (1043400.11 repeat5) represents an example of a cDNA sequence corresponding to repeat number 12 from the 5' variable region of O772P.

SEQ ID NO:546 (1043400.12 repeat1) represents an example of a cDNA sequence corresponding to repeat number 20 from the 5' variable region of O772P.

15 SEQ ID NO:547 (PB repeatA) represents an example of a cDNA sequence corresponding to repeat number 1 from the 5' variable region of O772P.

SEQ ID NO:548 (PB repeatB) represents an example of a cDNA sequence corresponding to repeat number 2 from the 5' variable region of O772P.

20 SEQ ID NO:549 (PB repeatE) represents an example of a cDNA sequence corresponding to repeat number 3 from the 5' variable region of O772P.

SEQ ID NO:550 (PB repeatG) represents an example of a cDNA sequence corresponding to repeat number 4 from the 5' variable region of O772P.

SEQ ID NO:551 (PB repeatC) represents an example of a cDNA sequence corresponding to repeat number 4 from the 5' variable region of O772P.

25 SEQ ID NO:552 (PB repeatH) represents an example of a cDNA sequence corresponding to repeat number 6 from the 5' variable region of O772P.

SEQ ID NO:553 (PB repeatJ) represents an example of a cDNA sequence corresponding to repeat number 7 from the 5' variable region of O772P.

30 SEQ ID NO:554 (PB repeatK) represents an example of a cDNA sequence corresponding to repeat number 8 from the 5' variable region of O772P.

SEQ ID NO:555 (PB repeatD) represents an example of a cDNA sequence corresponding to repeat number 9 from the 5' variable region of O772P.

SEQ ID NO:556 (PB repeatI) represents an example of a cDNA sequence corresponding to repeat number 10 from the 5' variable region of O772P.

5 SEQ ID NO:557 (PB repeatM) represents an example of a cDNA sequence corresponding to repeat number 11 from the 5' variable region of O772P.

SEQ ID NO:558 (PB repeat9) represents an example of a cDNA sequence corresponding to repeat number 12 from the 5' variable region of O772P.

10 SEQ ID NO:559 (PB repeat8.5) represents an example of a cDNA sequence corresponding to repeat number 13 from the 5' variable region of O772P.

SEQ ID NO:560 (PB repeat8) represents an example of a cDNA sequence corresponding to repeat number 14 from the 5' variable region of O772P.

SEQ ID NO:561 (PB repeat7) represents an example of a cDNA sequence corresponding to repeat number 15 from the 5' variable region of O772P.

15 SEQ ID NO:562 (PB repeat6) represents an example of a cDNA sequence corresponding to repeat number 16 from the 5' variable region of O772P.

SEQ ID NO:563 (PB repeat5) represents an example of a cDNA sequence corresponding to repeat number 17 from the 5' variable region of O772P.

20 SEQ ID NO:564 (PB repeat4) represents an example of a cDNA sequence corresponding to repeat number 18 from the 5' variable region of O772P.

SEQ ID NO:565 (PB repeat3) represents an example of a cDNA sequence corresponding to repeat number 19 from the 5' variable region of O772P.

SEQ ID NO:566 (PB repeat2) represents an example of a cDNA sequence corresponding to repeat number 20 from the 5' variable region of O772P.

25 SEQ ID NO:567 (PB repeat1) represents an example of a cDNA sequence corresponding to repeat number 21 from the 5' variable region of O772P.

SEQ ID NO:568 represents the cDNA sequence from the 3' constant region.

30 SEQ ID NO:569 represents a cDNA sequence containing the consensus sequences of the 21 repeats, the 3' constant region and the 3' untranslated region.

SEQ ID NO:570 represents the cDNA sequence of the consensus repeat sequence.

SEQ ID NO:571 represents the consensus amino acid sequence of one potential open reading frame of repeat number 1 from the 5' variable region of O772P.

5 SEQ ID NO:572 represents the consensus amino acid sequence of a second potential open reading frame of repeat number 1 from the 5' variable region of O772P.

SEQ ID NO:573 represents the consensus amino acid sequence of a third potential open reading frame of repeat number 1 from the 5' variable region of O772P.

10 SEQ ID NO:574 represents the consensus amino acid sequence of repeat number 2 from the 5' variable region of O772P.

SEQ ID NO:575 represents the consensus amino acid sequence of repeat number 3 from the 5' variable region of O772P.

15 SEQ ID NO:576 represents the consensus amino acid sequence of repeat number 4 from the 5' variable region of O772P.

SEQ ID NO:577 represents the consensus amino acid sequence of repeat number 5 from the 5' variable region of O772P.

SEQ ID NO:578 represents the consensus amino acid sequence of repeat number 6 from the 5' variable region of O772P.

20 SEQ ID NO:579 represents the consensus amino acid sequence of repeat number 7 from the 5' variable region of O772P.

SEQ ID NO:580 represents the consensus amino acid sequence of repeat number 8 from the 5' variable region of O772P.

25 SEQ ID NO:581 represents the consensus amino acid sequence of repeat number 9 from the 5' variable region of O772P.

SEQ ID NO:582 represents the consensus amino acid sequence of repeat number 10 from the 5' variable region of O772P.

SEQ ID NO:583 represents the consensus amino acid sequence of repeat number 11 from the 5' variable region of O772P.

30 SEQ ID NO:584 represents the consensus amino acid sequence of repeat number 12 from the 5' variable region of O772P.

SEQ ID NO:585 represents the consensus amino acid sequence of repeat number 13 from the 5' variable region of O772P.

SEQ ID NO:586 represents the consensus amino acid sequence of repeat number 14 from the 5' variable region of O772P.

5 SEQ ID NO:587 represents the consensus amino acid sequence of repeat number 15 from the 5' variable region of O772P.

SEQ ID NO:588 represents the consensus amino acid sequence of repeat number 16 from the 5' variable region of O772P.

10 SEQ ID NO:589 represents the consensus amino acid sequence of repeat number 17 from the 5' variable region of O772P.

SEQ ID NO:590 represents the consensus amino acid sequence of repeat number 18 from the 5' variable region of O772P.

SEQ ID NO:591 represents the consensus amino acid sequence of repeat number 19 from the 5' variable region of O772P.

15 SEQ ID NO:592 represents the consensus amino acid sequence of repeat number 20 from the 5' variable region of O772P.

SEQ ID NO:593 represents the consensus amino acid sequence of repeat number 21 from the 5' variable region of O772P.

20 SEQ ID NO:594 represents the amino acid sequence of the 3' constant region.

SEQ ID NO:595 represents an amino acid sequence containing the consensus sequences of the 21 repeats and the 3' constant region.

SEQ ID NO:596 represents the amino acid sequence of the consensus repeat sequence.

25 Figures 1A-1S (SEQ ID NO:1-71) depict partial sequences of polynucleotides encoding representative secreted ovarian carcinoma antigens.

Figures 2A-2C depict full insert sequences for three of the clones of Figure 1. Figure 2A shows the sequence designated O7E (11731; SEQ ID NO:72), Figure 2B shows the sequence designated O9E (11785; SEQ ID NO:73) and Figure 2C
30 shows the sequence designated O8E (13695; SEQ ID NO:74).

Figure 3 presents results of microarray expression analysis of the ovarian carcinoma sequence designated O8E.

Figure 4 presents a partial sequence of a polynucleotide (designated 3g; SEQ ID NO:75) encoding an ovarian carcinoma sequence that is a splice fusion
5 between the human T-cell leukemia virus type I oncoprotein TAX and osteonectin.

Figure 5 presents the ovarian carcinoma polynucleotide designated 3f (SEQ ID NO:76).

Figure 6 presents the ovarian carcinoma polynucleotide designated 6b (SEQ ID NO:77).

10 Figures 7A and 7B present the ovarian carcinoma polynucleotides designated 8e (SEQ ID NO:78) and 8h (SEQ ID NO:79).

Figure 8 presents the ovarian carcinoma polynucleotide designated 12c (SEQ ID NO:80).

15 Figure 9 presents the ovarian carcinoma polynucleotide designated 12h (SEQ ID NO:81).

Figure 10 depicts results of microarray expression analysis of the ovarian carcinoma sequence designated 3f.

Figure 11 depicts results of microarray expression analysis of the ovarian carcinoma sequence designated 6b.

20 Figure 12 depicts results of microarray expression analysis of the ovarian carcinoma sequence designated 8e.

Figure 13 depicts results of microarray expression analysis of the ovarian carcinoma sequence designated 12c.

25 Figure 14 depicts results of microarray expression analysis of the ovarian carcinoma sequence designated 12h.

Figures 15A-15EEE depict partial sequences of additional polynucleotides encoding representative secreted ovarian carcinoma antigens (SEQ ID NO:82-310).

30 Figure 16 is a diagram illustrating the location of various partial O8E sequences within the full length sequence.

Figure 17 is a graph illustrating the results of epitope mapping studies on O8E protein.

Figure 18 is graph of a fluorescence activated cell sorting (FACS) analysis of O8E cell surface expression.

5 Figure 19 is graph of a FACS analysis of O8E cell surface expression.

Figure 20 shows FACS analysis results for O8E transfected HEK293 cells demonstrating cell surface expression of O8E.

Figure 21 shows FACS analysis results for SKBR3 breast tumor cells demonstrating cell surface expression of O8E.

10 Figure 22 shows O8E expression in HEK 293 cells. The cells were probed with anti-O8E rabbit polyclonal antisera #2333L.

Figure 23 shows the ELISA analysis of anti-O8E rabbit sera.

Figure 24 shows the ELISA analysis of affinity purified rabbit anti-O8E polyclonal antibody.

15 Figure 25 is a graph determining antibody internalization of anti-O8E mAb showing that mAbs against amino acids 61-80 induces ligand internalization.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the therapy of cancer, such as ovarian cancer. The
20 compositions described herein may include immunogenic polypeptides, polynucleotides encoding such polypeptides, binding agents such as antibodies that bind to a polypeptide, antigen presenting cells (APCs) and/or immune system cells (*e.g.*, T cells).

Polypeptides of the present invention generally comprise at least an immunogenic portion of an ovarian carcinoma protein or a variant thereof. Certain
25 ovarian carcinoma proteins have been identified using an immunoassay technique, and are referred to herein as ovarian carcinoma antigens. An "ovarian carcinoma antigen" is a protein that is expressed by ovarian tumor cells (preferably human cells) at a level that is at least two fold higher than the level in normal ovarian cells. Certain ovarian carcinoma antigens react detectably (within an immunoassay, such as an ELISA or
30 Western blot) with antisera generated against serum from an immunodeficient animal

implanted with a human ovarian tumor. Such ovarian carcinoma antigens are shed or secreted from an ovarian tumor into the sera of the immunodeficient animal. Accordingly, certain ovarian carcinoma antigens provided herein are secreted antigens. Certain nucleic acid sequences of the subject invention generally comprise a DNA or
5 RNA sequence that encodes all or a portion of such a polypeptide, or that is complementary to such a sequence.

The present invention further provides ovarian carcinoma sequences that are identified using techniques to evaluate altered expression within an ovarian tumor. Such sequences may be polynucleotide or protein sequences. Ovarian carcinoma
10 sequences are generally expressed in an ovarian tumor at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in normal ovarian tissue, as determined using a representative assay provided herein. Certain partial ovarian carcinoma polynucleotide sequences are presented herein. Proteins encoded by genes comprising such polynucleotide sequences (or complements thereof) are also
15 considered ovarian carcinoma proteins.

Antibodies are generally immune system proteins, or antigen-binding fragments thereof, that are capable of binding to at least a portion of an ovarian carcinoma polypeptide as described herein. T cells that may be employed within the compositions provided herein are generally T cells (*e.g.*, CD4⁺ and/or CD8⁺) that are
20 specific for such a polypeptide. Certain methods described herein further employ antigen-presenting cells (such as dendritic cells or macrophages) that express an ovarian carcinoma polypeptide as provided herein.

Ovarian Carcinoma Polynucleotides

Any polynucleotide that encodes an ovarian carcinoma protein or a
25 portion or other variant thereof as described herein is encompassed by the present invention. Preferred polynucleotides comprise at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides, and more preferably at least 45 consecutive nucleotides, that encode a portion of an ovarian carcinoma protein. More preferably, a polynucleotide encodes an immunogenic portion of an ovarian carcinoma
30 protein, such as an ovarian carcinoma antigen. Polynucleotides complementary to any

such sequences are also encompassed by the present invention. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a
5 polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes an ovarian carcinoma protein or a portion thereof) or may comprise a variant of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the immunogenicity
10 of the encoded polypeptide is not diminished, relative to a native ovarian carcinoma protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native ovarian carcinoma protein or
15 a portion thereof.

The percent identity for two polynucleotide or polypeptide sequences may be readily determined by comparing sequences using computer algorithms well known to those of ordinary skill in the art, such as Megalign, using default parameters. Comparisons between two sequences are typically performed by comparing the
20 sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, or 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Optimal alignment of sequences for
25 comparison may be conducted, for example, using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. Preferably, the percentage of sequence identity is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the
30 window may comprise additions or deletions (*i.e.*, gaps) of 20 % or less, usually 5 to 15 %, or 10 to 12%, relative to the reference sequence (which does not contain additions or

deletions). The percent identity may be calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

5 Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native ovarian carcinoma protein (or a complementary
10 sequence). Suitable moderately stringent conditions include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

It will be appreciated by those of ordinary skill in the art that, as a result
15 of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences
20 provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

25 Polynucleotides may be prepared using any of a variety of techniques. For example, an ovarian carcinoma polynucleotide may be identified, as described in more detail below, by screening a late passage ovarian tumor expression library with antisera generated against sera of immunocompetent mice after injection of such mice with sera from SCID mice implanted with late passage ovarian tumors. Ovarian
30 carcinoma polynucleotides may also be identified using any of a variety of techniques designed to evaluate differential gene expression. Alternatively, polynucleotides may

be amplified from cDNA prepared from ovarian tumor cells. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

- 5 An amplified portion may be used to isolate a full length gene from a suitable library (e.g., an ovarian carcinoma cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for
10 identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

- For hybridization techniques, a partial sequence may be labeled (e.g., by nick-translation or end-labeling with ^{32}P) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured
15 bacterial colonies (or lawns containing phage plaques) with the labeled probe (see Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using
20 a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into a single contiguous sequence. A full length cDNA molecule can be
25 generated by ligating suitable fragments, using well known techniques.

- Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed
30 using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target

sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (see Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (e.g., NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence.

Certain nucleic acid sequences of cDNA molecules encoding portions of ovarian carcinoma antigens are provided in Figures 1A-1S (SEQ ID NO:1 to 71) and Figures 15A to 15EEE (SEQ ID NO:82 to 310). The sequences provided in Figures 1A-1S appear to be novel. For sequences in Figures 15A-15EEE, database searches revealed matches having substantial identity. These polynucleotides were isolated by serological screening of an ovarian tumor cDNA expression library, using a technique designed to identify secreted tumor antigens. Briefly, a late passage ovarian tumor expression library was prepared from a SCID-derived human ovarian tumor (OV9334) in the vector λ -screen (Novagen). The sera used for screening were obtained by

injecting immunocompetent mice with sera from SCID mice implanted with one late passage ovarian tumors. This technique permits the identification of cDNA molecules that encode immunogenic portions of secreted tumor antigens.

5 The polynucleotides recited herein, as well as full length polynucleotides comprising such sequences, other portions of such full length polynucleotides, and sequences complementary to all or a portion of such full length molecules, are specifically encompassed by the present invention. It will be apparent to those of ordinary skill in the art that this technique can also be applied to the identification of antigens that are secreted from other types of tumors.

10 Other nucleic acid sequences of cDNA molecules encoding portions of ovarian carcinoma proteins are provided in Figures 4-9 (SEQ ID NO:75-81), as well as SEQ ID NO:313-384. These sequences were identified by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least five fold greater in an ovarian tumor than in normal ovarian tissue, as determined using a representative
15 assay provided herein). Such screens were performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). SEQ ID NO:311 and 391 provide full length sequences incorporating certain of these nucleic acid sequences.

20 Any of a variety of well known techniques may be used to evaluate tumor-associated expression of a cDNA. For example, hybridization techniques using labeled polynucleotide probes may be employed. Alternatively, or in addition, amplification techniques such as real-time PCR may be used (*see* Gibson et al., *Genome Research* 6:995-1001, 1996; Heid et al., *Genome Research* 6:986-994, 1996). Real-
25 time PCR is a technique that evaluates the level of PCR product accumulation during amplification. This technique permits quantitative evaluation of mRNA levels in multiple samples. Briefly, mRNA is extracted from tumor and normal tissue and cDNA is prepared using standard techniques. Real-time PCR may be performed, for example, using a Perkin Elmer/Applied Biosystems (Foster City, CA) 7700 Prism instrument.
30 Matching primers and fluorescent probes may be designed for genes of interest using, for example, the primer express program provided by Perkin Elmer/Applied Biosystems

(Foster City, CA). Optimal concentrations of primers and probes may be initially determined by those of ordinary skill in the art, and control (e.g., β -actin) primers and probes may be obtained commercially from, for example, Perkin Elmer/Applied Biosystems (Foster City, CA). To quantitate the amount of specific RNA in a sample, a standard curve is generated alongside using a plasmid containing the gene of interest. Standard curves may be generated using the Ct values determined in the real-time PCR, which are related to the initial cDNA concentration used in the assay. Standard dilutions ranging from 10^{-10} to 10^{-6} copies of the gene of interest are generally sufficient. In addition, a standard curve is generated for the control sequence. This permits standardization of initial RNA content of a tissue sample to the amount of control for comparison purposes.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (see Adelman et al., *DNA* 2:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding an ovarian carcinoma antigen, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded polypeptide is generated *in vivo*.

A portion of a sequence complementary to a coding sequence (i.e., an antisense polynucleotide) may also be used as a probe or to modulate gene expression. cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells or tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of an ovarian carcinoma protein. Antisense technology can be used to control gene expression through triple-helix formation, which compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (see Gee et al., *In Huber and Carr, Molecular and Immunologic Approaches*,

Futura Publishing Co. (Mt. Kisco, NY; 1994). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (e.g., promoter, enhancer or transcription initiation site), and block transcription of the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

- 5 Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl- methyl-, thio- and
10 other modified forms of adenine, cytidine, guanine, thymine and uridine.

- Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of
15 particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

- 20 Within certain embodiments, polynucleotides may be formulated so as to permit entry into a cell of a mammal, and expression therein. Such formulations are particularly useful for therapeutic purposes, as described below. Those of ordinary skill in the art will appreciate that there are many ways to achieve expression of a polynucleotide in a target cell, and any suitable method may be employed. For
25 example, a polynucleotide may be incorporated into a viral vector such as, but not limited to, adenovirus, adeno-associated virus, retrovirus, or vaccinia or other pox virus (e.g., avian pox virus). Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of
30 transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also

be accomplished using an antibody, by methods known to those of ordinary skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (*i.e.*, an artificial membrane vesicle). The preparation and use of such systems is well known in the art.

Ovarian Carcinoma Polypeptides

10 Within the context of the present invention, polypeptides may comprise at least an immunogenic portion of an ovarian carcinoma protein or a variant thereof, as described herein. As noted above, certain ovarian carcinoma proteins are ovarian carcinoma antigens that are expressed by ovarian tumor cells and react detectably within an immunoassay (such as an ELISA) with antisera generated against serum from an immunodeficient animal implanted with an ovarian tumor. Other ovarian carcinoma proteins are encoded by ovarian carcinoma polynucleotides recited herein. Polypeptides as described herein may be of any length. Additional sequences derived from the native protein and/or heterologous sequences may be present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

20 An "immunogenic portion," as used herein is a portion of an antigen that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic portions generally comprise at least 5 amino acid residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of an ovarian carcinoma protein or a variant thereof. Preferred immunogenic portions are encoded by cDNA molecules isolated as described herein. Further immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with ovarian carcinoma protein-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "ovarian carcinoma protein-

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specific" if they specifically bind to an ovarian carcinoma protein (i.e., they react with the ovarian carcinoma protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera, antibodies and T cells may be prepared as described herein, and using well known techniques. An immunogenic portion of a native ovarian carcinoma protein is a portion that reacts with such antisera, antibodies and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (e.g., in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length protein. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ^{125}I -labeled Protein A.

As noted above, a composition may comprise a variant of a native ovarian carcinoma protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native ovarian carcinoma protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide is not substantially diminished. In other words, the ability of a variant to react with ovarian carcinoma protein-specific antisera may be enhanced or unchanged, relative to the native ovarian carcinoma protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native ovarian carcinoma protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with ovarian carcinoma protein-specific antibodies or antisera as described herein. Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (e.g., 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the native polypeptide. Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydropathic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells

include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available
5 filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic
10 means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is
15 commercially available from suppliers such as Applied BioSystems, Inc. (Foster City, CA), and may be operated according to the manufacturer's instructions.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises one polypeptide as described herein and a known tumor antigen, such as an ovarian
20 carcinoma protein or a variant of such a protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion
25 partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

Fusion proteins may generally be prepared using standard techniques,
30 including chemical conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a non-fused

protein, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see, for example, Stoute et al. New Engl. J. Med., 336:86-91, 1997*).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen present cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene 43:265-292, 1986*). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone: The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology 10:795-798, 1992*). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In general, polypeptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its original environment. For example, a naturally-occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector that is not a part of the natural environment.

Binding Agents

10 The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to an ovarian carcinoma protein. As used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to an ovarian carcinoma protein if it reacts at a detectable level (within, for example, an ELISA) with an ovarian carcinoma protein, and does not react
15 detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a "complex" is formed. The ability to bind may be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of
20 the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients
25 with and without a cancer, such as ovarian cancer, using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a ovarian carcinoma antigen will generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the
30 cancer. To determine whether a binding agent satisfies this requirement, biological

samples (e.g., blood, sera, leukophoresis, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the

desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized
5 animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks,
10 colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the
15 yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process
20 in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane,
25 *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides,
30 differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include

methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

5 A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-
10 containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

 Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker
15 group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

 It will be evident to those skilled in the art that a variety of bifunctional
20 or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

25 Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction
30 of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of

derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn *et al.*), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell *et al.*), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler *et al.*).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato *et al.*), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih *et al.*). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison *et al.* discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Also provided herein are anti-idiotypic antibodies that mimic an immunogenic portion of an ovarian carcinoma protein. Such antibodies may be raised against an antibody, or antigen-binding fragment thereof, that specifically binds to an

immunogenic portion of an ovarian carcinoma protein, using well known techniques. Anti-idiotypic antibodies that mimic an immunogenic portion of an ovarian carcinoma protein are those antibodies that bind to an antibody, or antigen-binding fragment thereof, that specifically binds to an immunogenic portion of an ovarian carcinoma
5 protein, as described herein.

T Cells

Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for an ovarian carcinoma protein. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be present within
10 (or isolated from) bone marrow, peripheral blood or a fraction of bone marrow or peripheral blood of a mammal, such as a patient, using a commercially available cell separation system, such as the CEPRATE™ system, available from CellPro Inc., Bothell WA (see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived
15 from related or unrelated humans, non-human animals, cell lines or cultures.

T cells may be stimulated with an ovarian carcinoma polypeptide, polynucleotide encoding an ovarian carcinoma polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific
20 for the polypeptide. Preferably, an ovarian carcinoma polypeptide or polynucleotide is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for an ovarian carcinoma polypeptide if the T cells kill target cells coated with an ovarian carcinoma polypeptide or expressing a gene encoding such a polypeptide. T cell specificity may be evaluated
25 using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.*
30 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be

accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (e.g., by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with an ovarian carcinoma polypeptide (200 ng/ml - 100 µg/ml, preferably 100 ng/ml - 25 µg/ml) for 3 - 7 days should result in at least a two fold increase in proliferation of the T cells and/or contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (e.g., TNF or IFN-γ) is indicative of T cell activation (see Coligan et al., Current Protocols in Immunology, vol. 1, Wiley Interscience (Greene 1998). T cells that have been activated in response to an ovarian carcinoma polypeptide, polynucleotide or ovarian carcinoma polypeptide-expressing APC may be CD4⁺ and/or CD8⁺. Ovarian carcinoma polypeptide-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from a patient or a related or unrelated donor and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4⁺ or CD8⁺ T cells that proliferate in response to an ovarian carcinoma polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to an ovarian carcinoma polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize an ovarian carcinoma polypeptide. Alternatively, one or more T cells that proliferate in the presence of an ovarian carcinoma polypeptide can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution. Following expansion, the cells may be administered back to the patient as described, for example, by Chang et al., *Crit. Rev. Oncol. Hematol.* 22:213, 1996.

Pharmaceutical Compositions and Vaccines

Within certain aspects, polypeptides, polynucleotides, binding agents and/or immune system cells as described herein may be incorporated into

pharmaceutical compositions or vaccines. Pharmaceutical compositions comprise one or more such compounds or cells and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds or cells and a non-specific immune response enhancer. A non-specific immune response enhancer may be any substance that enhances an immune response to an exogenous antigen. Examples of non-specific immune response enhancers include adjuvants, biodegradable microspheres (e.g., polylactic galactide) and liposomes (into which the compound is incorporated; see e.g., Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound within the composition or vaccine.

A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al.,

PNAS 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749, 5 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier 10 will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. 15 For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for 20 example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide) 25 and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. 30 Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune

responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI), Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ), alum, biodegradable microspheres, monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- γ , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6, IL-10 and TNF- β) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Ribi ImmunoChem Research Inc. (Hamilton, MT; see US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). Also preferred is AS-2 (SmithKline Beecham). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555. Another preferred adjuvant is a saponin, preferably QS21, which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO

96/33739. Other preferred formulations comprises an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210. Any vaccine provided herein may be prepared using well known methods that result in a combination
5 of antigen, immune response enhancer and a suitable carrier or excipient.

The compositions described herein may be administered as part of a sustained release formulation (*i.e.*, a formulation such as a capsule or sponge that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology and administered by, for example,
10 oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane. Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant
15 level of active component release. The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific
20 immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se*
25 and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic
30 cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to

be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (see Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*) and based on the lack of differentiation markers of B cells (CD19 and CD20), T cells (CD3), monocytes (CD14) and natural killer cells (CD56), as determined using standard assays. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (see Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor, mannose receptor and DEC-205 marker. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (e.g., CD54 and CD11) and costimulatory molecules (e.g., CD40, CD80 and CD86).

APCs may generally be transfected with a polynucleotide encoding a ovarian carcinoma antigen (or portion or other variant thereof) such that the antigen, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells
5 may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun
10 approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (e.g., vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently
15 conjugated to an immunological partner that provides T cell help (e.g., a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

Cancer Therapy

In further aspects of the present invention, the compositions described
20 herein may be used for immunotherapy of cancer, such as ovarian cancer. Within such methods, pharmaceutical compositions and vaccines are typically administered to a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a
25 cancer or to treat a patient afflicted with a cancer. Within certain preferred embodiments, a patient is afflicted with ovarian cancer. Such cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration
30 of radiotherapy or conventional chemotherapeutic drugs.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immuno response-modifying agents (such as tumor vaccines, bacterial adjuvants and/or
5 cytokines).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host
10 immune system. Examples of effector cells include T lymphocytes (such as CD8⁺ cytotoxic T lymphocytes and CD4⁺ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides
15 recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for
20 adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above,
25 immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example,
30 antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system.

Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see, for example, Cheever et al., Immunological Reviews 157:177, 1997.*)

Alternatively, a vector expressing a polypeptide recited herein may be introduced into stem cells taken from a patient and clonally propagated *in vitro* for autologous transplant back into the same patient.

Routes and frequency of administration, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration), orally or in the bed of a resected tumor. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 100 μ g to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical

outcome (e.g., more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to an ovarian carcinoma antigen generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

Screens for Identifying Secreted Ovarian Carcinoma Antigens

The present invention provides methods for identifying secreted tumor antigens. Within such methods, tumors are implanted into immunodeficient animals such as SCID mice and maintained for a time sufficient to permit secretion of tumor antigens into serum. In general, tumors may be implanted subcutaneously or within the gonadal fat pad of an immunodeficient animal and maintained for 1-9 months, preferably 1-4 months. Implantation may generally be performed as described in WO 97/18300. The serum containing secreted antigens is then used to prepare antisera in immunocompetent mice, using standard techniques and as described herein. Briefly, 50-100 μ L of sera (pooled from three sets of immunodeficient mice, each set bearing a different SCID-derived human ovarian tumor) may be mixed 1:1 (vol:vol) with an appropriate adjuvant, such as RIBI-MPL or MPL + TDM (Sigma Chemical Co., St. Louis, MO) and injected intraperitoneally into syngeneic immunocompetent animals at monthly intervals for a total of 5 months. Antisera from animals immunized in such a manner may be obtained by drawing blood after the third, fourth and fifth immunizations. The resulting antiserum is generally pre-cleared of *E. coli* and phage antigens and used (generally following dilution, such as 1:200) in a serological expression screen.

The library is typically an expression library containing cDNAs from one or more tumors of the type that was implanted into SCID mice. This expression library may be prepared in any suitable vector, such as λ -screen (Novagen). cDNAs that encode a polypeptide that reacts with the antiserum may be identified using standard techniques, and sequenced. Such cDNA molecules may be further characterized to

evaluate expression in tumor and normal tissue, and to evaluate antigen secretion in patients.

The methods provided herein have advantages over other methods for tumor antigen discovery. In particular, all antigens identified by such methods should
5 be secreted or released through necrosis of the tumor cells. Such antigens may be present on the surface of tumor cells for an amount of time sufficient to permit targeting and killing by the immune system, following vaccination.

Methods for Detecting Cancer

In general, a cancer may be detected in a patient based on the presence of
10 one or more ovarian carcinoma proteins and/or polynucleotides encoding such proteins in a biological sample (such as blood, sera, urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as ovarian cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein
15 generally permit detection of the level of protein that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, an ovarian carcinoma-associated sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

20 There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by
25 (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection
30 reagent that contains a reporter group and specifically binds to the binding

agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length ovarian carcinoma proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μ g, and preferably about 100 ng to about 1 μ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports
5 having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay.
10 This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a
15 different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically
20 blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20TM (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact
25 time (*i.e.,* incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with ovarian cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve
30 equilibrium may be readily determined by assaying the level of binding that occurs over

a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second
5 antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of
10 binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups
15 and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

20 To determine the presence or absence of a cancer, such as ovarian cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with
25 samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985,
30 p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (i.e., sensitivity) and false positive rates (100%-specificity)

that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered
5 positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or
10 strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of
15 bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the
20 presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a
25 positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 µg, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological
30 sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use ovarian carcinoma polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such ovarian carcinoma protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with an ovarian carcinoma protein in a biological sample. Within certain methods, a biological sample comprising CD4⁺ and/or CD8⁺ T cells isolated from a patient is incubated with an ovarian carcinoma protein, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with an ovarian carcinoma protein (e.g., 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of ovarian carcinoma protein to serve as a control. For CD4⁺ T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8⁺ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding an ovarian carcinoma protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of an ovarian carcinoma protein cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the ovarian carcinoma protein. The amplified cDNA is then separated and detected using techniques well

known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding an ovarian carcinoma protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

5 To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding an ovarian carcinoma protein that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably,
10 oligonucleotide primers and/or probes hybridize to a polynucleotide encoding a polypeptide described herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous
15 nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence provided herein. Techniques for both PCR based assays and hybridization assays are well known in the art (*see*, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

20 One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample such as a biopsy tissue and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification
25 may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered
30 positive.

In another embodiment, ovarian carcinoma proteins and polynucleotides encoding such proteins may be used as markers for monitoring the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

10 Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

15 As noted above, to improve sensitivity, multiple ovarian carcinoma protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

Diagnostic Kits

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to an ovarian carcinoma protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain

a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding an ovarian carcinoma protein in a biological sample. Such kits generally
5 comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding an ovarian carcinoma protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a
10 polynucleotide encoding an ovarian carcinoma protein.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

IDENTIFICATION OF REPRESENTATIVE OVARIAN CARCINOMA PROTEIN cDNAs

This Example illustrates the identification of cDNA molecules encoding
5 ovarian carcinoma proteins.

Anti-SCID mouse sera (generated against sera from SCID mice carrying
late passage ovarian carcinoma) was pre-cleared of E. coli and phage antigens and used
at a 1:200 dilution in a serological expression screen. The library screened was made
from a SCID-derived human ovarian tumor (OV9334) using a directional RH oligo(dT)
10 priming cDNA library construction kit and the λ Screen vector (Novagen). A
bacteriophage lambda screen was employed. Approximately 400,000 pfu of the
amplified OV9334 library were screened.

196 positive clones were isolated. Certain sequences that appear to be
novel are provided in Figures 1A-1S and SEQ ID NO:1 to 71. Three complete insert
15 sequences are shown in Figures 2A-2C (SEQ ID NO:72 to 74). Other clones having
known sequences are presented in Figures 15A-15EEE (SEQ ID NO:82 to 310).
Database searches identified the following sequences that were substantially identical to
the sequences presented in Figures 15A-15EEE.

These clones were further characterized using microarray technology to
20 determine mRNA expression levels in a variety of tumor and normal tissues. Such
analyses were performed using a Synteni (Palo Alto, CA) microarray, according to the
manufacturer's instructions. PCR amplification products were arrayed on slides, with
each product occupying a unique location in the array. mRNA was extracted from the
tissue sample to be tested, reverse transcribed and fluorescent-labeled cDNA probes
25 were generated. The microarrays were probed with the labeled cDNA probes and the
slides were scanned to measure fluorescence intensity. Data was analyzed using
Synteni's provided GEMtools software. The results for one clone (13695, also referred
to as O8E) are shown in Figure 3.

EXAMPLE 2

IDENTIFICATION OF OVARIAN CARCINOMA CDNAS USING MICROARRAY TECHNOLOGY

This Example illustrates the identification of ovarian carcinoma polynucleotides by PCR subtraction and microarray analysis. Microarrays of cDNAs
5 were analyzed for ovarian tumor-specific expression using a Synteni (Palo Alto, CA) microarray, according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997).

A PCR subtraction was performed using a tester comprising cDNA of
10 four ovarian tumors (three of which were metastatic tumors) and a driver of cDNA from five normal tissues (adrenal gland, lung, pancreas, spleen and brain). cDNA fragments recovered from this subtraction were subjected to DNA microarray analysis where the fragments were PCR amplified, adhered to chips and hybridized with fluorescently
15 labeled probes derived from mRNAs of human ovarian tumors and a variety of normal human tissues. In this analysis, the slides were scanned and the fluorescence intensity was measured, and the data were analyzed using Synteni's GEMtools software. In general, sequences showing at least a 5-fold increase in expression in tumor cells (relative to normal cells) were considered ovarian tumor antigens. The fluorescent
20 results were analyzed and clones that displayed increased expression in ovarian tumors were further characterized by DNA sequencing and database searches to determine the novelty of the sequences.

Using such assays, an ovarian tumor antigen was identified that is a splice fusion between the human T-cell leukemia virus type I oncoprotein TAX (*see* Jin et al., *Cell* 93:81-91, 1998) and an extracellular matrix protein called osteonectin. A
25 splice junction sequence exists at the fusion point. The sequence of this clone is presented in Figure 4 and SEQ ID NO:75. Osteonectin, unspliced and unaltered, was also identified from such assays independently.

Further clones identified by this method are referred to herein as 3f, 6b, 8e, 8h, 12c and 12h. Sequences of these clones are shown in Figures 5 to 9 and SEQ ID
30 NO:76 to 81. Microarray analyses were performed as described above, and are presented in Figures 10 to 14. A full length sequence encompassing clones 3f, 6b, 8e

and 12h was obtained by screening an ovarian tumor (SCID-derived) cDNA library. This 2996 base pair sequence (designated O772P) is presented in SEQ ID NO:311, and the encoded 914 amino acid protein sequence is shown in SEQ ID NO:312. PSORT analysis indicates a Type 1a transmembrane protein localized to the plasma membrane.

5 In addition to certain of the sequences described above, this screen identified the following sequences which are described in detail in Table 1:

Table 1

Sequence	Comments
OV4vG11 (SEQ ID NO:313)	human clone 1119D9 on chromosome 20p12
OV4vB11 (SEQ ID NO:314)	human UWGC:y14c094 from chromosome 6p21
OV4vD9 (SEQ ID NO:315)	human clone 1049G16 chromosome 20q12-13.2
OV4vD5 (SEQ ID NO:316)	human KIAA0014 gene
OV4vC2 (SEQ ID NO:317)	human KIAA0084 gene
OV4vF3 (SEQ ID NO:318)	human chromosome 19 cosmid R31167
OV4vC1 (SEQ ID NO:319)	novel
OV4vH3 (SEQ ID NO:320)	novel
OV4vD2 (SEQ ID NO:321)	novel
O815P (SEQ ID NO:322)	novel
OV4vC12 (SEQ ID NO:323)	novel
OV4vA4 (SEQ ID NO:324)	novel
OV4vA3 (SEQ ID NO:325)	novel
OV4v2A5 (SEQ ID NO:326)	novel
O819P (SEQ ID NO:327)	novel
O818P (SEQ ID NO:328)	novel
O817P (SEQ ID NO:329)	novel
O816P (SEQ ID NO:330)	novel
Ov4vC5 (SEQ ID NO:331)	novel
21721 (SEQ ID NO:332)	human lumican
21719 (SEQ ID NO:333)	human retinoic acid-binding protein II
21717 (SEQ ID NO:334)	human26S proteasome ATPase subunit
21654 (SEQ ID NO:335)	human copine I
21627 (SEQ ID NO:336)	human neuron specific gamma-2 enolase

Sequence	Comments
21623 (SEQ ID NO:337)	human geranylgeranyl transferase II
21621 (SEQ ID NO:338)	human cyclin-dependent protein kinase
21616 (SEQ ID NO:339)	human prepro-megakaryocyte potentiating factor
21612 (SEQ ID NO:340)	human UPH1
21558 (SEQ ID NO:341)	human RalGDS-like 2 (RGL2)
21555 (SEQ ID NO:342)	human autoantigen P542
21548 (SEQ ID NO:343)	human actin-related protein (ARP2)
21462 (SEQ ID NO:344)	human huntingtin interacting protein
21441 (SEQ ID NO:345)	human 90K product (tumor associated antigen)
21439 (SEQ ID NO:346)	human guanine nucleotide regulator protein (tim1)
21438 (SEQ ID NO:347)	human Ku autoimmune (p70/p80) antigen
21237 (SEQ ID NO:348)	human S-laminin
21436 (SEQ ID NO:349)	human ribophorin I
21435 (SEQ ID NO:350)	human cytoplasmic chaperonin hTRiC5
21425 (SEQ ID NO:351)	human EMX2
21423 (SEQ ID NO:352)	human p87/p89 gene
21419 (SEQ ID NO:353)	human HPBRII-7
21252 (SEQ ID NO:354)	human T1-227H
21251 (SEQ ID NO:355)	human cullin I
21247 (SEQ ID NO:356)	kunitz type protease inhibitor (KOP)
21244-1 (SEQ ID NO:357)	human protein tyrosine phosphatase receptor F (PTPRF)
21718 (SEQ ID NO:358)	human LTR repeat
OV2-90 (SEQ ID NO:359)	novel
Human zinc finger (SEQ ID NO:360)	
Human polyA binding protein (SEQ ID NO:361)	
Human pleitrophin (SEQ ID NO:362)	
Human PAC clone 278C19 (SEQ ID NO:363)	
Human LLRep3 (SEQ ID NO:364)	
Human Kunitz type protease inhib (SEQ ID NO:365)	
Human KIAA0106 gene (SEQ ID NO:366)	
Human keratin (SEQ ID NO:367)	
Human HIV-1TAR (SEQ ID NO:368)	
Human glia derived nexin (SEQ ID NO:369)	

Sequence	Comments
Human fibronectin (SEQ ID NO:370)	
Human ECMproBM40 (SEQ ID NO:371)	
Human collagen (SEQ ID NO:372)	
Human alpha enolase (SEQ ID NO:373)	
Human aldolase (SEQ ID NO:374)	
Human transf growth factor BIG H3 (SEQ ID NO:375)	
Human SPARC osteonectin (SEQ ID NO:376)	
Human SLP1 leucocyte protease (SEQ ID NO:377)	
Human mitochondrial ATP synth (SEQ ID NO:378)	
Human DNA seq clone 461P17 (SEQ ID NO:379)	
Human dbpB pro Y box (SEQ ID NO:380)	
Human 40 kDa keratin (SEQ ID NO:381)	
Human arginosuccinate synth (SEQ ID NO:382)	
Human acidic ribosomal phosphoprotein (SEQ ID NO:383)	
Human colon carcinoma laminin binding pro (SEQ ID NO:384)	

This screen further identified multiple forms of the clone O772P, referred to herein as 21013, 21003 and 21008. PSORT analysis indicates that 21003 (SEQ ID NO:386; translated as SEQ ID NO:389) and 21008 (SEQ ID NO:387; translated as SEQ ID NO:390) represent Type 1a transmembrane protein forms of
5 O772P. 21013 (SEQ ID NO:385; translated as SEQ ID NO:388) appears to be a truncated form of the protein and is predicted by PSORT analysis to be a secreted protein.

Additional sequence analysis resulted in a full length clone for O8E (2627 bp, which agrees with the message size observed by Northern analysis; SEQ ID
10 NO:391). This nucleotide sequence was obtained as follows: the original O8E sequence (OrigO8Econs) was found to overlap by 33 nucleotides with a sequence from an EST clone (IMAGE#1987589). This clone provided 1042 additional nucleotides upstream of the original O8E sequence. The link between the EST and O8E was confirmed by sequencing multiple PCR fragments generated from an ovary primary tumor library
15 using primers to the unique EST and the O8E sequence (ESTxO8EPCR). Full length status was further indicated when anchored PCR from the ovary tumor library gave

several clones (AnchoredPCR cons) that all terminated upstream of the putative start methionine, but failed to yield any additional sequence information. Figure 16 presents a diagram that illustrates the location of each partial sequence within the full length O8E sequence.

- 5 Two protein sequences may be translated from the full length O8E. For "a" (SEQ ID NO:393) begins with a putative start methionine. A second form "b" (SEQ ID NO:392) includes 27 additional upstream residues to the 5' end of the nucleotide sequence.

EXAMPLE 3

- 10 This example discloses the identification and characterization of antibody epitopes recognized by the O8E polyclonal anti-sera.

Rabbit anti-sera was raised against E. coli derived O8E recombinant protein and tested for antibody epitope recognition against 20 or 21 mer peptides that correspond to the O8E amino acid sequence. Peptides spanning amino acid regions 31 to 65, 76 to 110, 136 to 200 and 226 to 245 of the full length O8E protein were recognized by an acid eluted peak and/or a salt eluted peak from affinity purified anti-O8E sera. Thus, the corresponding amino acid sequences of the above peptides constitute the antibody epitopes recognized by affinity purified anti-O8E antibodies.

- 20 ELISA analysis of anti-O8E rabbit sera is shown in Figure 23, and ELISA analysis of affinity purified rabbit anti-O8E polyclonal antibody is shown in Figure 24.

For epitope mapping, 20 or 21 mer peptides corresponding to the O8E protein were synthesized. For antibody affinity purification, rabbit anti-O8E sera was run over an O8E-sepharose column, then antibody was eluted with a salt buffer containing 0.5 M NaCl and 20 mM PO₄, followed by an acid elution step using 0.2 M Glycine, pH 2.3. Purified antibody was neutralized by the addition of 1M Tris, pH 8 and buffer exchanged into phosphate buffered saline (PBS). For enzyme linked immunosorbant assay (ELISA) analysis, O8E peptides and O8E recombinant protein were coated onto 96 well flat bottom plates at 2 µg/ml for 2 hours at room temperature (RT). Plates were then washed 5 times with PBS + 0.1 % Tween 20 and blocked with PBS + 1 % bovine serum albumin (BSA) for 1 hour. Affinity purified anti-O8E antibody, either an acid or salt eluted fraction, was then added to the wells at 1 µg/ml

and incubated at RT for 1 hr. Plates were again washed, followed by the addition of donkey anti-rabbit-Ig-horseradish peroxidase (HRP) antibody for 1 hour at RT. Plates were washed, then developed by the addition of the chromagenic substrate 3, 3', 5, 5'-tetramethylbenzidine (TMB) (described by Bos *et al.*, *J. of Immunoassay* 2:187-204 (1981); available from Sigma (St. Louis, MO)). The reaction was incubated 15 minutes at RT and then stopped by the addition of 1 N H₂SO₄. Plates were read at an optical density of 450 (OD450) in an automated plate reader. The sequences of peptides corresponding to the OE8 antibody epitopes are disclosed herein as SEQ ID NO: 394-415. Antibody epitopes recognized by the O8E polyclonal anti-sera are disclosed herein in Figure 17.

EXAMPLE 4

This example discloses IHC analysis of O8E expression in ovarian cancer tissue samples.

For immunohistochemistry studies, paraffin-embedded formalin fixed ovarian cancer tissue was sliced into 8 micron sections. Steam heat induced epitope retrieval (SHIER) in 0.1 M sodium citrate buffer (pH 6.0) was used for optimal staining conditions. Sections were incubated with 10% serum/PBS for 5 minutes. Primary antibody (anti-O8E rabbit affinity purified polyclonal antibody) was added to each section for 25 min followed by a 25 min incubation with an anti-rabbit biotinylated antibody. Endogenous peroxidase activity was blocked by three 1.5 min incubations with hydrogen peroxidase. The avidin biotin complex/horse radish peroxidase system was used along with DAB chromogen to visualize antigen expression. Slides were counterstained with hematoxylin. One (papillary serous carcinoma) of six ovarian cancer tissue sections displayed O8E immunoreactivity. Upon optimization of the staining conditions, 4/5 ovarian cancer samples stained positive using the O8E polyclonal antibody. O8E expression was localized to the plasma membrane.

Six ovarian cancer tissues were analyzed with the anti-O8E rabbit polyclonal antibody. One (papillary serous carcinoma) of six ovarian cancer tissue samples stained positive for O8E expression. O8E expression was localized to the surface membrane.

EXAMPLE 5

This example discloses O8E peptides that are predicted to bind HLA-A2 and to be immunogenic for CD8 T cell responses in humans.

Potential HLA-A2 binding peptides of O8E were predicted by using the full-length open-reading frame (ORF) from O8E and running it through "Episeek," a program used to predict MHC binding peptides. The program used is based on the algorithm published by Parker, K.C. *et al.*, *J. Immunol.* 152(1):163-175 (1994) (incorporated by reference herein in its entirety). 10-mer and 9-mer peptides predicted to bind HLA-0201 are disclosed herein as SEQ ID NO: 416-435 and SEQ ID NO: 436-455, respectively.

EXAMPLE 6

This example discloses O8E cell surface expression measured by fluorescence activated cell sorting.

For FACS analysis, cells were washed with ice cold staining buffer (PBS/1% BSA/azide). Next, the cells were incubated for 30 minutes on ice with 10 micrograms/ml of affinity purified rabbit anti-B305D polyclonal antibody. The cells were washed 3 times with staining buffer and then incubated with a 1:100 dilution of a goat anti-rabbit Ig (H+L)-FITC reagent (Southern Biotechnology) for 30 minutes on ice. Following 3 washes, the cells were resuspended in staining buffer containing prodium iodide, a vital stain that allows for identification of permeable cells, and analyzed by FACS. O8E surface expression was confirmed on SKBR3 breast cancer cells and HEK293 cells that stably overexpress the cDNA for O8E. Neither MB415 cells nor HEK293 cells stably transfected with a control irrelevant plasmid DNA showed surface expression of O8E (Figures 18 and 19).

EXAMPLE 7

This example further evaluates the expression and surface localization of O8E.

For expression and purification of antigen used for immunization, O8E expressed in an E. coli recombinant expression system was grown overnight in LB Broth with the appropriate antibiotics at 37°C in a shaking incubator. The next morning,

10 ml of the overnight culture was added to 500 ml of 2x YT plus appropriate antibiotics in a 2L-baffled Erlenmeyer flask. When the Optical Density (at 560 nanometers) of the culture reached 0.4-0.6 the cells were induced with IPTG (1 mM). 4 hours after induction with IPTG the cells were harvested by centrifugation. The cells
5 were then washed with phosphate buffered saline and centrifuged again. The supernatant was discarded and the cells were either frozen for future use or immediately processed. Twenty milliliters of lysis buffer was added to the cell pellets and vortexed. To break open the E. coli cells, this mixture was then run through the French Press at a pressure of 16,000 psi. The cells were then centrifuged again and the supernatant and
10 pellet were checked by SDS-PAGE for the partitioning of the recombinant protein. For protein that localized to the cell pellet, the pellet was resuspended in 10 mM Tris pH 8.0, 1% CHAPS and the inclusion body pellet was washed and centrifuged again. This procedure was repeated twice more. The washed inclusion body pellet was solubilized with either 8 M urea or 6 M guanidine HCl containing 10 mM Tris pH 8.0 plus 10 mM
15 imidazole. The solubilized protein was added to 5 ml of nickel-chelate resin (Qiagen) and incubated for 45 min to 1 hour at room temperature with continuous agitation. After incubation, the resin and protein mixture were poured through a disposable column and the flow through was collected. The column was then washed with 10-20 column volumes of the solubilization buffer. The antigen was then eluted from the column using
20 8M urea, 10 mM tris pH 8.0 and 300 mM imidazole and collected in 3 ml fractions. A SDS-PAGE gel was run to determine which fractions to pool for further purification. As a final purification step, a strong anion exchange resin such as Hi-Prep Q (Biorad) was equilibrated with the appropriate buffer and the pooled fractions from above were loaded onto the column. Each antigen was eluted off of the column with an increasing
25 salt gradient. Fractions were collected as the column was run and another SDS-PAGE gel was run to determine which fractions from the column to pool. The pooled fractions were dialyzed against 10 mM Tris pH 8.0. This material was then evaluated for acceptable purity as determined by SDS-PAGE or HPLC, concentration as determined by Lowry assay or Amino Acid Analysis, identity as determined by amino terminal
30 protein sequence, and endotoxin level as determined by the Limulus (LAL) assay. The

proteins were then vialled after filtration through a 0.22 micron filter and the antigens were frozen until needed for immunization.

For generation of polyclonal anti-sera, 400 micrograms of each prostate antigen was combined with 100 micrograms of muramyldipeptide (MDP). Equal
5 volume of Incomplete Freund's Adjuvant (IFA) was added and then mixed. Every four weeks animals were boosted with 100 micrograms of antigen mixed with an equal volume of IFA. Seven days following each boost the animal was bled. Sera was generated by incubating the blood at 4°C for 12-24 hours followed by centrifugation.

For characterization of polyclonal antisera, 96 well plates were coated
10 with antigen by incubating with 50 microliters (typically 1 microgram) at 4°C for 20 hrs. 250 microliters of BSA blocking buffer was added to the wells and incubated at RT for 2 hrs. Plates were washed 6 times with PBS/0.01% tween. Anti-O8E rabbit sera or affinity purified anti-O8e antibody was diluted in PBS. Fifty microliters of diluted antibody was added to each well and incubated at RT for 30 min. Plates were washed as
15 described above before 50 microliters of goat anti-rabbit horse radish peroxidase (HRP) at a 1:10000 dilution was added and incubated at RT for 30 min. Plates were washed as described above and 100 microliters of TMB microwell Peroxidase Substrate was added to each well. Following a 15 minute incubation in the dark at room temperature the colorimetric reaction was stopped with 100 microliters of 1N H2SO4 and read
20 immediately at 450 nm. All polyclonal antibodies showed immunoreactivity to the O8E antigen.

For recombinant expression in mammalian HEK293 cells, full length O8E cDNA was subcloned into the mammalian expression vectors pcDNA3.1+ and pCEP4 (Invitrogen) which were modified to contain His and FLAG epitope tags,
25 respectively. These constructs were transfected into HEK293 cells (ATCC) using Eugene 6 reagent (Roche). Briefly, HEK293 cells were plated at a density of 100,000 cells/ml in DMEM (Gibco) containing 10% FBS (Hyclone) and grown overnight. The following day, 2 ul of Eugene6 was added to 100 ul of DMEM containing no FBS and incubated for 15 minutes at room temperature. The Eugene6/DMEM mixture was then
30 added to 1ug of O8E/pCEP4 or O8E/pcDNA3.1 plasmid DNA and incubated for 15 minutes at room temperature. The Eugene/DNA mix was then added to the HEK293

cells and incubated for 48-72 hrs at 37°C with 7% CO₂. Cells were rinsed with PBS then collected and pelleted by centrifugation. For Western blot analysis, whole cell lysates were generated by incubating the cells in Triton-X100 containing lysis buffer for 30 minutes on ice. Lysates were then cleared by centrifugation at 10,000rpm for 5 minutes at 4 C. Samples were diluted with SDS-PAGE loading buffer containing beta-mercaptoethanol, then boiled for 10 minutes prior to loading the SDS-PAGE gel. Protein was transferred to nitrocellulose and probed using anti-O8E rabbit polyclonal sera #2333L at a dilution of 1:750. The blot was revealed with a goat anti-rabbit Ig coupled to HRP followed by incubation in ECL substrate.

For FACS analysis, cells were washed further with ice cold staining buffer (PBS+1%BSA+Azide). Next, the cells were incubated for 30 minutes on ice with 10ug/ml of Protein A purified anti-O8E polyclonal sera. The cells were washed 3 times with staining buffer and then incubated with a 1:100 dilution of a goat anti-rabbit Ig(H+L)-FITC reagent (Southern Biotechnology) for 30 minutes on ice. Following 3 washes, the cells were resuspended in staining buffer containing Propidium Iodide (PI), a vital stain that allows for the identification of permeable cells, and analyzed by FACS.

From these experiments, the results of which are illustrated in Figures 20-21, O8E expression was detected on the surface of transfected HEK293 cells and SKBR3 cells by FACS analysis using rabbit anti-O8E sera. Expression was also detected in transfected HEK293 cell lysates by Western blot analysis (Figure 22).

EXAMPLE 8

GENERATION AND CHARACTERIZATION OF ANTI-O8E MABS.

Mouse monoclonal antibodies were raised against E. coli derived O8E proteins as follows. A/J mice were immunized intraperitoneally (IP) with Complete Freund's Adjuvant (CFA) containing 50 µg recombinant O8E, followed by a subsequent IP boost with Incomplete Freund's Adjuvant (IFA) containing 10µg recombinant O8E protein. Three days prior to removal of the spleens, the mice were immunized intravenously with approximately 50µg of soluble O8E recombinant protein. The spleen of a mouse with a positive titer to O8E was removed, and a single-cell suspension made and used for fusion to SP2/0 myeloma cells to generate B cell

hybridomas. The supernatants from the hybrid clones were tested by ELISA for specificity to recombinant O8E, and epitope mapped using peptides that spanned the entire O8E sequence. The mAbs were also tested by flow cytometry for their ability to detect O8E on the surface of cells stably transfected with O8E and on the surface of a breast tumor cell line.

For ELISA analysis, 96 well plates were coated with either recombinant O8E protein or overlapping 20-mer peptides spanning the entire O8E molecule at a concentration of either 1-2µg/ml or 10µg/ml, respectively. After coating, the plates were washed 5 times with washing buffer (PBS + 0.1% Tween-20) and blocked with PBS containing 0.5% BSA, 0.4% Tween-20. Hybrid supernatants or purified mAbs were then added and the plates incubated for 60 minutes at room temperature. The plates were washed 5 times with washing buffer and the secondary antibody, donkey-anti mouse Ig linked to horseradish peroxidase (HRP)(Jackson ImmunoResearch), was added for 60 minutes. The plates were again washed 5 times in washing buffer, followed by the addition of the peroxidase substrate. Of the hybridoma clones generated, 15 secreted mAbs that recognized the entire O8E protein. Epitope mapping revealed that of these 15 clones, 14 secreted mAbs that recognized the O8E amino acid residues 61-80 and one clone secreted a mAb that recognized amino acid residues 151-170.

For flow cytometric analysis, HEK293 cells which had been stably transfected with O8E and SKBR3 cells which express O8E mRNA, were harvested and washed in flow staining buffer (PBS+1%BSA+Azide). The cells were incubated with the supernatant from the mAb hybrids for 30 minutes on ice followed by 3 washes with staining buffer. The cells were incubated with goat-anti mouse Ig-FITC for 30 minutes on ice, followed by three washes with staining buffer before being resuspended in wash buffer containing propidium iodide. Flow cytometric analysis revealed that 15/15 mAbs were able to detect O8E protein expressed on the surface of O8E-transfected HEK293 cells. 6/6 mAbs tested on SKBR3 cells were able to recognize surface expressed O8E.

EXAMPLE 9

EXTENDED DNA AND PROTEIN SEQUENCE ANALYSIS OF SEQUENCE O772P

A full-length sequence encompassing clones 3f, 6b, 8e, and 12 was obtained by screening an ovarian tumor (SCID-derived) cDNA library described in detail in Example 2. This 2996 base pair sequence, designated O772P, is presented in SEQ ID NO: 311, and the encoded 914 amino acid protein sequence is shown in SEQ ID NO: 312. The DNA sequence O772P was searched against public databases including Genbank and showed a significant hit to Genbank Accession number AK024365 (SEQ ID NO: 457). This Genbank sequence was found to be 3557 base pairs in length and encodes a protein 1156 amino acids in length (SEQ ID NO: 459). A truncated version of this sequence, residues 25-3471, in which residue 25 corresponds to the first ATG initiation codon in the Genbank sequence, (SEQ ID NO: 456), encodes a protein that is 1148 amino acids in length (SEQ ID NO: 458). The published DNA sequence (SEQ ID NO: 457) differs from O772P in that it has a 5 base pair insertion corresponding to bases 958-962 of SEQ ID NO: 457. This insertion results in a frame shift such that SEQ ID NO: 457 encodes an additional N-terminal protein sequence relative to O772P (SEQ ID NO: 312). In addition, O772P encodes a unique N-terminal portion contained in residues 1-79 (SEQ ID NO: 460). The N-terminal portion of SEQ ID NO: 456, residues 1-313, also contains unique sequence and is listed as SEQ ID NO: 461.

EXAMPLE 10

THE GENERATION OF POLYCLONAL ANTIBODIES FOR IMMUNOHISTOCHEMISTRY
AND FLOW CYTOMETRIC ANALYSIS OF THE CELL ASSOCIATED EXPRESSION
PATTERN OF MOLECULE O772P

The O772P molecule was identified in Examples 2 and 9 of this application. To evaluate the subcellular localization and specificity of antigen expression in various tissues, polyclonal antibodies were generated against O772P. To produce these antibodies, O772P-1 (amino acids 44-772 of SEQ ID NO:312) and O772P-2 (477-914 of SEQ ID NO:312) were expressed in an E. coli recombinant expression system and grown overnight at 37°C in LB Broth. The following day, 10ml

of the overnight culture was added to 500ml of 2xYT containing the appropriate antibiotics. When the optical density of the cultures (560 nanometers) reached 0.4-0.6 the cells were induced with IPTG. Following induction, the cells were harvested, washed, lysed and run through a French Press at a pressure of 16000 psi. The cells were then centrifuged and the pellet checked by SDS-PAGE for the partitioning of the recombinant protein. For proteins that localize to the cell pellet, the pellet was resuspended in 10mM Tris, pH 8.0, 1% CHAPS and the inclusion body pellet washed and centrifuged. The washed inclusion body was solubilized with either 8M urea or 6M guanidine HCL containing 10mM Tris, pH 8.0, plus 10mM imidazole. The solubilized protein was then added to 5ml of nickel-chelate resin (Qiagen) and incubated for 45 minutes at room temperature.

Following the incubation, the resin and protein mixture was poured through a column and the flow through collected. The column was washed with 10-20 column volumes of buffer and the antigen eluted using 8M urea, 10mM Tris, pH 8.0, and 300. mM imidazole and collected in 3ml fractions. SDS-PAGE was run to determine which fractions to pool for further purification. As a final purification step, a strong anion exchange resin was equilibrated with the appropriate buffer and the pooled fractions were loaded onto the column. Each antigen was eluted from the column with an increasing salt gradient. Fractions were collected and analyzed by a SDS-PAGE to determine which fractions from the column to pool. The pooled fractions were dialyzed against 10mM Tris, pH 8.0, and the resulting protein was submitted for quality control for final release. The release criteria were: (a) purity as determined by SDS-PAGE or HPLC, (b) concentration as determined by Lowry assay or Amino Acid Analysis, (c) identity as determined by amino terminal protein, and (d) endotoxin levels as determined by the Limulus (LAL) assay. The proteins were then filtered through a 0.22 μ M filter and frozen until needed for immunizations.

To generate polyclonal antisera, 400 μ g of O772P-1 or O772P-2 was combined with 100 μ g of muramyl dipeptide (MDP). The rabbits were immunized every 4 weeks with 100 μ g of antigen mixed with an equal volume of Incomplete Freund's Adjuvant (IFA). Seven days following each boost, the animals were bled and sera was generated by incubating the blood at 4°C for 12-24 hours followed by centrifugation.

To characterize the antisera, 96 well plates were coated with antigen followed by blocking with BSA. Rabbit sera was diluted in PBS and added to each well. The plates were then washed, and goat anti-rabbit horseradish peroxidase (HRP). The plates were again washed and TMB microwell Peroxidase Substrate was added. 5 Following this incubation, the colormetric reaction was stopped and the plates read immediately at 450nm. All polyclonal antibodies showed immunoreactivity to the appropriate antigen.

Immunohistochemistry analysis of O772P expression was performed on paraffin-embedded formalin fixed tissue. O772P was found to be expressed in normal 10 ovary and ovarian tumor, but not in normal heart, kidney, colon, lung or liver. Additionally, immunohistochemistry and flow cytometric analysis indicates that O772P is a plasma membrane-associated molecule. O772P contains 1 plasma transmembrane domain predicted to be encoded by amino acids 859-880. The N-terminus of O772P is extracellular and is encoded by amino acids 1-859, while the C-terminus is intracellular. 15 Sequence analysis shows that there are 17 potential N-linked glycosylation sites.

EXAMPLE 11

O772P IS EXPRESSED ON THE SURFACE OF PRIMARY OVARIAN TUMOR CELLS

For recombinant expression in mammalian cells, the O772P-21008 (SEQ ID NO:387) and O772P full length cDNA (SEQ ID NO:311 encoding the protein of 20 SEQ ID NO:312) were subcloned into mammalian expression vectors pBIB or pCEP4 respectively. These constructs were transfected into HEK293 cells using Fugene 6 (Roche). The HEK cells were then plated at a density of 100,000 cells/ml in DMEM containing fetal bovine serum (FBS) and grown overnight. The following day, 2µl of Fugene 6 was added to 100µl of DMEM, which contained no FBS, and incubated for 15 25 minutes at room temperature. The Fugene 6/DMEM mixture was then added to 1µg of O772P/pBIB or O772P/pCEP4 plasmid DNA and incubated for an additional 15 minutes at room temperature. The Fugene 6/DNA mix was then added to the HEK293 cells and incubated for 48-72 hours at 37°C with 7% CO₂. The cells were rinsed and pelleted by centrifugation.

For Western Blot analysis, whole cell lysates were generated by incubating the cells in lysis buffer followed by clarification by centrifugation. The samples were diluted and run on SDS-PAGE. The gel was then transferred to nitrocellulose and probed using purified anti-O772P-2 rabbit polyclonal antibody. The blot was revealed with a goat anti-rabbit Ig coupled to HRP followed by incubation in ECL substrate. Western Blot analysis revealed that O772P-21008 could be detected in HEK293 cells that had been transfected with O772P.

To determine the cell expression profile of O772P in cells, primary ovarian tumor cells were grown in SCID mice. The cells were retrieved from the mice and analyzed by flow cytometry. Briefly, cells washed in cold staining buffer containing PBS, 1% BSA, and Na Azide. The cells were incubated for 30 minutes with 10µg/ml of purified anti-O772P-1 and O772P-2 polyclonal sera. Following this incubation, the cells were washed three times in staining buffer and incubated with goat anti-rabbit Ig (H+L) conjugated to FITC (Southern Biotechnology). The cells were washed and resuspended in staining buffer containing Propidium Iodide (PI), a vital stain that identifies non-viable cells. The cells were then analyzed using Fluorescence Activated Cell Sorting (FACS). FACS analysis revealed that O772P was present on the cells surface. Surface expression of O772P on tumor cells allows for immune targeting by therapeutic antibodies.

EXAMPLE 12

FUNCTIONAL CHARACTERIZATION OF ANTI-O8E MONOCLONAL ANTIBODIES

Mouse monoclonal antibodies (mAb) raised against E. coli derived O8E, as described in Example 8, were tested for their ability to promote O8E antigen internalization. Internalization of the antibody was determined using an in vitro cytotoxicity assay. Briefly, HEK293 and O8E/HEK transfected cells were plated into 96 well plates containing DME plus 10% heat-inactivated FBS in the presence of 50ng/well of purified anti-O8E or control antibodies. The isotype of the anti-O8E mAbs are as follows: 11A6-IgG1/kappa, 15C6-IgG2b/kappa, 18A8-IgG2b/kappa, and 14F1-IgG2a/kappa. W6/32 is a pan anti-human MHC class I mouse monoclonal antibody that serves as a positive control, and two irrelevant mAbs, Ir-Pharm and Ir-

Crxa were included as negative controls. Following incubation with the O8E specific antibodies or the relevant controls antibodies, the mAb-zap, a goat anti-mouse Ig-saporin conjugated secondary antibody (Advanced Targeting Systems) was added at a concentration of 100ng/ml to half of the wells, and the plates were incubated for 48 to 72 hours at 37°C in a 7% CO₂ incubator. This assay takes advantage of the toxic nature of saporin, a ribozyme inactivating protein, which when internalized has a cytotoxic effect. Following incubation with the mAb-zap, internalization was quantitated by the addition of MTS reagent, followed by reading the OD490 of the plate on a microplate ELISA reader. Figure 25 depicts the results from these assays. The top panel represents HEK cells that have not been transfected with O8E and therefore O8E antibody should not bind and be internalized. Levels of proliferation were the same in all samples whether they were incubated with or without the mAb-zap, with the exception of the positive control Ab, W6/32. The lower panel represents cells that have been transfected with O8E and therefore should bind O8E specific antibodies. Antibodies from the hybridomas 11H6, 14F1, and 15C6, which recognize the amino acids 61-80 of O8E were able to promote internalization of the O8E surface protein as measured by decreased levels of proliferation due to the toxic nature of the mAb-zap (See Figure 25). The antibody generated by the hybridoma 18A8, which recognizes amino acids 151-170 of O8E, was unable to promote internalization as determined by normal levels of proliferation either in the absence or presence of the mAb-zap.

EXAMPLE 13

CHARACTERIZATION OF THE OVARIAN TUMOR ANTIGEN, O772P

The cDNA and protein sequences for multiple forms of the ovarian tumor antigen O772P have been described in the above (e.g., Examples 2 and 9). A Genbank search indicated that O772P has a high degree of similarity with FLJ14303 (Accession # AK024365; SEQ ID NO:457 and 463). Protein sequences corresponding to O772P and FLJ14303 are disclosed in SEQ ID NO:478 and 479, respectively. FLJ14303 was identical to the majority of O772P, with much of the 3'-end showing 100% homology. However, the 5'-end of FLJ14303 was found to extend further 5' than O772P. In addition, FLJ14303 contained a 5 bp insert (SEQ ID NO:457) resulting in a

frame shift of the amino-terminus protein sequence such that FLJ14303 utilizes a different starting methionine than O772P and therefore encodes a different protein. This insertion was present in the genomic sequence and seen in all EST clones that showed identity to this region, suggesting that FLJ14303 (SEQ ID NO:457) represents a splice variant of O772P, with an ORF that contains an extended and different amino-terminus. The additional 5'-nucleotide sequence included repeat sequences that were identified during the genomic mapping of O772P. The 5'-end of O772P and the corresponding region of FLJ14303 showed between 90-100% homology. Taken together, this suggests that O772P and FLJ14303 are different splice variants of the same gene, with different unique repeat sequences being spliced into the 5'-end of the gene.

The identification of an additional ten or more repeat sequences within the same region of chromosome 19, indicates that there may be many forms of O772P, each with a different 5'-end, due to differential splicing of different repeat sequences. Northern blot analysis of O772P demonstrated multiple O772P-hybridizing transcripts of different sizes, some in excess 10kb.

Upon further analysis, 13 additional O772P-related sequences were identified, the cDNA and amino acid sequences of which are described in Table 2.

Table 2

SEQ ID NO:	Description	Transmembrane Domains
464	LS #1043400.1 (cDNA)	nd
465	LS #1043400.10 (cDNA)	0
466	LS #1043400.11 (cDNA)	2
467	LS #1043400.12 (cDNA)	2
468	LS #1043400.2 (cDNA)	nd
469	LS #1043400.3 (cDNA)	
470	LS #1043400.5 (cDNA)	nd
471	LS #1043400.8 (cDNA)	1
472	LS #1043400.9 (cDNA)	0

473	LS #1043400.6 (cDNA)	nd
474	LS #1043400.7 (cDNA)	nd
475	LS #1043400.4 (cDNA)	nd
476	LS #1397610.1 (cDNA)	0
477	1043400.10 Novel 5' (cDNA)	-
480	LS #1043400.9 (amino acid)	-
481	LS #1043400.8B (amino acid) Contains a transmembrane domain	-
482	LS #1043400.8A (amino acid)	-
483	LS #1043400.12 (amino acid) Contains a transmembrane domain	-
484	LS #1043400.11B (amino acid) Contains a transmembrane domain	-
485	LS #1043400.11A (amino acid)	-
486	LS #1043400.10 (amino acid)	-
487	LS #1043400.1 (amino acid)	-

nd=not determined

Initially it appeared that these sequences represented overlapping and/or discrete sequences of O772P splice forms that were capable of encoding polypeptides unique to the specific splice forms of O772P. However, nucleotide alignment of these sequences failed to identify any identical regions within the repeat elements. This indicates that the sequences may represent different specific regions of a single O772P gene, one that contains 16 or more repeat domains, all of which form a single linear transcript. The 5'-end of sequence LS #1043400.10 (Table 2; SEQ ID NO:465) is unique to both O772P and FLJ14303 and contains no repeat elements, indicating that this sequence may represent the 5'-end of O772P.

Previously, transmembrane prediction analysis had indicated that O772P contained between 1 and 3 transmembrane spanning domains. This was verified by the

use of immunohistochemistry and flow cytometry, which demonstrated the existence of a plasma membrane-associated molecule representing O772P. However, immunohistochemistry also indicated the presence of secreted form(s) of O772P, possibly resulting from an alternative splice form of O772P or from a post-translational cleavage event. Analysis of several of the sequences presented in Table 2 showed that sequences 1043400B.12, 1043400.8B, and 1043400.11B all contained transmembrane regions, while 1043400.8A, 1043400.10, 1043400.1, 1043400.11A, and 1043400.9 were all lacking transmembrane sequences, suggesting that these proteins may be secreted.

10 Analysis indicates a part of O772P is expressed and/or retained on the plasma membrane, making O772P an attractive target for directing specific immunotherapies, e.g., therapeutic antibodies, against this protein. The predicted extracellular domain of O772P is disclosed in SEQ ID NO:489 and secretion of O772P is likely to occur as a result of a cleavage event within the sequence:

15 SLVEQVFLDKTLNASFHWLGSTYQLVDIHVTEMESSVYQP.

Proteolytic cleavage is most likely to occur at the Lysine (K) at position 10 of SEQ ID NO:489. The extracellular, transmembrane, and cytoplasmic regions of O772P are all disclosed in SEQ ID NO:488:

Extracellular:

20 SLVEQVFLDKTLNASFHWLGSTYQLVDIHVTEMESSVYQPTSSSS
TQHFYLNFTITNLPYSQDKAQPGTTNYQRNKRNIEDALNQLFRNSSIKSYFSDCQ
VSTFRSVPNRHHTGVDSL CNFSPLARRVDRVAIYEEFLRMTRNGTQLQNFTLDR
SSVLVDGYFPNRNEPLTGNSDLPF

Transmembrane:

25 WAVILIGLAGLLGLITCLICGVLVTT

Cytoplasmic:

RRRKKEGEYNVQQQCPGYYSQSHLDLEDLQ

EXAMPLE 14

IMMUNOHISTOCHEMISTRY (IHC) ANALYSIS OF O8E EXPRESSION IN OVARIAN CANCER
AND NORMAL TISSUES

In order to determine which tissues express the ovarian cancer antigen
5 O8E, IHC analysis was performed on a diverse range of tissue sections using both
polyclonal and monoclonal antibodies specific for O8E. The generation of O8E specific
polyclonal antibodies is described in detail in Example 8. The monoclonal antibodies
used for staining were 11A6 and 14F1, both of which are specific for amino acids 61-80
of O8E and 18A8, which recognizes amino acids 151-170 of O8E (see Example 12 for
10 details on generation).

To perform staining, tissue samples were fixed in formalin solution for
12-24 hours and embedded in paraffin before being sliced into 8 micron sections.
Steam heat induced epitope retrieval (SHEIR) in 0.1M sodium citrate buffer (pH 6.0)
was used for optimal staining conditions. Sections were incubated with 10%
15 serum/PBS for 5 minutes. Primary antibody was then added to each section for 25
minutes followed by 25 minutes of incubation with either anti-rabbit or anti-mouse
biotinylated antibody. Endogenous peroxidase activity was blocked by three 1.5 minute
incubations with hydrogen peroxidase. The avidin biotin complex/horse radish
peroxidase (ABC/HRP) system was used along with DAB chromogen to visualize the
20 antigen expression. Slides were counterstained with hematoxylin to visualize the cell
nuclei.

Results using rabbit affinity purified polyclonal antibody to O8E (a.a. 29-
283; for details on the generation of this Ab, see Example 3) are presented in Table 3.
Results using the three monoclonal antibodies are presented in Table 4.

Table 3

Immunohistochemistry analysis of O8E using polyclonal antibodies

Tissue	O8E Expression
Ovarian Cancer	Positive
Breast Cancer	Positive

Normal Ovary	Positive
Normal Breast	Positive
Blood Vessel	Positive
Kidney	Negative
Lung	Negative
Colon	Negative
Liver	Negative
Heart	Negative

Table 4

Immunohistochemistry analysis of O8E using monoclonal antibodies

Normal Tissue	11A6		18A8		14F1	
	Endothelial	Epithelial	Endothelial	Epithelial	Endothelial	Epithelial
	1					
Skin	2	2	0	0	1	1
Skin	1	1	0	0	1	1
Breast	0	1	n/a	n/a	1	1
Colon	0	0	0	0	0	0
Jejunum	0	0	0	0	0	0
Colon	0	0	0	0	0	0
Colon	0	0	0	0	0	0
Ovary	0	0	0	0	1	0
Colon	0	0	0	0	0	1
Liver	0	0	0	0	1	2
Skin	0	0	0	0	1	0
Duodenum and Pancreas	0	0	0	0	0	0
Appendix	0	0	0	0	0	0
Ileum	0	0	0	0	0	0

0=no staining, 1=light staining, 2=moderate staining, n/a=not available

EXAMPLE 15

EPIOTOPE MAPPING OF O772P POLYCLONAL ANTIBODIES

To perform epitope mapping of O772P, peptides were generated, the sequences of which were derived from the sequence of O772P. These peptides were 15 mers that overlapped by 5 amino acids and were generated via chemical synthesis on membrane supports. The peptides were covalently bound to Whatman 50 cellulose support by their C-terminus with the N-terminus unbound. In order to determine epitope specificity, the membranes were wet with 100% ethanol for 1 minute, and then blocked for 16 hours in TBS/Tween/Triton buffer (50mM Tris, 137 mM NaCl, 2.7 mM KCl, 0.5% BSA, 0.05% Tween 20, 0.05% Triton X-100, pH 7.5). The peptides were then probed with 2 O772P specific antibodies, O772P-1 (amino acids 44-772 of SEQ ID NO:312) and O772P-2 (477-914 of SEQ ID NO:312; see Example 10 for details of antibody generation), as well as irrelevant rabbit antibodies for controls. The antibodies were diluted to 1µg/ml and incubated with the membranes for 2 hours at room temperature. The membranes were then washed for 30 minutes in TBS/Tween/Triton buffer, prior to being incubated with a 1:10,000 dilution of HRP-conjugated anti-rabbit secondary antibody for 2 hours. The membranes were again washed for 30 minutes in TBS/Tween/Triton and anti-peptide reactivity was visualized using ECL. Specific epitope binding specificity for each of the O772P-polyclonal antibodies is described in Table 5.

Table 5

SEQ ID NO:	Peptide #	Anti-O772P1	Anti-O772P2	Peptide Sequence
490	2	***	-	TCGMRRTCSTLAPGS
491	6	*	*/-	CRLTLRPEKDGAT
492	7	*	-	DGTATGVDAICTHHP
493	8	-	-	CTHHPDPKSPRLDRE
494	9	***	***	RLDREQLYWELSOLT
495	11	*/-	-	LGPYALDNDSLFVNG
496	13	****	-	SVSTTSTPGTPTYVL
497	22	-	-	LRPEKDGEATGVDAI
498	24	**	*/-	DPTGPGLDREQLYLE
499	27	*/-	-	LDRDSLTVNGFTTHRS
500	40	*/-	-	GPYSLDKDSLVLNGY
501	41	-	-	YLVNGYNEPGPDEPPT
502	47	***	***	ATFNSTEGVLQHLLR

503	50	-	***	QLISLRPEKDGAATG
504	51	-	**	GAATGVDTTCTYHPD
505	52	-	*/-	TYHPDPVGPGLDIQQ
506	53	-	*	LDIQQLYWELSOLTH
507	58	-	*	HIVNWNLSNPDPTSS
508	59	-	*	DPTSSEYITLLRDIQ
509	60	-	*	LRDIQDKVTTLTKGS
510	61	-	***	LYKGSQQLHDTFRFCL
511	71	-	**	DKAQPGTTNYQRNKR

*= relative reactive level, -; no binding, ***; maximal binding

EXAMPLE 16

IDENTIFICATION OF A NOVEL N-TERMINAL REPEAT STRUCTURE ASSOCIATED WITH O772P

5 Various O772P cDNA and protein forms have been identified and characterized as detailed above (e.g., Examples 1, 2, 9, and 14). Importantly, O772P RNA and protein have been demonstrated to be over-expressed in ovarian cancer tissue relative to normal tissues and thus represents an attractive target for ovarian cancer diagnostic and therapeutic applications.

10 Using bioinformatic analysis of open reading frames (ORFs) from genomic nucleotide sequence identified previously as having homology with O772P, multiple nucleotide repeat sequences were identified in the 5' region of the gene encoding the O772P protein. A number of these repeat sequences were confirmed by RT-PCR using primers specific for the individual repeats. Fragments which contained
15 multiple repeats were amplified from cDNA, thus confirming the presence of specific repeats and allowing an order of these repeats to be established.

Unexpectedly, when various sets of O772P sequences derived from different database and laboratory sources were analyzed, at least 20 different repeat structures, each having substantial levels of identity with each other (see Table 6), were
20 identified in the 5' region of the O772P gene and the corresponding N-terminal region of the O772P protein. Each repeat comprises a contiguous open reading frame encoding a polypeptide unit that is capable of being spliced to one or more other repeats such that concatomers of the repeats are formed in differing numbers and orders. Interestingly, other molecules have been described in the scientific literature that have repeating
25 structural domains analogous to those described herein for O772P. For example, the

mucin family of proteins, which are the major glycoprotein component of the mucous which coats the surfaces of cells lining the respiratory, digestive and urogenital tracts, have been shown to be composed of tandemly repeated sequences that vary in number, length and amino acid sequence from one mucin to another (Perez-Vilar and Hill, J. Biol. Chem. 274(45):31751-31754, 1999).

The various identified repeat structures set forth herein are expected to give rise to multiple forms of O772P, most likely by alternative splicing. The cDNA sequences of the identified repeats are set forth in SEQ ID NOs:513-540, 542-546, and 548-567. The encoded amino acid sequences of the repeats are set forth in SEQ ID NOs:574-593. In many instances these amino acid sequences represent consensus sequences that were derived from the alignment of more than one experimentally derived sequence.

Each of these splice forms is capable of encoding a unique O772P protein with multiple repeat domains attached to a constant carboxy terminal protein portion of O772P that contains a trans membrane region. The cDNA sequence of the O772P constant region is set forth in SEQ ID NO:568 and the encoded amino acid sequence is set forth in SEQ ID NO:594.

All of the available O772P sequences that were obtained were broken down into their identifiable repeats and these sequences were compared using the Clustal method with weighted residue weight table (MegAlign software within DNASTAR sequence analysis package) to identify the relationship between the repeat sequences. Using this information, the ordering data provided by the RT-PCR, and sequence alignments (automatic and manual) using SeqMan (DNASTAR), one illustrative consensus full length O772P contig was identified comprising 20 distinct repeat units. The cDNA for this O772P cDNA contig is set forth in SEQ ID NO:569 and the encoded amino acid sequence is set forth in SEQ ID NO:595. This form of the O772P protein includes the following consensus repeat structures in the following order:

SEQ ID NO:572- SEQ ID NO:574- SEQ ID NO:575-SEQ ID NO:576-
SEQ ID NO:577- SEQ ID NO:578- SEQ ID NO:579- SEQ ID NO:580- SEQ ID
NO:581- SEQ ID NO:582- SEQ ID NO:583- SEQ ID NO:584- SEQ ID NO:585- SEQ

ID NO:586- SEQ ID NO:587- SEQ ID NO:588- SEQ ID NO:589- SEQ ID NO:590-
SEQ ID NO:591- SEQ ID NO:592- SEQ ID NO:593.

SEQ ID NO:595, therefore, represents one illustrative full-length
consensus sequence for the O772P protein. As discussed above, however, based on
5 current knowledge of this protein and based upon scientific literature describing
proteins containing analogous repeating structures, many other forms of O772P are
expected to exist with either more or less repeats. In addition, many forms of O772P
are expected to have differing arrangements, e.g., different orders, of these N-terminal
repeat structures. The existence of multiple forms of O772P having differing numbers
10 of repeats is supported by Northern analysis of O772P. In this study, Northern
hybridization of a O772P-specific probe resulted in a smear of multiple O772P-
hybridizing transcripts, some in excess 10kb.

Thus, the variable repeat region of the O772 protein can be illustratively
represented by the structure $X_n - Y$, wherein X comprises a repeat structure having at
15 least 50% identity with the consensus repeat sequence set forth in SEQ ID NO:596; n is
the number of repeats present in the protein and is expected to typically be a integer
from 1 to about 35; Y comprise the O772P constant region sequence set forth in SEQ
ID NO:594 or sequences having at least 80% identity with SEQ ID NO:594. Each X
present in the X_n repeat region of the O772 molecule is different.

20 To determine the consensus sequences of each of the 20 repeat regions,
sequences that were experimentally determined for a discrete repeat region were aligned
and a consensus sequence determined. In addition to determining the consensus
sequences for individual repeat regions, a consensus repeat sequence was also
determined. This sequence was obtained by aligning the 20 individual consensus
25 sequences. Variability of the repeats was determined by aligning the consensus amino
acid sequences from each of the individual repeat regions with the over all repeat
consensus sequence. Identity data is presented in Table 6.

Table 6

Percent identities of Repeat Sequences with Reference to the Consensus Repeat Sequence

Repeat Number (amino acid)	SEQ ID NO:	Percent Identity to Consensus Repeat Sequence
2	574	88
3	575	84
4	576	88
5	577	89
6	578	93
7	579	90
8	580	91
9	581	88
10	582	85
11	583	86
12	584	87
13	585	87
14	586	89
15	587	89
16	588	89
17	589	83
18	590	84
19	591	83
20	592	57
21	593	68

5 From the foregoing it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration,

various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

CLAIMS

What is Claimed:

1. An O772P polypeptide having the structure:
 X_n-Y
wherein X comprises a sequence having at least 50% identity with the consensus O772P repeat sequence set forth in SEQ ID NO: 596;
Y comprises a sequence having at least 80% identity with the O772P constant region sequence set forth in SEQ ID NO: 594;
n is an integer from 1 to 35;
wherein each X present in said polypeptide is different.
2. The polypeptide of claim 1, wherein X comprises a sequence selected from the group consisting of any one of SEQ ID NOs: 574-593.
3. The polypeptide of claim 1, wherein Y comprises the sequence set forth in SEQ ID NO: 594.
4. The polypeptide of claim 1, wherein n is an integer from 15 to 25.
5. The polypeptide of claim 1, wherein n is 20.
6. The polypeptide of claim 1, wherein said polypeptide comprises SEQ ID NO: 595.
7. The polypeptide of claim 1, wherein said polypeptide is overexpressed in ovarian cancer cells compared with normal tissues.
8. An O772P polypeptide having the structure:
 X_n-Y

wherein X comprises an O772P repeat sequence selected from the group consisting of any one of SEQ ID NOs: 574-593;

Y comprises a sequence having at least 90% identity with the O772P constant region sequence set forth in SEQ ID NO: 594;

n is an integer from 15 to 25;

wherein each X present in said polypeptide is different.

9. The polypeptide of claim 8, wherein n is 20.
10. The polypeptide of claim 8, wherein said polypeptide comprises SEQ ID NO: 595.
11. The polypeptide of claim 8, wherein said polypeptide is overexpressed in ovarian cancer cells compared with normal tissues.
12. An O772P polypeptide having the structure:
 X_n -Y
wherein n is 20 and X comprises the following O772P repeat sequences:
SEQ ID NO: 574 - SEQ ID NO: 575 - SEQ ID NO: 576 - SEQ ID NO: 577 - SEQ ID NO: 578 - SEQ ID NO: 579 - SEQ ID NO: 580 - SEQ ID NO: 581 - SEQ ID NO: 582 - SEQ ID NO: 583 - SEQ ID NO: 584 - SEQ ID NO: 585 - SEQ ID NO: 586 - SEQ ID NO: 587 - SEQ ID NO: 588 - SEQ ID NO: 589 - SEQ ID NO: 590 - SEQ ID NO: 591 - SEQ ID NO: 592 - SEQ ID NO: 593; and
Y comprises the sequence set forth in SEQ ID NO: 594.
13. The polypeptide of claim 12, wherein said polypeptide comprises SEQ ID NO: 595.
14. The polypeptide of claim 12, wherein said polypeptide is overexpressed in ovarian cancer cells compared with normal tissues.

15. An O772P polynucleotide having the structure:

X_n -Y

wherein X comprises an O772P repeat sequence selected from the group consisting of any one of SEQ ID NOs: 512-540, 542-546 and 548-567;

Y comprises a sequence having at least 95% identity with the O772P constant region sequence set forth in SEQ ID NO: 568;

n is an integer from 1 to 35;

wherein each X present in said polypeptide is different.

16. The polynucleotide of claim 15, wherein said polynucleotide comprises SEQ ID NO: 569.

17. The polynucleotide of claim 15, wherein n is from 15 to 25.

18. The polynucleotide of claim 15, wherein n is 20.

19. The polynucleotide of claim 15, wherein said polynucleotide is overexpressed in ovarian cancer cells compared with normal tissues.

20. An isolated polynucleotide comprising a sequence selected from the group consisting of:

- (a) sequences provided in SEQ ID NOs: 464-477 and 512-569;
- (b) complements of the sequences provided in SEQ ID NOs: 464-477 and 512-569;
- (c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NOs: 464-477 and 512-569;
- (d) sequences that hybridize to a sequence provided in SEQ ID NOs: 464-477 and 512-569, under highly stringent conditions;
- (e) sequences having at least 75% identity to a sequence of SEQ ID NOs: 464-477 and 512-569;

(f) sequences having at least 90% identity to a sequence of SEQ ID NOs: 464-477 and 512-569; and

(g) degenerate variants of a sequence provided in SEQ ID NOs: 464-477 and 512-569.

21. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

(a) sequences encoded by a polynucleotide of claim 20; and

(b) sequences having at least 80% identity to a sequence encoded by a polynucleotide of claim 20; and

(c) sequences having at least 90% identity to a sequence encoded by a polynucleotide of claim 20.

22. An expression vector comprising a polynucleotide of claim 20 operably linked to an expression control sequence.

23. A host cell transformed or transfected with an expression vector according to claim 22.

24. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a polypeptide of claim 21.

25. A method for detecting the presence of a cancer in a patient, comprising the steps of:

(a) obtaining a biological sample from the patient;

(b) contacting the biological sample with a binding agent that binds to a polypeptide of claim 21;

(c) detecting in the sample an amount of polypeptide that binds to the binding agent; and

(d) comparing the amount of polypeptide to a predetermined cut-off value and therefrom determining the presence of a cancer in the patient.

26. A fusion protein comprising at least one polypeptide according to claim 21.

27. A method for stimulating and/or expanding T cells specific for a tumor protein, comprising contacting T cells with at least one component selected from the group consisting of:

- (a) polypeptides according to claim 21;
- (b) polynucleotides according to claim 20; and
- (c) antigen-presenting cells that express a polynucleotide according to claim 20,

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

28. An isolated T cell population, comprising T cells prepared according to the method of claim 27.

29. A composition comprising a first component selected from the group consisting of physiologically acceptable carriers and immunostimulants, and a second component selected from the group consisting of:

- (a) polypeptides according to claim 21;
- (b) polynucleotides according to claim 20;
- (c) antibodies according to claim 24;
- (d) fusion proteins according to claim 26;
- (e) T cell populations according to claim 28; and
- (f) antigen presenting cells that express a polypeptide according to claim 21.

30. A method for stimulating an immune response in a patient, comprising administering to the patient a composition of claim 29.

31. A method for the treatment of a ovarian cancer in a patient, comprising administering to the patient a composition of claim 29.

32. A method for determining the presence of a cancer in a patient, comprising the steps of:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with an oligonucleotide that hybridizes to a polynucleotide sequence according to claim 21 under moderately stringent conditions;
- (c) detecting in the sample an amount of said polynucleotide that hybridizes to the oligonucleotide; and
- (d) comparing the amount of said polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence of the cancer in the patient.

33. An O772 polypeptide comprising at least an antibody epitope sequence set forth in any one of SEQ ID NOs: 490-511.

34. An O8E polypeptide comprising at least an antibody epitope sequence set forth in any one of SEQ ID NOs: 394-415.

35. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a polypeptide of claim 1.

1/101

11729.1 contg

TTAGAGAGGCACAGAAGGAAGAAGAGTTAAAAGCAGCAAAGCCGGGTTTTTTGTTTTGTTTTGTTTTGTTTTG
TTTTGAGATGGAGTCTCACTCTGTTGCCCAAGCTGGAGTACAACGGCATGATCTCAGCTCGCTGCAACCTCCGC
CTCCACGTTCAAGTGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGCGCCCGCCACCACGCTCA
GCTAATTTTTTTGTAATTTTAGTAGAGACAGGGTTTCACCAGGTTGGCCAGGCTGCTCTTGAATCCTGACCT
CAGGTGATCCACCCGCTCGGCCTCCCAAGTGCTGGGATTACAGGCGTGAGCCACCACGCCCGGCCCCCAAAG
CTGTTTCTTTTGCTTTAGCGTAAAGCTCTCCTGCCATGCAGTATCTACATAACTGACGTGACTGCCAGCAAGC
TCAGTCACTCCGTGGTC

11729-45.21.21.cons1

TAGGATGTGTTGGACCCTCTGTGTCAAAAAAACCTCACAAAGAATCCCTGCTCATTACAGAAGAAGATGCAT
TAAAAATATGGGTATTTTCACTTTTTATCTGAGGACAAGTATCCATTAATTATTGTGTGAGAAGAGATTGAA
TACCTGCTTAAGAAGCTTACAGAAGCTATGGGAGGAGGTTGGCAGCAAGAACAATTTGAACATTATAAAATCAA
CTTTGATGACAGTAAAAATGGCCTTTCTGCATGGGAACTTATTGAGCTTATTGGAAATGGACAGTTTAGCAAAG
GCATGGACCGGCAGACTGTGTCTATGGCAATTAATGAAGTCTTTAATGAATTAATTAGATGTGTTAAAGCAG
GGTTACATGATGAAAAAGGGCCACAGACGGAAAACTGGACTGAAAGATGGTTTGTACTAAACCCCAACATAAT
TTCTTACTATGTGAGTGAGGATCTGAAGGATAAGAAAGGAGACATTCTCTTGATGAAAATTGCTGTGTAGAGT
CCTTGCTGACAAAGATGGAAA

11729-45.21.21.cons2

TTAGAGAGGCACAGAAGGAAGAAGAGTTAAAAGCAGCAAAGCCGGGTTTTTTGTTTTGTTTTGTTTTGTTTTG
TTTTGAGATGGAGTCTCACTCTGTTGCCCAAGCTGGAGTACAACGGCATGATCTCAGCTCGCTGCAACCTCCGC
CTCCACGTTCAAGTGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGCGCCCGCCACCACGCTCA
GCTAATTTTTTTGTAATTTTAGTAGAGACAGGGTTTCACCAGGTTGGCCAGGCTGCTCTTGAATCCTGACCT
CAGGTGATCCACCCGCTCGGCCTCCCAAGTGCTGGGATTACAGGCGTGAGCCACCACGCCCGGCCCCCAAAG
CTGTTTCTTTTGCTTTAGCGTAAAGCTCTCCTGCCATGCAGTATCTACATAACTGACGTGACTGCCAGCAAGC
TCAGTCACTCCGTGGTC

11731.1contig

TCTTTTCTTTCGATTTCTTCAATTTGTCAGGTTTGATTTTATGAAGTTGTTCAAGGGCTAACTGCTGTGTAT
TATAGCTTTCTCTGAGTTCCTTCAGCTGATTGTTAAATGAATCCATTTCTGAGAGCTTAGATGCAGTTTCTTTT
TCAAGAGCATCTAATTGTTCTTTAAGTCTTTGGCATAATCTTCTTTTCTGATGACTTTTTATGAAGTAACT
GATCCCTGAATCAGGTGTGTTACTGAGCTGCATGTTTTAATCTTTCTGTTAATAGCTGCTTCTCAGGGACCA
GATAGATAAGCTTATTTGATATTCTTAAGCTCTTGTGAAGTTGTTTGATTTCATAATTTCCAGGTACAC
TGTTTATCCAAAATCTTAGCTCAGTCTTTTGTTGTTGCTTTCTGATTGGACATCTTGTAGTCTGCCTGAGAT
CTGCTGATGXTTTCATTCACTGCTCCAGTTCAGGTGGAGACTTXXCTTTCTGGAGCTCAGCCTGACAATGC
CTTCTTGXTCCCT

Fig. 1A

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11731.2contig

AGCCAGATGGCTGAGAGCTGCAAGAAGAAGTCAGGATCATGATGGCTCAGTTTCCACAGCGATGAATGGAGGG
CCAAATATGTGGGCTATTACATCTGAAGAACGTACTAAGCATGATAAACAGTTTGATAACCTCAAACCTTCAGG
AGGTTACATAACAGGTGATCAAGCCCGTACTTTTTCTACAGTCAGGTCTGCCGGCCCCGGTTTTAGCTGAAA
TATGGGCCCTTATCAGATCTGAACAAGGATGGGAAGATGGACCAGCAAGAGTTCTCTATAGCTATGAACTCATC
AAGTTAAAGTTGCAGGGCCAAACAGCTGCCTGTAGTCCTCCTCTATCATGAAACAACCCCTATGTTCTCTCC
ACTAATCTCTGCTCGTTTTGGGATGGGAAGCATGCCCAATCTGTCCATTTCATCAGCCATTGCCTCCAGTTGCAC
CTATAGCAACACCCTTGTCTTCTGCTACTTCAGGGACCAGTATTCCTCCCCTAATGATGCCTGCCCTAGTG
CCTTCTGTTAGTA

11734.1contig

AATAGATTTAATGCAGAGTGTCAACTTCAATTGATTGATAGTGGCTGCCTAGAGTGCTGTGTTGAGTAGGTTTC
TGAGGATGCACCTGGCTTGAAGAGAAAGACTGGCAGGATTAACAATATCTAAAATCTCACTTGTAGGAGAAAC
CACAGGCACCAGAGCTGCCACTGGTGTGGCACCAGCTCCACCAAGGCCAGCGAAGAGCCCAAATGTGAGAGTG
GCGGTCAAGCTGGCACCAGCACTGAAGCCACCCTGGTGTGGCAGTGGCACTGGCACTGTTATTGGTACTGGT
ACTGGCACCAGTGGTGGCACTGCCACTCTCTGGGCTTTGGCTTTAGCTTCTGCTCCCGCTGGATCCGGGCTT
TGGCCAGGGTCCGATATCAGCTTCGTCCAGTTGCAGGGCCCGGCAGCATTCTCCGAGCCGAGCCCAATGCC
ATTGAGCTCTAATCTCGGCCCTAGCCTTGGCTTCAGCTGCAGCCTCAGCTGCAGCCTTCAAATCCGCTTCCAT
CGCTCTCGGTAC

11734.2contig

GCCAAGAAAGCCCSAAAGGTGAAGCATCTGGATGGGAAGAGGATGGCAGCAGTGATCAGAGTCAGGCTTCTGG
AACCACAGGTGGCCGAAGGGTCTCAAAGGCCCTAATGGCCTCAATGGCCCGCAGGGCTTCAAGGGGTCCCATAG
CCTTTTGGGCCCGCAGGGCATCAAGGACTCGGTTGGCTGCTTGGGCCCGGAGAGCCTTGCTCTCCCTGAGATCA
CCTAAAGCCCGTAGGGGCAAGGCTCGCCGTAGAGCTGCCAAGCTCCAGTCATCCCAAGAGCCTGAAGCACCACC
ACCTCGGATGTGGCCCTTTTGAAGGAGGGCAATGATTTGGTGAAGTACCTTTTGGCTAAAGACCAGACGA
AGATTCCCATCAAGCGCTCGGACATGCTGAAGGACATCATCAAGAATACACTGATGTGTACCCCGAAATCATT
GAACGAGCAGGCTATTCTTGGAGAAGGTATTTGGGATTCAATTGAAGGAAATTGATAAGAATGACCCTTGTA
CATTTCTCTCAGC

11736.1contg

GAGGTCTCACTATGTTGCCAGGCTGTTCTTGAACCTCCTGGGATCAAGCAATCCACCCATGTTGGTCTCCAAA
GTGCTGGGATCATAGCGTGAGCCACCTCACCCAGCCACCAATTTCAATCAGGAAGACTTTTTCTTCTTCAA
GAAGTGAAGGGTTTCCAGAGTATAGCTACACTATTGCTTGCCCTGAGGGTGACTACAAAATTGCTTGCTAAAAGG
TTAGGATGGGTAAAGAATTAGATTTTCTGAATGCAAAAATAAATGTGAATAATGAACCTTAGGTAATACATA
TTCATAAAATAATTATTCACATATTTCTGATTTATCACAGAAATAATGTATGAAATGCTTTGAGTTTCTTGGG
GTAAACTCCATTACTCATCCCAAGAAACCATATTATAAGTATCACTGATAATAAGAACAACAGGACCTTGTCT
AAATCTGGATAAGAGAAATAGTCTCTGGGTGTTGXTCTTAATTGATAAAATTTACTTGTCATCTTTAGTT
CAGAATCACAAAA

Fig. 1B

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11736.2contig

AAGCGGAAATGAGAAAGGAGGGGAAATCATGTGGTATTGAGCGGAAACTGCTGGATGACAGGGCTCAGTCCCTG
TTGGAGAACTCTGGGTGGTGCTGTAGAACAGGGCCACTCACAGTGGGGTGACAGACCAGCACGGCTCTGTGAC
CTGTTTGTACAGGTCCATGATGAGGTAAACAATACTGAGTATAAGGGTTGGTTAGAACTCTTACAGCAA
TTTGACAAAGTAATCTTCTGTGCACTGAATCTAAGAAAAAATGGGGCTGTATTTGTATGTTCTTTTTTTCA
TTTCATGTTCTGAGTTACCTATTTTTATTGCATTTTACAAAAGCATCCTCCATGAAGGACCGGAAGTTAAAA
CAAAGCAGGTCTTTATCACAGCACTGCTGTAGAACACAGTTCAGAGTTATCCACCAAGGAGCCAGGGAGCTG
GGCTAAACCAAGAATTTTGCTTTTGGTTAATCATCAGGTACTTGAGTTGGAATTGTTTAAATCCCATCATTAC
CAGGCTGGAXGTG

11739-1&2

CCGCGGCTCCTGTCCAGACCCTGACCCTCCCTCCAAGGCTCAACCGTCCCCAACAACCGCCAGCCTTGACT
GATGTCGGCTGCGAGAGCCTGTGCTTAAGTAAGAATCAGGCCTTATTGGAGACATTCAAGCAAAGGTTGGACAA
CTACTTTTCCAGAACAGAAAGGAACTCATGCATCAGAAAAGGTGACTAATAAAGGTACCAGAAGAATATGGCT
GCACAAATACCAGAATCTGATCAGATAAAACAGTTTAAGGAATTTCTGGGGACCTACAATAAACTTACAGAGAC
CTGCTTTTGGACTGTGTTAGAGACTTCACAACAAGAGAAGTAAACCTGAAGAGACCCTGTTTCAAGACATT
GCTTACAGAAATATTTAAAAATGACACAAAGAATATCCATGAGATTTTCAAGGAATATCATATTCAGCAGAAATGAA
GCCCTGGCAGCCAAAGCAGGACTCCTTGGCCAACCCAGATAGAGAAGTCTGATGGATGAAGTTTGTATGAAAG
ATTGCCAACAGCTGCTTTATTGGAATGAGGACTCATCTGATAGAATCCCTGAAAGCAGTAGCCACCATGTTT
AACCATCTGTCTGACTGTTTGGCAAATGGAACCGCTGGAGAAACAAAATTGCTATTTACCAGGAATAATCAC
AATAGAAGGTCTTATTGTTTCAAGTAAATAAAGATGCAACATTTGTTGAGGCCATTGATTGAGCAGCTTGGT
CACTTGATTAGAAAAATAAACCATTGTTTCTTCAATTGTGACTGTTAATTTTAAAGCAACTTATGTGTTTCGATC
ATGTATGAGATAGAAAAATTTTATTACTCAAAGTAAAAATAAATGGA

11740.1.contig

GAAAAAAATATAAACACACTTTTGCSAAAACGGTGGCCCTAAAAGAGGAAAAAGAAATTCACCAATATAAATC
CAATTTTATGAAAACAGCAATTTAATCCAAGAATCACTTTTGTAATGAAGCTAGCAAGTGATGATATGATAA
AATAAACGTGGAGGAAATAAAACACAAGACTTGGCATAAGATATATCCACTTTTGATATTAAGCTTGTGAAGC
ATATTCTTCGACAAATTTGTGAAAGCGTTCCTGATCTTGCTTCTCCATTTCAAATAAGGAGGCATATCACAT
CCCAAGAGTAACAGAAAAAGAAAAAGACATTTTGCATTTTGAGATGAACCAAGACACAAAACAAAACGAAC
AAAGTGTCTATGCTAATTTAGCCTCTGAAATAAACCTTGAACATCTCCTACAAGGCACCGTGATTTTGTAAAT
TCTAACCTGAAGAAATGTGATGACTTTTGTGGACATGAAAATCAGATGAGAAAAGTGTGGTCTTTCCAAGCCT
GAACTCCCCTGAAAACCTTTGCA

Fig. 1C

SUBSTITUTE SHEET (RULE 26)

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11766.1.contig

CTGGGATCATTTCTCTTGATGTCATAAAAGACTCTTCTTCTTCTCTTCATCCTCTTCTTCATCCTCTTCTGTGTA
CAGTGCTGCCGGGTACAACGGCTATCTTTGTCTTTATCCTGAGATGAAGATGATGCTTCTGTTTTCTCCTACCAT
AACTGAAGAAATTCGCTGGAAGTCGTTTGACTGGCTGTTTCTCTGACTTCACCTTCTTTGTCAAACCTGAGTC
TTTTACCTCATGCCCTCAGCTTCCACAGCATCTTCATCTGGATGTTTATTTTTCAAAGGGCTCACTGAGGAA
ACTTCTGATTGAGAGTCGAAGAGTCACTGTGATTTTTCTCCTCATTTTGCTGCAAATTTGCTCTTTGCTGTC
TGTGCTCTCAGGCAACCAATTTGTTGTCATGGGGGTGACAAAGAAACCTTTGGTCGATTAAGTGGCCTGGGTG
TCCCAGGCCCATTTATATTAGACCTCTCAGTATAGCTTGGTGAATTTCCAGGAAACATAACACCATTTCATTCGA
TTTAAACTATTGGAATTGGTTTT

11766.2.contig

GAGGGTTGGTGGTAGCGGCTTGGGGAGGTGCTCGCTCTGTGCGTCTTGCTCTCTCGCACGCTTCCCCGGCTCC
CTTCGTTTTCCCCCCCCGGTGCCTGCGTGCCGGAGTGTTGCGAGGGAGGGGAGGGCGTGGGGGGGTGGGG
GGAGGCGTTCCGGTCCCAAGAGACCCGCGGAGGGAGGGGAGGCTGTGAGGGACTCCGGGAAGCCATGGACGT
CGAGAGGCTCCAGGAGGCGCTGAAAGATTTGAGAAGAGGGGAAAAAGGAAGTTGTCTGTCTGATCAGT
TTCTTTGTATGTAGCCAAGACTGGAGAAACAATGATTGAGTGGTCCAATTTAAAGGCTATTTATTTTCAAA
CTGGAGAAAGTGATGGATGATTCAGAACTTCAGCTCCTGAGCCAAGAGGTCTCCCAACCCTAATGTCGA

11773.2.contig

AAGCAGGCGGCTCCCGGCTCGCAGGGCCGTGCCACCTGCCCGCCCGCCGCTCGCTCGCTCGCCCGCCGCGCC
GCGCTGCCGACCGCCAGCATGCTGCCGAGAGTGGGCTGCCCGCGCTGCCGXTGCCG

11775-1&2

ATCTCTGTATGCCAAATATTTAATAATAATCTTTGAAACAAGTTCAGATGAAATAAAATCAAAGTTTGCAAA
AACGTGAAGATTAACCTAATTGTCAAATATTCCTCATTGCCCAAATCAGTATTTTTTTATTTCTATGCAAAA
GTATGCCCTTCAAAGTCTTAAATGATATATGATATGATACACAAACAGTTTTCAAATAGTAAAGCCAGTCATC
TTGCAATTGTAAGAAATAGGTAAGATTATAAGACACCTTACACACACACACACACACACAGTGTGCACG
CCAATGACAAAAACAATTTGGCCTCTCCTAAATAAGAACATGAAGACCTTAATTGCTGCCAGGAGGGAACA
CTGTGTACCCCTCCCTACAATCCAGGTAGTTTCTTTAATCCAATAGCAAATCTGGGCATATTTGAGAGGAGT
GATTCTGACAGCCACGTTGAAATCCTGTGGGGAACCATTCATGTCCACCCACTGGTGGCCTGAAAAATGCCAA
TAATTTTTCGCTCCCACTTCTGCTGCTGCTCTTCCACATCCTCACATAGACCCAGACCCGCTGGCCCTGGC
TGGGCATCGCATTTGCTGGTAGAGCAAGTCATAGGTCTCGTCTTTGACGTACAGAAGCGATACACCAAATGGC
TGTCGGTCATTGTCATAACCAGAGA

Fig. 1D

SUBSTITUTE SHEET (RULE 26)

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11777.1&2.cons

CAGACGGGGTTTCACTATGTTGGCTAGGCTGGTCTTGAACCTCTGACTTCAGGTGATCTGCCTGCCTTGGCCTC
CCAAAGTGCTGGGATTACAGGCATAAGCCACTGCGCCCGGCTGATCTGATGGTTTCATAAGGCTTTTCCCCCTT
TTGCTCAGCACTTCTCCTTCTGCGCCATGTGAAGAAGGACATGTTTGCTTCCCCTTCCACCACGATTGTAAG
TTGTTTCTGAGGCCTCCCCGGCCATGCTGAACCTGTGAGTCAATTAACCTCTTTCCTTTATAAATTATCCAGT
TTTGGGTATGCTTTATTAGTAGAATGAGAACAGACTAATACAACCCTTAAGGAGACTGACGGAGAGGATTCT
TCCTGGATCCAGCACTTCTCTGAATGCTACTGACATTCTTCTTGAGGACTTTAACTGGGAGATAGAAAACA
GATTCCATGGCTCAGCAGCCTGAGAGCAGGGAGGGAGCCAAGCTATAGATGACATGGGCAGCCTCCCCTGAGGC
CAGGTGTGGCCGAACCTGGGCAGTGTGCGACCCACCCACCCAGGGCCAAGTCTGTCTTGGAGAGCCAAGCC
TCAATCACTGCTAGCCTCAAGTGTCCCAAGCCACAGTGGCTAGGGGACTCAGGGAACAGTCCCAGTCTGCC
CTACTTCTCTTACCTTTACCCTCATACCTCCAAAGTAGACCATGTTTCATGAGGTCCAAAGG

11779.2.contig

AAGCGAGGAAGCCACTGCGGCTCCTGGCTGAAAAGCGGCGCCAGGCTCGGGAACAGAGGGAACGCGAAGAACAG
GAGCGGAAGCTGCAGGCTGAAAGGGACAAGCGAATGCGAGAGGAGCAGTGGCCCGGGAGGCTGAAGCCCGGGC
TGAACGTGAGGCGGAGGCGCGGAGACGGGAGGAGCAGGAGGCTCGAGAGAAGGCGCAGGCTGAGCAGGAGGAGC
AGGAGCGACTGCAGAAGCAGAAAGAGGAAGCGGAGCCGCTCCGGAAGAAGCTGAGCGCCAGCGCCAGGAG
CGGGAAGGCACTTTGAGAAGGAGGAACAGGAGAGACAAGAGCGAAGAAAGCGGCTGGAGGAGATAATGAAGAG
GACTCGGAAATCAGAAGCCGCGGAAACCAAGAAGCAGGATGCAAGGAGACCGCAGCTAACAAATTCGGGCCAG
ACCCTTGTGAAAGCTGTAGAGACTCGGCCCTCTGGGCTTCCAGAAAGGATTCTATTGCAGAAAGGAAGGAGCTX
GGCCCCCAXGGA

11781 & 37.cons

CTCTGTGGAAAAGTATGAGGAATGAATTTACCATTACCCATGTTCTCATCCCCAAGCAAAGTGCTGGGTCTGA
TTACTGCAACACAGAGAACGAAGAAGAACTTTTCTCATACAGGATCAGCAGGGCTCATCACTGGGCTGGA
TTCATACTACCCACACAGACCGGTTTCTCTCCAGTGTGACCTACACACTCACTGCTTTACCAGATGATG
TTGCCAGAGTCAGTAGCCATTGTTTGCTCCCCAAGTTCAGGAACTGGATTCTTTAACTAACTGACCATGG
ACTAGAGGAGATTTCTTCTGTGCGCAGAAAGGATTTATCCACACAGCAAGGATCCACCTCTGTTCTGTAGCT
GCAGCCACGTGACTGTTGTGGACAGAGCAGTGACCATCACAGACCTTCGATGAGCGTTTGAGTCCAACACCTTC
CAAGAACAACAAACCATATCAGTGTACTGTAGCCCTTAATTTAAGCTTTCTAGAAAGCTTTGGAAGTTTTG
TAGATAGTAGAAAGGGGGCATCACXTGAGAAAGAGCTGATTTTGTATTTAGGTTTGAAAGAAATACTGAA
CATATTTTTTAGGCAAGTCAGAAAGAGAACATGGTCACCCAAAAGCAACTGTAACCTCAGAAATTAAGTTACTCA
GAAATTAAGTAGCTCAGAAATTAAGAAAGAAATGGTATAATGAACCCCATATACCCTTCTTCTGGATTACCA
ATTGTTAACTTTTTTCTCTCAGCTATCCTTCTAATTTCTCTAATTTCAATTTGTTTATATTTACCTCTG
GGCTCAATAAGGGCATCTGTGCAGAAATTTGGAAGCCATTTAGAAATCTTTTGATTTTCTGTGTTTATGG
CAATATGAATGAGCTTATTACTGGGTGAGGGACAGCTTACTCCATTTGACCAGATTGTTTGGCTAACACATC
CCGAAGAATGATTTTGTGAGGAATTATTGTTATTTAATAAATATTTAGGATATTTTCTCTACAATAAAGTA
ACAAT

Fig. 1E

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11781-76-87-37

CTCTGTGGAAACTGATGAGGAATGAATTTACCATTACCCATGTTCTCATCCCCAAGCAAAGTGCTGGGTCTGA
TTACTGCAACACAGAGAACGAAGAAGAACTTTTCTCATACAGGATCAGCAGGGCCTCATCACACTGGGCTGGA
TTCTACTACCCACACAGACCGGTTTCTCTCCAGTGTGACCTACACACTCACTGCTCTTACCAGATGATG
TTGCCAGAGTCAGTAGCCATTGTTTGCTCCCCAAGTTCAGGAACTGGATTCTTTAACTAACTGACCATGG
ACTAGAGGAGATTTCTTCTGTGCGCCAGAAAGGATTTTCATCCACACAGCAAGGATCCACCTCTGTTCTGTAGCT
GCAGCCACGTGACTGTTGTGGACAGAGCAGTGACCATCACAGACCTTCGATGAGCGTTTGAGTCCAACACCTTC
CAAGAACAACAAACCATATCAGTGTACTGTAGCCCCCTTAATTTAAGCTTTCTAGAAAGCTTTGGAAGTTTTG
TAGATAGTAGAAAAGGGGGCATCACCTGAGAAAGAGCTGATTTTGATTTTCAGGTTTGAAAAGAAATAACTGAA
CATATTTTTTAGGCAAGTCAGAAAGAGAACATGGTCACCCAAAAGCAACTGTAACCTAGAAATTAAGTTACTCA
GAAATTAAGTAGCTCAGAAATTAAGAAAGAATGGTATAATGAACCCCATATACCCTTCCTTCTGGATTCACCA
ATTGTTAACATTTTTTCTCTCAGCTATCCTTCTAATTTCTCTAATTTCAATTTGTTTATATTTACCTCTG
GGCTCAATAAGGGCATCTGTGCAGAAATTTGGAAGCCATTTAGAAAATCTTTTGGATTTTCTGTGTTTATGG
CAATATGAATGGAGCTTATTACTGGGGTGAGGACAGCTTACTCCATTTGACCAGATTGTTTGGCTAACACATC
CCGAAGAATGATTTTGTGAGGAATTATTGTTATTTAATAATATTTTCAAGATATTTTCTCTACAATAAAGTA
ACAATTA

11784-1 & 2

GGACGACAAGGCCATGGCGATATCGGATCCGAATTCAGCCTTTGGAATTAATAAACCTGGAACAGGGAAGGT
GAAAGTTGGAGTGAGATGTCTTCCATATCTATACCTTTGTGCACAGTTGAATGGGAAGCTTTGGGTTTAGGGC
ATCTTAGAGTTGATTGATGGAAAAAGCAGACAGGAAGTGGTGGGAGGTCAAGTGGGAAGTTGGTGAATGTGGA
ATAACTTACCTTTGTGCTCCACTTAAACCAGATGTGTGCAGCTTTCTGACATGCAAGGATCTACTTTAATTC
CACACTCTCATTAATAAATTAATAAAAGGGAATGTTTTGGCACCTGATATAATCTGCCAGGCTATGTGACAGT
AGGAAGGAATGGTTTCCCTAACAAGCCCAATGCACTGGTCTGACTTTATAAATTATTTAATAAATGAAGTAT
TATC

11785.2.contig

GGCAGTGACATTCACCATCATGGGAACCACTTCCCTTTTCTTCAAGATTCTCTGTAGTGAAGAGAGCACCCA
GTGTTGGGCTGAAAACATCTGAAAGTAGGGAGAAGAACCTAAAATAATCAGTATCTCAGAGGGCTCTAAGGTGC
CAAGAAGTCTCACTGGACATTTAAGTGCCAAACAAAGGCATACTTTGGAATCGCCAAGTCAAACTTTCTAAT
TCTGTCTCTCTCAGAGACAAGTGAGACTCAAGAGTCTACTGCTTTAGTGGCAACTACAGAAAAGTGGTGTACC
CAGAAAAACAGGAGCAATTAGAAATGGTTCCAATATTTCAAAGCTCCGCAACAGGATGTGCTTTCTTTGCCC
ATTTAGGGTTTCTTCTTTCTTTCTTTTATTAACT

Fig. 1F

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11718-182 cons

TGCGCTGAAAACAACGGCTCCTTTACTGTAAAAATGCAGCCACAGGTGCTTAGCCGTGGGCATCTCAACCACC
AGCCTCTGTGGGGGGCAGGTGGGCGTCCCTGTGGGCCCTCTGGGCCCAAGTCCAGCCTCTGTCTCTGCCTTCCG
TTCTTCGACAGTGTCCCGGCATCCCTGGTCACTTGGTACTTGGCGTGGGCTCCTGTGCTGCTCCAGCAGCTC
CTCCAGGXGGTCGGCCCGCTTCACCGCAGCCTCATGTTGTGTCCGGAGGCTGCTCACGGCTCCTCCTTCTCG
CGAGGGCTGTCTTCACCTCCGGXGCACCTCCTCCAGCTCCAGCTGCTGGCGGGCTGCAGCGTGGCCAGCTCG
GCCTTGGCCTGCCGCGTCTCCTCCTCARAGGCTGCCAGCGGTCTCGAACTCCTGGCGSATCACCTGGGCCAG
GTTGCTGCGCTCGCTAGAAAGCTGCTCGTTCACCGCTGGCGATCCTCCAGCGCCGCTCCTTCTGCCGCACAA
GGCCCTGCAGACGAGATTCTGCCCTCGGCCTCCCAAGTGGCCCTTCACTCCGAGCACCGCTCCTGAAGC
TTCCGCTCCGACTGCTCCAGCTCGGAGAGCTCGGCCTCGTACTTGTCCGTAAGCGCTTGATGCGGCTCTCGGC
AGCCTTCTCACTCTCCTTGGCCAGGCCATGTGGCCTCCAGCGGTGAATGACCAGCTCAATCTCCTTGT
CCCGGCTTTCGGATTCTTCCCTCAGCTCCTGTTCCCGTTCCAGCAGCCAGCCTCCTCCTTCTGCTGCGG
CGGCCTCCACGCTGCCCTCTCCAGCTCCAGCTGCTGCTTCAGGTATTAGCTCCATCTGGCGGGCTGCAG
CGTGGCCA

13690.4

CAACTTATTACTTGAAATTATAATATAGCCTGTCCGTTTGCTGTTCCAGGCTGTGATATATTTTCTAGTGGT
TTGACTTTAAAAATAAATAAGGTTAATTTTCTCCCC

13693.1

TGCAAGTCACGGGAGTTTATTTATTTAATTTTTTTTCCCAGATGGAGACTCTGTGCGCCAGGCTGGAGTGCAAT
GGTGTGATCTTGGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCACAGCCTCCCGAGTAGC
TGGGATTACAGGTGCCCGCCACACCCAGCTAATTTTATTTTTAGTAAAGACAGGGTTTCCCATGTTG
GCCAGGCTGGTCTTGAACCTTGACCTCAGGTGATCCACCTGCTCGGCCTCCCAAAGTGTGGGATTACAGGC
GTGAGCTACCGTGCCTGGCCAGCCACTGGAGTTAAAGGACAGTCATGTTGCTCCAGCCTAAGGCGGCATTT
TCCCCATCAGAAAGCCCGGGCTCCTGTACCTCAAATAGGACCTGTAAAGTCAGTCAGTGAAGTCTCTGC
CTAACTGGCCACCCGGGGCATTGGCNTCTGACACAGCCTTGCCAGGANGCCTGCATCTGCAAAAGAAAAGTT
CACTTCCTTTCCG

13694.1

CAGAGAATCTKAGAAAGATGTCGCGTTTTCTTTTAAATGAATGAGAGAAGCCATTTGTATCCCTGAATCATTGA
GAAAAGGCGGGTGGCGACAGCGGCGACCTAGGGATCGATCTGGAGGGACTTGGGGAGCGTGCAGAGACCTCT
AGCTCGAGCGCGAGGGACCTCCCGCCGGGATGCCCTGGGGAGCAGATGGACCCTACTGGAAGTCAGTTGGATTCA
GATTTCTCTCAGCAAGATACTCCTTGCCTGATAATTGAAGATTCTCAGCCTGAAAGCCAGGTTCTAGAGGATGA
TTCTGGTTCTCACTTCAGTATGCTATCTCGACACCTTCTTAATCTCCAGACGCACAAAGAAAATCCTGTGTTGG
ATGTTGNGTCCAATCCTTGAACAAACAGCTGGAGAAGAACGAGGAGACCGGTAATAGTGGGTTCAATGAACATT
TGAAAGAAAACCAGGTTGCAGACCCTG

Fig. 1G

SUBSTITUTE SHEET (RULE 26)

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13694.2

GACTGTCTGAACAAGGGACCTCTGACCAGAGAGCTGCAGGAGATGCAGAGTGGTGGCAGGAGTGGAAGCCAAA
GAACACCCACCTTCTCCCTTGAAGGAGTAGAGCAACCATCAGAAGATACTGTTTTATTGCTCTGGTCAAACAA
GTCTTCCTGAGTTGACAAAACCTCAGGCTCTGGTGACTTCTGAATCTGCAGTCCACTTTCATAAGTTCTTG
CAGACAACGTGTTCTTTGCTTCATAGCAGCAACAGATGCTTTGGGGCTAAAAGGCATGTCCTCTGACCTTGCA
GGTGGTGGATTTGCTCTTTTACAACATGTACATCCTTACTGGGCTGTGCTGTACAGGATGTCCTTGCTGGA
CTGTTCTGCTATGGGATATCTTCGTTGGACTGTTCTTCATGCTTAATTGCAGTATTAGCATCCACATCAGAÇA
GCCTGGTATAACCAGAGTTGGTGGTTACTGATTGTAGCTGCTCTTTGTCCACTTCATATGGCACAAGTATTTTC
CTCAACATCCTGECTCTGGGAAG

13695.1

GAAATGTATATTTAATCATTCTCTTGAACGATCAGAACTCTRAATCAGTTTTCTATAACARCATGTAATACAG
TCACCGTGGCTCCAAGGTCAGGAAGGCAGTGGTTAACACATGAAGAGTGTGGGAAGGGGGCTGGAACAAAGT
ATTCTTTTCCTTCAAAGCTTCATTCTCAAGGCCTCAATTCAGCAGTCAATTGCTTCTGCTTTCAAAGTCTGT
GTGTGCTTCATGGAAGGTATATGTTGTTGCTTAAATTTGAATGTGGCCAGGAAGGTCTGGAGATCTAAATT
CAGAGTAAGAAAACCTGAGCTAGAACTCAGGCATTTCTCTTACAGAACTTGGCTTGCAGGGTAGAATGAANGGA
AAGAACTTAGAAGCTCAACAAGCTGAAGATAATCCCATCAGGCATTTCCCATAGGCCTTGCAACTCTGTTAC
TGAGAGATGTTATCCTG

13695.2

AGTCTGGAGTGAGCAACAAGAGCAAGAAACAARRAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAA
ATCTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTCTGTGAACTAGACAAGTGTGTTAAGAGTGATAA
GTAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCTGTCACCTGGGGAGTGAGA
GGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTGTAATGTTGCTCTGAGGAAGCCCC
TGGAAGTCTATCCCAACATATCCACATCTTATATCCACAAATTAAGCTGTAGTATGTACCCTAAGACGCTGC
TAATTGACTGCCACTTCGCAACTCAGGGGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATG
CTTCCCAAGGTGCCTTGGCTTCTTCCCACTGACAAATGCCCAAGTTGAGAAAAATGATCATAATTTTAGCA
AAACCGAGCAATCGGCGACCCC

13697.1

TAGCTGTCTTCCTCACTCTTATGGCAATGACCCATATCTTAATGGATTAAGATAATGAAAGTGATTTCTTAC
ACTCTGTATCTATCACCAGAAGCTGAGGTGATAGCCCGCTTGTCATTGTTCATCCATATTCTGGGACTCAGGCGG
GAACTTTCTGGAATATTGCCAGGGAGCATGGCAGAGGGGCACAGTGCATTCTGGGGGAATGCACATTGGCTCAG
CCTGGGTAATGAGTGATATACATTACCTCTGTTCACTCACTTATGCCCAGCACCAGTCAAGGCCCCACCAA
TACCAGAGCCCAAGAAATGATGCTGTTGATATGTTTTGCTGTGTCCCAACCCAAATCTCATCTTGAATTGT
AAGCTCCATAATTCCCATGTGTTGTGGGAGGGACCTGGTG

Fig. 1H

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13697.2

ATCATGAGGATGTTACCAAAGGGATGGTACTAAACCATTGTATTGCTGTGTTTCACACTGCTTTGAAGATAC
TACCTGAGACTGGGTAATTTATAAACAAAAGAGATTAAATTGACTCACAGTTCTGCATGGCTGAAGAGGGCTCA
GGAACTTACAGTCATGGTGAAGGCAAAGGAGGAGCAAGGCATGTCTTACATGTCAGTAGGAGAGAGAGCGAG
AGCAGGAGAACCTGCCACTTATAAACCATTCAGATCTCATAACTCCCTATCATGAGAAAAACATGGAGGAAACC
ACCCTCATGATCCAATCACCTCCCGCCAGGTCCCTCCCTCGACACGTGGGGATTATAATTGAGGATTAGAGGGA
CACAGAGACAAACCATATCATCATTATGAGAAATCCACCCTCATAGTCCAATCAGCTCCTACCAGGCCCCACC
TCCAACACTGGGGATTGCAATTCAACATGAGATTGGATGGGGACACAGATTCAAACCATATCATAC

13699.1&2

CATGGCCTTTCTCCTTAGAGGCCAGAGGTGCTGCCCTGGCTGGGAGTGAAGCTCCAGGCACTACCAGCTTTCTT
GATTTTCCCGTTTGGTCCATGTGAAGAGCTACCACGAGCCCCAGCCTCACAGTGTCCACTCAAGGGCAGCTTGG
TCCTCTTGTCTGCAGAGGCAGGCTGGTGTGACCTGGGAACTTGACCGGGGAACAACAGGTGGCCAGAGTGA
GTGTGGCCTGGCCCCCAACCTAGTGTCCGTCCCTCTCTCTGAGGCCAGTCTTGAGTTAAAGGCATTAAG
TGTTAGATACAAGCTCCTTGTGGCTGGAAAAACCCCTCTGCTGATAAAGCTCAGGGGGCACTGAGGAAGCAG
AGGCCCTTGGGGGTGCCCTCCTGAAGAGAGCGTCAGGCCATCAGCTCTGTCCCTCTGGTGTCCCACGTCTGT
TCCTCACCCCTCCATCTCTGGGAGCAGCTGCACCTGACTGGCCACGCGGGGGCAGTGGAGGCACAGGCTCAGGT
GGCCGGGCTACCTGGCACCCTATGGCTTACAAAGTAGAGTTGGCCAGTTTCTTCCACCTGAGGGGAGCACTC
TGACTCCTAACAGTCTTCTTGGCTGCCATCATCTGGGGTGGCTGGCTGTCAAGAAAGGCCGGGCATGCTTTC
TAAACACAGCCACAGGAGGCTTGTAGGGCATCTTCCAGGTGGGGAAACAGTCTTAGATAAGTAAGGTGACTTGC
CTAAGGCCTCCAGCACCTTGATCTTGGAGTCTCACAGCAGACTGCATGTSAACTGGAACCGAAAAACATG
CCTCAGTATAAAA

13703.3

CCAGAACCTCCTTCTCTTTGGAGAATGGGGAGGCCCTTGGAGACACAGAGGTTTCACCTTGGATGACCTCTA
GAGAAATTGCCAAGAAGCCACCTTCTGGTCCCAACCTGCAGACCCACAGCAGTCAGTTGGTCAGGCCCTGC
TGTAAGAGTCACTTGGCTCCATTGCCTGCTTCCAACCAATGGGCAGGAGAGAAGGCCCTTATTTCTGCCCCAC
CATTCTCCTGTACCAGCACCTCCGTTTTAGTCAAGYGTGTCCAGCAACGGTACCCTTACACAGTCA

13705.1

TGCATGTAGTTTTATTTATGTGTTTTSGTCTGGAAAACCAAGTGTCCAGCAGCATGACTGAACATCACTCACT
TCCCCTACTTGATCTACAAGGCCAACGCCGAGAGCCAGACCAGGATTCAAACACACTGCACGAGAATATTGT
GGATCCGCTGTGAGGTAAGTGTCCGTCACTGACCCARACGCTGTACGTGGCACATGACTGTACAGTGCCACGT
AACAGCACTGTACTTTTCTCCATGAACAGTTACCTGCCATGTATCTACATGATTGAGAACATTTTGACAGTT
AATTCTGACACTTGAATAATCCCATCAAAAACCGTAAATCACTTTGATGTTTGAACGACAACATAGCATCAC
TTTACGACAGAATCATCTGGAAAAACAGAACGAATACATACATCTTAAAAATGCTGGGGTGGGCCAGGCA
CAGCTTACGCCTGTAATCCAGCACTTTGGGAGGCTTAAGCGGGTG

Fig. 11

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13705.2

TGGGGCGGAAAGAAGCCAAGGCCAAGGAGCTGGTGCGGCAGCTGCAGCTGGAGGCCGAGGAGCAGAGGAAGCAG
AAGAAGCGGCAGAGTGTGTGCGGCCTGCACAGATACCTTCACTTGCTGGATGGAAATGAAAATTACCCGTGTCT
TGTGGATGCAGACGGTGATGTGATTTCCCTCCACCAATAACCAACAGTGAGAAGACAAAGGTTAAGAAAACGA
CTTCTGATTTGTTTTGGAAGTAACAAGTGCCACCAGTCTGCAGATTTGCAAGGATGTCATGGATGCCCTCATT
CTGAAAATGGCAAGAAATGAAAAAGTACACTTTAGAAAATAAAGAGGAAGGATCACTCTCAGATACTGAAGCCG
ATGCAGTCTCTGGACAACCTCCAGATCCACAAACGAATCCAGTGCTGGAAGGACGGGCCCTTCTTCTGGTG
GTGGAACANGTCCCGGTGGTGATCTTGAANGGAACCTGAANGTGGTGTACCCCGTCCAAGGCCGACCTTGGC
CAC

13707.4

TCCCGCGCTCGCAGGGCNCGTGCCACCTGCCYGTCCGCCGCTCGCTCGCTCGCCCGCCGCGCCGCGCTGCCGA
CCGYCAGCATGCTGCCGAGAGTGGGTGCCCGCGCTGCCGCTGCCGCGCCGCGCGCTGCTGCCGCTGCTGCCG
CTGCTGCTGCTGC

13708.1&2

GGCGGGTAGGCATGGAAGTGAAGAAGCAAGAAGCTTTCAGACTACGTGGGGAAGAATGAAAAACCAAAT
ATCGCCAAGATTAGCAAGGGGACAGGGAGCTCCAGCCGAGAGCCTATTATTAGCAGTGAGGAGCAGAAGCA
GCTGATGCTGTACTATCACAGAAGACAAGAGGAGCTCAAGAGATTGGAAGAAAATGATGATGATGCCTATTTAA
ACTCACCATGGGCGGATAACACTGCTTTGAAAAGACATTTTCATGGAGTGAAAGACATAAAGTGGAGACCAAGA
TGAAGTTCACCAGCTGATGACACTTCAAAGAGATTAGCTCACCT

13709.1

TCTGAAGGTTAAATGTTTCATCTAAATAGGGATAATGRTAAACACCTATAGCATAGAGTTGTTTGAGATTAAAT
GAGATAATACATGTAAAATTATGTGCTGGCATAACAGCAAGATTGTTGTTGTTGTTGATGATGATGATGATGAT
GATAATATTTTCTATCCCACTGCACAACCTGCTTGAACCTATTAGATAATCAATACATGTTTCTTGAAGTGA
ATCAATTTCCCATGTTGTCTGACTGATGAAGCCCTACATTTTCTTAGAGGAGATGACATTTGAGCAAGATC
TTAAAGAAAATCAGATGCCTTCACTGACCACTGCTTGGTGATCCCATGGCACTTTGTACATCTCTCCATTAGC
TCTCATCTCACCAGCCCATCATTATTGTATGTGCTGCTTCTGAAGCTTGCAAGCTGGCTACCATCMGGTAGAAT
AAAAATCATCTTTCATAAAATAGTGACCTCCTTTTTTATTGCAATTTCCAAAGCCAAGCACCGTGGGANGG
TAG

Fig. 1J

SUBSTITUTE SHEET (RULE 26)

11/101

13709.2

TATGAAGAAGGAAAAGAAGATAATTTGTGAAAGAAATGGGTCCAGTTACTAGTCTTTGAAAAGGGTCAGTCTG
TAGCTCTTCTTAATGAGAATAGGCAGCTTTTCAGTTGCTCAGGGTCAGATTTCTTAGTGGTGTATCTAATCACA
GGAAACATCTGTGGTTCCCTCCAGTCTCTTTCTGGGGGACTTGGGCCACTTCTCATTTTCAATTAATTAGAGGA
AATAGAAGCTCAAAGTACAATTTACTGTTGTTTAAACAATGCCACAAAGACATGGTTGGGAGCTATTTCTTGATTT
GTGTAAGTGTCTGTTTGTGTGCTCATAATGGTTCCAAAATTTGGGTGCTGGCCAAAGAGAGATACTGTTACA
GAAGCCAGCAAGAAGACCTCTGTTTCATTACACCCCCGGGGATATCAGGAATTGACTCCAGTGTGTGCAATCC
AGTTTGGCCTATCTTCT

13712.1&2

TGAGGGACTGATTGGTTTGCTCTCTGCTATTCAATCCCCAAGCCCACTTGTTCTGCAGCGTCTCCTTCTCA
TTCCCTTTAGTTGTACCTCTCTTTCATCTGAGACCTTCTTCTTGATGTCGCCCTTTCTTCTTGTCTTTT
TCTGATGTTCTGCTCAGCATGTTCTGGGTGCTTCTCATCTGCATCATCTTTCAGATGCTGTAGCTTCTTCT
CCTCTTCTGCTCCTTTCTTTTCTTTTCTTTTGGGGGGCTTGCTCTGACTGCAGTTGAGGGGCCCAAGG
TCTTGGCTTTGAGACGAGCCAGGAAGGCTGCTCTGGGGCTTAGGCSAGCAAGCTTGGCCTTCATTGTGAT
CCCAAGACGGGCAGCCTTGTGTGCTGTTGCGCCCTCACAGGCTTGAGAGCAGCATCTCATAGTCAGAATCTTTG
GGGACTTGGACCCCTGGTGTGCTCATCTGCAGCTCTCCAAGTCTTTGTTGGCTTCTCTCCACCTGAAGTC
AATGTAGCCATCTTCACAAACCTTCTGATACAGCAAGTTGGGCTTGGGATGATTATAACGGGTGGTCTCCTTAGA
AAGGCTCCTTATCTGTACTCCATCCTGCCAGTTTCCACTACCAAGTTGGCCGAGTCTTGTGAAGAGCTCAT
TCCACCAAGTGGTTGTGAAGTCTTGGCAGGGTCATGTCTACCCCATGAGTGTCTTGTTCAGYGTACCCCTG
AGAGCCTGAGTGATACCATCTCCTTCCG

13714.1&2

GACAACATGAAATAAATCCTAGAGGACAAAATTAACCTCAATAGAGTGTAGTCTAGTTAAAACTCGAAAAATG
AGCAAGTCTGGTGGGAGTGGAGGAAGGGCTATACTATAAATCCAAGTGGGCTCCTGATCTTAACAAGCCATGC
TCATTATACACATCTCTGAAGTGGACATACCACTTTACGCAAGAAACAGGGCTTGAAGTCTTAAGGGAAAT
AACATGCAGCACCCACATCTAACCTACCTGCCGGGTAGGTACCATCCTGCTTGGCTGAATCAGTGCTC

13716.1&2

TTGGAATTAATAAACCTGGAACAGGGAAGGTGAAAGTTGGAGTGAGATGTCTTCATATCTATACCTTTGTGC
ACAGTTGAATGGGAAGTGTGGGTTAGGGCATCTTAGAGTTGATTGATGGAAGGAGACAAGAACTGGTG
GGAGGTCAAGTGGGGAAGTTGGTGAATGTGGAATAACTTACCTTTGTGCTCCACTTAAACAGATGTGTTGCAG
CTTCTGACATGCAAGGATCTACTTTAATCCACTCTCATTATAAATTAATAAAAGGGAATGTTTGGC
ACCTGATATAATCTGCCAGGCTATGTGACAGTAGGAAGGAATGTTTCCCTAACAGCCCAATGCACTGGTCT
GACTTTATAAATTATTTAATAAAATGAATATTATC

Fig. 1K

12/101

13718.2

AAACTGGACCTGCAACAGGGACATGAATTTACTGCGGGTCTGAGCAAGCTCAGCCCTCTACCTCAGGGCCCC
ACAGCCATGACTACCTCCCCAGGAGCGGGAGGGTGAAGGGGGCCTGTCTCTGCAAGTGGAGCCAGAGTGGAGG
AATGAGCTCTGAAGACACAGCACCCAGCCTTCTCGCACCAGCCAAGCCTTAAGTGCCTGCCTGACCCTGAACCA
GAACCCAGCTGAAGTGCCTTCCAAGGGACAGGAAGGCTGGGGGAGGGAGTTTACAACCAAGCCATTCCACCC
CCTCCCTGCTGGGGAGAATGACACATCAAGCTGCTAACAAATTGGGGGAAGGGGAAGGAAGAACTCTGAAAA
CAAAATCTTGT

13722.3

CATGCGTTTCACCACTGTTGGCCAGGCTGGTCTCGAACTCCTGGCCTCAAGCAATCCACCCGCCTCAGCCTCCA
AAAGTGCTGGGATTACAGATGTGAGCCATGGCACCATGCCAAAAGGCTATATTCCTGGCTCTGTGTTCCGAGA
CTGCTTTTAAATCCCACTTCTCTACATTTAGATTAAAAAATATTTTATTCATGGTCAATCTGGAACATAATTAC
TGCACTTAAGTTTCCACTGATGTATATAGAAGGCTAAAGGCACAATTTTATCAAATCTAGTAGAGTAACCAA
ACATAAAATCATTAAATTAATTTCAACTTAATACTAATTGACATTCCTCAAAAGAGCTGTTTCAATCCTGATA
GGTCTTTATTTTCAAATATATTTGCCATGGGATGCTAATTTGCAATAAGGCGCATAATGAGAATACCCCA
AACTGGA

13722.4

GTTGGACCCCCAGGGACTGGAAGACACTTCTTGCCCGAGCTGTGGCGGGAGAAGCTGATGTTCTTTTTATTA
TGCTTCTGGATCCGAATTTGATGAGATGTTTGTGGGTGTGGGAGCCAGCCGTATCAGAAATCTTTTAGGGAAG
CAAAGGCGAATGCTCCTTGTTATATTTATTTGATGAATTAGATTCTGTTGGTGGGAAGAGAATTGAATCTCCA
ATGCACTCCATATTCAAGGCAGACCATAAATCAACTTCTTGCTGAAATGGATGGTTTTAAACCCAATCAAGGAGT
TATCATAATAGGAGCCACAACTTCCAGAGGCATTAGATAATGCCTTAATACCGTCTGGTCTGTTTTGACATG
CAAGTTACAGTTCCAAGGCCAGATGTAAAAGGTCGAACAGAAATTTGAAATGGTATCTCAATAAAATAAAGTT
TGATCAATCCCGTTGATCCAGAAATTATAGCTCGAGGTACTGGTGGCTTTTCCGGAAGCAGAGTTGGGAGAAT
CTT

13724-13698-13748

GCCTACAACATCCAGAAAGAGTCTACCTGCACCTGGTGTCTCGTCTCAGAGGTGGGATGCAGATCTTCGTGAA
GACCTGACTGGTAAGACCATCACTCTCGAAGTGGAGCCAGTGACACCATYGAGAAGCTCAAAGCAAAGATCC
ARGACAAGGAAGGCRTYCCTCCTGACCAGCAGAGTTGATCTTTGCCGGAAGCAGCTGGAAGATGGDCGCACC
CTGTCTGACTACAACATCCAGAAAGAGTCYACCTGCACCTGGTGTCTCGTCTCAGAGGTGGGATGCARATCTT
CGTGAAGACCCTGACTGGTAAGACCATCACCTCGAGGTGGAGCCAGTGACACCATCGAGAATGTCAAGGCAA
AGATCCAAGATAAGGAAGGCATCCCTCCTGATCAGCAGAGGTTGATCTTTGCTGGGAAACAGCTGGAAGATGGA
CGCACCTGTCTGACTACAACATCCAGAAAGAGTCCACTCTGCACTTGGTCTCGCTTGAGGGGGGTGTCTA
AGTTTCCCTTTTAAAGGTTTCAACAAATTCATTGCACTTTCCTTTCAATAAAGTTGTTGCATTCCC

Fig. 1L

SUBSTITUTE SHEET (RULE 26)

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13730.1

GAAGTGGGCTGAGCCCAAGTCATGCCCTGTGTCCGCATCTGCCGTGTACCTCTGTCCTGCCCTCACCCC
TCCCTCCTGGTCTTCTGAGCCAGCACCATCTCCAAATAGCCTATTCTTCCTGCAAATCACACACATGCGGG
CCACACATACCTGCTGCCCTGGAGATGGGAAGTAGGAGAGATGAATAGAGGCCATACATTGTACAGAAGGAG
GGGCAGGTGCAGATAAAGCAGCAGACCCAGCGGCAGCTGAGGTGCATGGAGCAGGTTGGGGCCGGCATTGGG
CTGAGCACCTGATGGGCCTCATCTCGTGAATCCTCGAGGCAGCGCCACAGCAGAGGAGTTAAGTGGCACCTGGG
CCGAGCAGAGCAGGAGACTGAGGGTCAGAGTGGAGGCTAAGCTGCCCTGGAACCTCAATCTTGCTGCCCTCC
TAGTATGAAGCCCCCTTCTGCCCTACAATTCCTGA

13732.1

ATGGATCTTACTTTGCCACCCAGGTTGGAGTGCAGTGCATCTTGGCTCACTGCAGCCTTAACCTCCAGG
CTCAAGCTATCCTCCTGCCAAAGCCTTCCACATAGCTGGGACTACAGGTACACNGCCACCACACCAGCTAAAA
TTTTTGATTTTTGTAGAGACGGGATCTCGCCACGTTGCCAGGCTGGTCCCATCCTGACCTCAAGCAGATCT
GCCACCTCAGCCCCCAAGCTGCTAGGATTACAGGCGTGAGCCACCGCAGCCTTTGTTTTGCTTTAAT
GGAATCACCAGTTCCTCCGTGTCTCAGCAGCAGCTGTGAGAAATGCTTTGCATCTGTGACCTTTATGAAGGG
GAACCTCCATGCTGAATGAGGGTAGGATTACATGCTCCTGTTTCCGGGGGTCAAGAAAGCCTCAGACTCCAGC
ATGATAAGCAGGGTGAG

13732.2

ATAGGGGCTTTAAGGAGGGAATTCAGGTTCAATGAGGTGTAAGGCCAGGGCTCTTATCCAGTAAGACTGGGGT
CCTTAGATGAGAAAGAGACACCCGAGGTCTTCTCTGCGGTGTGAGGATGCATCAAGAAGGCGGCCGTCTGC
AAGCGAAGGAGAGGCCGACAGAAACCGACCTTCATCTTGACTTGACGCTCTAGAACTGAGAAAAATAAC
TGCTGTTGGTTAAGCCACCCAGTTTGTAGTATTCTTATGCTTCTTAAGCAGACTAACAACAAACACCCA
AAATTAACCTGATGGCTTCGCTGTCTTCTGTAATAATGCTATGAGAGAACTTTCACTCACTGTTTTGAGTTT
CTCCCTCAGTCCCTGGTCTTCTTCTCACATAATCCCAATTTCAATTTATAGTTTCATGGCCAGGCAGAGTCA
TTCATCACGGCATCTCCTGAGCTAAACCAGCACCTGCTCTGCTCACTTCTTGACTGGCTGCTCATCATCAGCCC
TCTTGAGAGATTTCAATTCCTCCGTGCCAGGTACTTCACGCACCAAGCTCA

Fig. 1M

SUBSTITUTE SHEET (RULE 26)

13735.1

13735.2

13736.1

13737.1&2

Fig. 1N

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13738.1

TTTGACTTTAGTAGGGGTCTGAACTATTTATTTTACTTTGCCMGTAATTTARACCYTATATATCTTTCTTA
TGCCATCTTATCTTCTAATGBCAAGGGAACAGWTGCTAAMCTGGCTTCTGCATTWATCACATTAATAATGGCTT
TCTTGGAATCTTCTTGATATGAATAAAGGATCTTTTAVAGCCATCATTTAAAGCMGNTTCTCTCCAACACG
AGTCTGCTASGGGGGGKAGCTGTGAACTCTGGCTGAAGGCTTTCCATACACACTGCAATGACMTGGTTTCT
GACCAGBTGAGTTA

13738.2

AGAGAAGCCCCATAAATGCAATCAGTGTGGGAAGGCCCTTCAGTCAGAGCTCAAGCCTTTTCTCCATCATCGGG
TTCATACTGGAGAGAAACCCTATGTATGTAATGAATGCGGCAGAGCCTTTGGTTTTAACTCTCATCTTACTGAA
CACGTAAGGATTCACACAGGAGAAAAACCCATGTTTTGTAATGAGTGCGGCAAAGCCTTTCTCGGAGTTCCAC
TCTTGTTGAGCATCGAAGAGTTCACACTGGGGAGAAGCCCTACAGTGCGTTGAATGTGGGAAAGCTTTGAGCC
AGAGCTCCAGCTCACCTACATCAGCCGAGTTCACACTGGAGAGAAGCCCTATGACTGTGGTGACTGTGGGAA
GGCCTTCAGCCGAGGTCAACCTCATTGAGCATCAGAAAGTTCACAGCGGAGAGACTCGTAAGTGCAGAAAAC
ATGGTCCAGCCTTTGTTGATGGCTCCAGCCTCACAGCAGATGGACAGATTCCCACTGGAGAGAAGCACGGCAGA
ACCTTTAACCATGGTGCAAATCTCATTCTGGCTGGACAGTTT

13739.1&2

GAGACAGGGTCTCACTTTGTCAACCCAGGCTGGAATGCAGTGGTGGATCTTACGTAGCTCACTGCAGCCCTGAC
CTCCTGGACTCAAACAATTCTCCTGCCTCAGCCCTGCAAGTAGCTGGGACTGTGGGTGCATGCCACCATGCCCTG
GCTAACTTTTGTAGTTTTGTAAAGATGGGTTTTGCCATGTTGCATGCTGGTCTTGAATCCTGAGCTCAA
ACGATCTGCCACCTCGGCCCTCCAGAATGTTGGGATTACAGGGGTAACCAACACGCTGGCCCCATTAGGGT
ATTCTTAGCATCCACTTGCTCACTGAGATTAATCATAAGAGATGATAAGCACTGGAAGAAAAAATTTTACTA
GGCTTTGGATATTTTTCTTTTTTCACTTTTATACAGAGGATTGGATCTTTAGTTTTCTTTAACTGATAATA
AAACATTGAAAGGAAATAAGTTTACCTGAGATTCACAGAGATAACCGGCATCACTCCCTTGCTCAATTCAGTC
TTTACCACATCAATTATTTTCAAGGTCAGGATAAAGGCCCTTAGTCTGCTTTTGCACATTTTTCTTCCACTTT
TTTGTAAACCTGTTGCCTGACAAATGGAATTGACAGCGTATGCCATGACTATTCCATTGTGAGGCATACGCTG
TCAATTTTTCCACCAATCCCTTGCTCTCTTTGGAGAGATCTTCTATCAGCTAGTCCTTTGGCAAAAGTAATT
GCAACTTCTTCTAGGTATTCTATTGTCCGTTCCACTGGTGGAACCCCTGGGACCAGGACTAAAACCTCCAG

13741.1

ATCTCATATATATATTTCTTCTGACTTTATTTGCTTGCTTCTGNCACGCATTTAAAATATCACAGAGACCAAA
ATAGAGCGGCTTTCTGGTGGAACGCATGGCAGTCACAGGACAAAATACAAAAGTGGGGCTCTGTCTTCTCAT
ACATCATACAATTTTCAAGTATTTTTTATGTACAAAGAGCTACTCTATCTGAAAAAATTTAAAAATAAAT
GAGACAAGATAGTTTATGCATCCTAGGAAGAAAGAAATGGGAAGAAAGAACGGGGCAGTTGGGTACAGATTCTG
TCCCCTGTTCCAGGGACCACTACCTTCTGCCACTGAGTTCCCCACAGCCTCACCCATCATGTACAGGGCA
AGTGCCAGGGTAGGTGGGGACCACTGGAGACAGGAACCAACATACTTTGGCTGGAAGATAAGGAGAAAGT
CTCAGAAACACACTGGTGGGAAGCAATCCACNCGCGGTGCCCCANGAGCTTCCACCTGCTGCTGGCTCCCTG
GGTGGCTTTGGGAACAGCTTGGGCAGGCCCTTTTGGGTGGGGNCCAACCTGGGCCTTTGGGCCGTGTGAAAG

Fig. 10

SUBSTITUTE SHEET (RULE 26)

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13742.1

AAACATTGAGATGGAATGATAGGGTTTCCAGAATCAGGTCCATATTTTAACTAAATGAAAATTATGATTATA
GCCTTCTCAAATACCTGCCATACTTGATATCTCAACCAGAGCTAATTTTACCTCTTTACAAATTAATAAGCAA
GTAAGTGGATCCACAATTTATAACCTGTCAATTTTTCTGTATTAAACCTCTATCATAGTTTAAGCCTATTA
GGGTACTTAATCCTTACAAATAAACAGGTTTAAATCACCTCAATAGGCAACTGCCCTTCTGGTTTTCTTCTTT
GACTAAACAATCTGAATGCTTAAGATTTTCCACTTTGGGTGCTAGCAGTACACAGTGTTACACTCTGTATTCCA
GACTTCTTAAATTATAGAAAAAGGAATGTACACTTTTTGTATTCTTTCTGAGCAGGGCCGGGAGGCAACATCAT
CTACCATGGTAGGGACTTGTATGCATGGACTACTTTA

14351.1

ACTCTGTCGCCAGGCTGGAGCCABTGGMCGGATCTCGACTCCCTGCAAGCTMCGCCTCACAGGWTATGCCA
TTCTCCTGCCTCAGCATCTGGAGTAGCTGGGACTACAGGCGCCAGCCACCATGCCAGCTAATTTTT

14351.2

ACCTTAAAGACATAGGAGAATTTATACTGGGAGAGAAAGCTTACAAATGTAAGGTTTCTGACAAGACTTGGGAG
TGATTCACACCTGGAACAACATACTGGACTTCACACTGGABAGAAACCTTACAAGTGAATGAGTGTGGCAAG
CCTTGGCAAGCAGTCAACACTTATTCACCATCAGGCAATTCA

14354.2

AGTCAGGATCATGATGGCTCAGTTTCCACAGCGATGAATGGAGGGCCAAATATGTGGGCTATTACATCTGAAG
AACGTAAGCATGATAAACAGTTTGATAACCTCAAACCTCAGGAGGTTACATAACAGGTGATCAAGCCCGT
ACTTTTTTCTACAGTCAGGTCTGCCGGCCCCGGTTTTAGCTGAAATATGGGCCTTATCAGATCTGAACAAGGA
TGGGAAGATGGACCAGCAAGAGTTCTCTATAGCTATGAAACTCATCAAGTTAAAGTTGCAGGGCCAACAGCTGC
CTGTAGTCCCTCCCTCTATCATGAAACAACCCCTATGTTCTCTCCACTAATCTCTGCTCGTTTTGGGATGGGA
AGCATGCCCAATCTGTCCATTCATCAGCCATTGCCTCCAGTTGCACCTATAGCAACACCCTTGTCTTCTGCTAC
TTCAGGGACCAGTATTCCTCCCTAATGATGCCTGCT

14354.1

CTTTCGATTTCTTCAATTTGTCACGTTTGATTTTATGAAGTTGTTCAAGGGCTAACTGCTGTGTATTATAGCT
TTCTCTGAGTTCCTTCAGCTGATTGTTAAATGAATCCATTTCTGAGAGCTTAGATGCAGTTTCTTTTTCAAGAG
CATCTAATTGTTCTTAAAGTCTTTGGCATAATTCTTCTTTCTGATGACTTTCTATGAAGTAACTGATCCCT
GAATCAGGTGTGTTACTGAGCTGCATGTTTTAATTCCTTTGTTTAAAGCTGCTTCTCAGGGACCAGATAGAT
AAGCTTATTTTGATATTCCTTAAGCTCTGGTGAAGTTGTTGATTTCCATAATTTCCAGGTCACACTGGTTAT
CCCAAACCTCT

Fig. 1P

SUBSTITUTE SHEET (RULE 26)

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16431.1.2

GTGGAGGTGAAACGGAGGCAAGAAAGGGGGCTACCTCAGGAGCGAGGGACAAAGGGGGCGTGAGGCACCTAGGC
CGCGGCACCCCGCGACAGGAAGCCGTCCTGAACGGGGCTACCGGTAGGGGAAGGGCCCGCTAGTCCTCGCA
GGGCCCCAGAGCTGGAGTCGGCTCCACAGCCCCGGGCGTCGGCTTCTCACTTCTTGACCTCCCGGGGCCCCG.
GGCCTGAGGACTGGCTCGGCGGAGGAGAAGAGGAAACAGACTTGAGCAGCTCCCCGTTGTCTCGCAACTCCAC
TGCCGAGGAACCTCATTTCCTTCCTCGCTCCTTCACCCCCACCTCATGTAGAAAGGTGCTGAAGCGTCCGGA
GGGAAGAAGAACCTGGGCTACCGTCCTGGCCTTCCMCCCCCTTCCCGGGGCGCTTGGTGGGCGTGAGTTGG
GGTTGGGGGGGTGGTGGGGGTTCTTTTGGAGTGCTGGGGAACTTTTTCCCTTCTTCAGGTCAGGGGAAAG
GGAATGCCAATTCAGAGAGACATGGGGCAAGAAGGACGGGAGTGAGGAGCTTCTGGAACTTTGCAGCCGTC
ATCGGGAGGCGGCAGCTTAACAGCAGAGAGCGTACCGCTTGGTATCGAAGCACAAGCGGCATAAGTCCAAAC
ACTCCAAGACATGGGGTTGGTGACCCCGAAGCAGCATCCTGGGCACAGTTATCAVACCTTTGGTGGAGTAT
GATGATATCAGCTCTGATTCCGACACCTTCTCGATGACATGGCCTTCAAAGTAGACCGAAGGGAGAACGACGA
ACGTCGTGGATCAGATCGGAGCGACCGCTGCACAAACATCGTCACCACCAGCAGAGCGTTCCCGGGACTTAC
TAAAAGCTAAACAGACCG

16432-1

GACATGTTTGCTGCAGGGGACCAGAGACAATGGGATTAGCCAGTGCTCACTGTTCTTTATGCTTCCAGAGAGG
ATGGGACAGCTCTCAGGTCAGAATCCAGGCTGAGAAGGCCATGCTGGTTGGGGGCCCCCGAAGCACGGTCCG
GATCCTCCCTGGCATCAGCGTAGACCCGCTGCTCAGGCTTGGGGTACCAAACTCATGCTCTGTACTGTTTTGGC
CCCATGCGGTGAGAGGAAAACCTAGAAAAAGATTGGTCTGCTAAGGAATCAGTGCCCCCTCATCTCCGAT
CCAATGCTGGTGACAACATATTCCTCTCCAGGACACAGACTCGGTGACTCCACACTGGGCTGAGTGGCCTCT
GGAGGCTCGTGGCCTAAGGCAGGGCTCCGTAAGGCTGATCGGCTGAAGTGGGTGGGGTGAGGGTTCTGACCCT
TCGCTTCCCATCCATAACCGCTGTCAATGAGCTCACACTGTGGTCA

16432-2

GATGGCATGGTCGTTGCTAATGTGCTGCTGGGATGGAGCACTTCCTCCTGTGAGCCAGGGGACCCGCTGTC
CCTGGAGCTTGGGGCAAGGAGGGAAGAGTGATACCAGGAAGGTGGGGCTGCAGCCAGGGGCCAGAGTCAGTTCA
GGGAGTGGTCCTCGGCCCTCAAAGCTCCTCGGGGAGTGCTCAGGAGTGATGGTGGCTGGAGTTTGCCCCAAC
TTCCCTGGCCACCCTGGAAGGTGCTGGCTGCTCCAGGCCTTAGGCTGGGCTGATGGGTTTCTCCAGGACACA
AGTATCATTAAAGCCACCCTCTCCTCAGCTTGTGAGGCCGACATGTGGGACAGGCTGTGCTCACAACCCCTC
GCCTGCCCTGCCCTCATCAGGAGGAGCCAGTGGAACCTTCGAAAGCTCCAGCATCTCAGCAGCCCTCAAAA
GTCGTCCTGGGGCAAGCTCTGGTTCTCCTGACTGGAGGTCTCTGGGCTTGGCCTGCTCTCTCTCGC

17184.3

TAAAAAGTGTAACAAAGGTTTATTTAGACTTTCTTCATGCCCCAGATCCAGGATGTCTATGTAAACCGTTAT
CTTACAAAGAAAGCACAATATTTGGTATAAACTAAGTCAGTGACTTGCTTAACTGAAATAGCGTCCATCCAAAA
GTGGGTTTAAAGGTAAAACTACCTGACGATATTGGCGGGATCCTGCAGTTTGGACTGCTTGCCGGGTTTGTCCA
GGGTTCCGGGCTGTTCTTGGCACTCATGGGACAGGCATCCTGCTGCTGTGGGGCCCCGCTGGAGCCCTTA
CGTGAAGCTGAAGGTATCGACCSTAGGGGGCTTAGGGCAGTGGGACCTTCATCCGGAACTAACAAGGTGCGG
GAGAGGCCTCTTGGGCTATGTGGG

Fig. 1Q

SUBSTITUTE SHEET (RULE 26)

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17184.4

CAAGCGTTCCTTTATGGATGTAAATTCAAACAGTCATGCTGAGCCATCCCGGGCTGACAGTCACGTTWAAGACA
CTAGGTCGGGCGCCACAGTGCCACCCAAGGAGAAGAAGAAATTTGGAATTTTCCATGAAGATGTACGGAAATCT
GATGTTGAATATGAAAATGGCCCCAAATGGAATTCAAAAGGTTACCACAGGGGCTGTAAAGACCTAGTGACCC
TCCTAAGTGGGAAAGAGGAATGGAGAATAGTATTTCTGATGCATCAAGAACATCAGAATATAAACTGAGATCA
TAATGAAGGAAAATTCATATCCAATATGAGTTTACTCAGAGACAGTAGAACTATTCCCAGG

17185.1

TAGGAATAACAAATGTTTATTCAGAAATGGATAAGTAATACATAATCACCCCTTCATCTCTTAATGCCCTTCCT
CTCCTTCTGCACAGGAGACACAGATGGGTAACATAGAGGCATGGGAAGTGGAGGAGGACACAGGACTAGCCAC
CACCTTCTCTTCCCGGTCTCCAAGATGACTGCTTATAGAGTGGAGGAGGCAACAGGTCCTCAATGTACCA
GATGGTCACCTATAGCACCAGCTCCAGATGGCCACGTGGTTGCAGCTGCACTCAATGAACTCTGTGACAACCA
GAAGATACCTGCTTTGGGATGAGAGGGAGGATAAAGCCATGCAGGGAGGATATTTACCATCCCTACCCTAAGCA
CAGTGCAAGCAGTGAGCCCCGGCTCCAGTACCTGAAAAACCAAGGCCTACTGNCTTTTGGATGCTCTCTTGG
GCCACG

17188.2

AAGCCTCCTGCCCTGGAATCTGGAGCCCTTGGAGCTGAGCTGGACGGGGCAGGGAGGGGCTGAGAGGCAAGA
CCGTCTCCCTCTGCTGCAGCTGCTTCCCAGCAGCCACTGCTGGGCACAGCAGAAACGCCAGCAGAGAAAATG
GGAGCCGAGAGTCTTAGCCCTGGAGCTGAGGCTGCCCTCTGGGCTGACCCGCTGGCTGTACGTGGCCAGAACTG
GGGTGGCATCTGGCATCCATTTGAGGCCAGGGTGGAGGAAAGGGAGGCCAACAGAGGAAAACCTATTCTGCT
GTGACAACACAGCCCTTGTCCACGCAGCCTAAGTGCAGGGAGCGTGATGAAGTCAGGCAGCCAGTCGGGGAGG
ACGAGGTAACCTCAGCAGCAATGTACCTTGTAGCCTATGCGCTCAATGGCCGGAGGGGCAGCAACCCCCGCA
CACGTACGCCAACAGCAGTGCCCTCTGCAGGCCAACAGAGCGATGATGGACTTGAGCGCCGTGTTT

17190.1

GTTTGGCAGAAGACATGTTTAATAACATTTTCATATTTAAAAATACAGCAACAATTCTCTATCTGTCCACCAT
CTTGCCCTGCCCTTCTGGGGCTGAGGCAGACAAAGGAAAGGTAATGAGGTTAGGGCCCCAGGCGGGCTAAGT
GCTATTGGCCTGCTCCTGCTCAAAGAGAGCCATAGCCAGCTGGGCACGGCCCCCTAGCCCTCCAGGTTGCTGA
GGCGGCAGCGGTGGTAGAGTTCTTCACTGAGCCGTGGGCTGCAGTCTCGCAGGGAGAATTCTGCACCAGCCCT
GGCTCTACGGCCCCGAAAGAGGTGGAGCCCTGAGAACCGGAGGAAAACATCCATCACCTCCAGCCCTCCAGGGC
TTCTCCTCTTCTGGCCTGCCAGTTCACCTGCCAGCCGGGCTCGGGCCGCCAGGTAGTCAGCGTTGTAGAAGC
AGCCCTCCGCAGAAGCCTGCCGGTCAAATCTCCCGCTATAGGAGCCCCCGGAGGGGTGAGCACC

Fig. 1R

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17190.2

CAAGTTGAACGTCAGGCTTGGCAGAGGTGGAGTGTAGATGAAAACAAAGGTGTGATTATGAAGAGGATGTGAGT
CCTTTGGGTGTAGGAGAGAAAGGCTGTTGAGCTTCTATTTCAAGATACTTTTACCTGTGCAAAAAGCACATTTT
CCACCTCCTTCTCATGGCATTGTGTAGGTGAGTATGATTCCTATTCCATCTGCATTTTAGAGGTGAAGAATA
ACGTACAAGGGATTCAGTGATTAGCAAGGGACCCCTCACTAAGTGTGATGGAGTTAGGACAGAGCTCAGCTGT
TTGAATCTCAGAGCCAGGCAGCTGGAGCTGGGTAGGATCCTGGAGCTGGCACTAATGTGAGGTGCATTCCTC
CAACCCAGGCTCAGATCCGGAACCTGACCGTGCTGACCCCGAAGGGGAGGCAGGGCTGAGCTGGCCCGTTGGG
CTCCCTGCTCCTTTCACACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTCACAGAGCAGC

17191.2889.2

TGGCCTGGGCAGGATTGGGAGAGAGGTAGCTACCCGGATGCAGTCCTTTGGGATGAAGACTATAGGGTATGACC
CCATCATTTCCCAGAGGTCTCGGCCTCCTTTGGTGTTGAGCAGCTGCCCCCTGGAGGAGATCTGGCCTCTCTGT
GATTTCACTACTGTGCACACTCCTCTCCTGCCCTCCACGACAGGCTTGCTGAATGACAACACCTTTGCCAGTG
CAAGAAGGGGGTGCGTGTGGTGAAGTGTGCCCGTGGAGGGATCGTGGACGAAGGCGCCCTGCTCCGGGCCCTGC
AGTCTGGCCAGTGTGCCGGGGCTGCACTGGACGTGTTTACGGAAGAGCCGCCACGGGACCGGGCCTTGGTGGAC
CATGAGAATGTATCAGCTGTCCCACTGGGTGCCAGCACCAAGGAGGCTCAGAGCCGCTGTGGGGAGGAAAT
TGCTGTTCAGTTCGTGGACATGGTGAAGGGGAAATCTCTACGGGGGTTGTGAATGCCAGGCCCTT

Fig. 1S

SUBSTITUTE SHEET (RULE 26)

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AGCCAGATGGCTGAGAGCTGCAAGAAGAAGTCAGGATCATGATGGCTCAGTTTCCACAGCGATGAATGGAGGG
CCAAATATGTGGGCTATTACATCTGAAGAACGTACTAAGCATGATAAACAGTTTGATAACCTCAAACCTTCAGG
AGGTTACATAACAGGTGATCAAGCCCGTACTTTTCTACAGTCAGGTCTGCCGGCCCCGGTTTTAGCTGAAA
TATGGGCCTTATCAGATCTGAACAAGGATGGGAAGATGGACCAGCAAGAGTTCTCTATAGCTATGAAACTCATC
AAGTTAAAGTTGCAGGGCCAACAGCTGCCTGTAGTCCCTCCCTCATCATGAAACAACCCCTATGTTCTCTCC
ACTAATCTCTGCTCGTTTTGGGATGGGAAGCATGCCAATCTGTCCATTATCAGCCATTGCTCCAGTTGCAC
CTATAGCAACACCTTGTCTTCTGCTACTTCAGGGACCAGTATTCTCCCTAATGATGCCTGCTCCCTAGTG
CCTTCTGTAGTACATCCTCATTACCAATGGAAGTCCAGTCTCATTGAGCCTTATCCATTCTTATTCTTC
TTCAACATTGCCTCATGCATCATCTTACAGCCTGATGATGGGAGGATTTGGTGGTGCTAGTATCCAGAAGGCCC
AGTCTCTGATTGATTTAGGATCTAGTAGCTCAACTTCTCAACTGCTTCCCTCTCAGGGAAGTCACTAAGACA
GGGACCTCAGAGTGGGCGAGTTCTCAGCCTTCAAGATTAAAGTATCGGCAAAATTTAATAGTCTAGACAAGG
CATGAGCGGATACCTCTCAGGTTTTCAAGCTAGAAATGCCCTTCTCAGTCAAATCTCTCTCAAAGTCAAGTAG
CTACTATTTGAGTCTGGCTGACATCGATGGTGACGGACAGTTGAAAGCTGAAGAATTTATTCTGGCGATGCAC
CTCACTGACATGGCCAAAGCTGGACAGCCACTACCACTGACGTTGCCCTCCGAGCTTGCCCTCCATCTTTCAG
AGGGGAAAGCAAGTTGATTCTGTTAATGGAAGTCTGCCTTCATATCAGAAAAACAAGAAGAAGAGCCTCAGA
AGAAAGTCCAGTTACTTTTGAGGACAAACGGAAAGCCAAGTATGAACGAGGAAACATGGAGCTGGAGAAGCGA
CGCCAGTGTTGATGGAGCAGCAGCAGAGGGAGGCTGAACGCAAGCCAGAAAGAGAAGGAAGAGTGGGAGCG
GAAACAGAGAGAACTGCAAGAGCAAGAATGGAAGAAGCAGCTGGAGTTGGAGAAACGCTTGGAGAAACAGAGAG
AGCTGGAGAGACAGCGGAGGAGAGAGAGGAGAAAGGAGATAGAAAGACGAGAGGCAGCAAAACAGGAGCTTGAG
AGACAACGCCGTTTGAATGGGAAAGACTCCGTCGGCAGGAGCTGCTCAGTCAGAAGACCAGGGAACAAGAAGA
CATTGTGAGGCTGAGCTCCAGAAAGAAAAGTCTCCACCTGGAAGTGAAGCAGTGAATGGAAAACATCAGCAGA
TCTCAGGCAGACTACAAGATGTCCAAATCAGAAAGCAACACAAAAGACTGAGCTAGAAGTTTTGGATAAACAG
TGTGACCTGGAAATTATGGAATCAACAAGTCAACAAGAGCTTAAGGAATATCAAAATAAGCTTATCTATCT
GGTCCCTGAGAAGCAGCTATTAACGAAAGAAATTAACCATGCAGCTCAGTAACACACCTGATTGAGGATCA
GTTTACTTCATAAAAGTCATCAGAAAAGGAAGATTATGCCAAAGACTTAAAGAACATTAGATGCTCTTGAA
AAAGAACTGCATCTAAGCTCTCAGAAATGGATTATTTAACAATCAGCTGAAGGAACTCAGAGAAAGCTATAA
TACACAGCAGTTAGCCCTTGAACAAGTTCATAAAATCAACGTGACAAATTGAAGGAAATCGAAAGAAAAGAT
AGAGCAAAAAAAAAAAAA

Fig. 2A

SUBSTITUTE SHEET (RULE 26)

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ATGGCAGTGACATTACCATCATGGGAACCACTTCCCTTTTCTTCAGGATTCTCTGTAGTGGGAAGAGAGCACC
CAGTGTTGGGCTGAAAACATCTGAAAGTAGGGAGAAGAACCTAAAATAATCAGTATCTCAGAGGGCTCTAAGGT
GCCAAGAAGTCTCACTGGACATTTAAGTGCCAACAAAGGCATACTTTCGGAATCGCCAAGTCAAACTTTCTAA
CTTCTGTCTCTCTCAGAGACAAGTGAGACTCAAGAGTCTACTGCTTTAGTGGCAACTACAGAAAAGTGGTGTTA
CCCAGAAAAACAGGAGCAATTAGAAATGGTTCCAATATTTCAAAGCTCCGCAACAGGATGTGCTTTCCTTTGC
CCATTTAGGGTTTCTTCTTTTCCTTCTCTTTATTAACCACTA

Fig. 2B

SUBSTITUTE SHEET (RULE 26)

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ATATCTAGAAGTCTGGAGTGAGCAACAAGAGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGA
ACAAGATAAATCTATCTTCAAAGACATATTAGAAGTTGGGAAAAATAATTCATGTGAAGTACAGCAAGTGTGTTAA
GAGTGATAAGTAAAAATGCACGTGGAGACAAGTGACATCCCAGATCTCAGGGACCTCCCCCTGCCTGTACCTGG
GGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTAGTTATATGTGCTGTAATGTTGCTCTGA
GGAAGCCCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATCCACAAATTAAGCTGTAGTATGTACCCTA
AGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACCTT
TTTATGATGCTTCCAAAGGTGCCTTGGCTTCTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATA
ATTTTAGCATAAACAGAGCAGTCGGCGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAACAA
ATGCGGGTTTATTTCTCAGATGATGTTTCATCCGTGAATGGTCCAGGGAAGGACCTTTCACCTTGACTATATGGC
ATTATGTCATCACAAGCTCTGAGGCTTCTCCTTTCCATCCTGCGTGGACAGCTAAGACCTCAGTTTTCAATAGC
ATCTAGAGCAGTGGGACTCAGCTGGGGTGATTTCCGCCCCCATCTCCGGGGGAATGTCTGAAGACAATTTTGTT
ACCTCAATGAGGGAGTGGAGGAGGATACAGTGCTACTACCAACTAGTGGATAAAGGCCAGGGATGCTGCTCAAC
CTCCTACCATGTACAGGACGTCTCCCCATTACAACCTACCAATCCGAAGTGTCAACTGTGTCAGGACTAAGAAA
CCCTGGTTTTGAGTAGAAAAGGGCTGGAAAGAGGGGAGCCAACAAATCTGTCTGCTTCTCACAATTAGTCATT
GGCAATAAGCATTCTGTCTCTTTGGCTGCTGCCTCAGCACAGAGAGCCAGAACTCTATCGGGCACCAGGATAA
CATCTCTCAGTGAACAGAGTTGACAAGGCCTATGGGAAATGCCTGATGGGATTATCTTCAGCTTGTTGAGCTTC
TAAGTTTCTTTCCCTTCATTCTACCCTGCAAGCCAAGTTCTGTAAGAGAAATGCCTGAGTTCTAGCTCAGGTTT
TCTTACTCTGAATTTAGATCTCCAGACCCTTCTGGCCACAATTCAAATTAAGGCAACAAACATATACCTTCCA
TGAAGCACACAGACTTTTGAAGCAAGGACAATGACTGCTTGAATTGAGGCTTGAGGAATGAAGCTTTGAA
GGAAAAGAATACTTTGTTTCCAGCCCCCTTCCCACTCTTCATGTGTTAACCCTGCCTTCTGGACCTTGGGA
GCCACGGTGACTGTATTACATGTTGTTATAGAAAAGTATTTAGAGTTCTGATCGTTCAAGAGAATGATTAAA
TATACATTTCTTA

Fig. 2C

SUBSTITUTE SHEET (RULE 26)

Element Display									
Unit Exp	Probe 1	Exp	Probe 2	180° ME Elements	Fluor. Wave	PRF (Hz)	SR	AS	PRF (Hz)
+1.7	35A Ovary T (links)	1	272A Denervic cells	422400818 (420)	422400818 (C-11)	2393	1.3	50	1430
+1.5	355A Ovary T	1	57 Ovary N	422200828 (420)	422400818 (C-11)	365	2.7	54	882
+1.8	261A Ovary T	1	510 Skeletal muscle N	422300824 (420)	421000198 (C-11)	1288	5.9	51	707
+3.1	328A Ovary T	1	572 Spleen N	422000829 (420)	421000198 (C-11)	9590	4.1	50	1180
+1.2	308A Ovary T	1	540 PBLIC (activated)	422300835 (420)	421000198 (C-11)	916	3.8	50	618
+4.7	288A Ovary T	1	575 Heart N	422900824 (420)	421000198 (C-11)	2305	1.1	53	489
+1.4	525 Ovary T	1	574 Bone Marrow N	422100818 (420)	421000198 (C-11)	933	3.5	53	743
	393A Ovary T (links)	1	576 Colon N	422300839 (420)	421000198 (C-11)	1842	10.1	55	371
+1.8	522 Ovary T	1	578 Kidney N	422800827 (420)	421000198 (C-11)	953	9.9	58	857
+3.2	3485 QT1-P (SCD)	1	3485 QT1-P (SCD)	422000827 (420)	421000198 (C-11)	1882	13.2	57	584
+1.5	262A Ovary T	1	584A Large Intestine N	422400822 (420)	421000198 (C-11)	1488	7.5	55	865
+1.1	515 Ovary T (links)	1	5710 Small Intestine N	422000834 (420)	421000198 (C-11)	509	9.4	51	573
+1.1	288A Ovary T	1	5712 Lung N	422400825 (420)	421000198 (C-11)	700	4.5	54	551
+2.1	201A Ovary T	1	56 Spleen N	422000820 (420)	421000198 (C-11)	825	4.8	48	1385
+7.5	525 Ovary T	1	556 Spinal Cord N	422300838 (420)	421000198 (C-11)	8889	22.2	50	502
+1.9	206A Ovary T	1	270A Liver N	422000808 (420)	421000198 (C-11)	2251	14.7	46	1259
+1.9	393A Ovary T (SCD)	1	572 Skin N	422000801 (420)	421000198 (C-11)	552	2.4	72	1028
+5.5	318A Ovary T	1	559 Pancreas	422000807 (420)	421000198 (C-11)	8138	35.5	50	1448
+3.5	263A Ovary T	1	573 Breast N	422100823 (420)	421000198 (C-11)	439	3.2	51	1531
+3.3	392A Ovary T	1	5718 Brain N	422000810 (420)	421000198 (C-11)	387	3.2	50	1278
+4.8	208A Ovary T	1	527 Ovary N	422500813 (420)	421000198 (C-11)	4242	22.2	58	883

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TCGAGCGGCCGCCCGGGCAGGTCCTTCAGACTTGGACTGTGTCACTGCCAGGCTTCCAGGGCTCCAATTGC
AGACGGCCTGTTGTGGGACAGTCTCTGTAATCGCGAAAGCAACCATGGAAGACCTGGGGGAAAACACCATGGTT
TTATCCACCCTGAGATCTTTGAACAACTTCATCTCTCAGCGTGCGGAGGGAGGCTCTGGACTGGATATTTCTAC
CTCGGCCGCGACCACGCT

Fig. 4

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TAGCGYGGTCGCGGCGAGGYCTGCTTYTCTGTCCAGCCCAGGGCCTGTGGGGTCAGGGCGGTGGGTGCAGATG
GCATCCACTCCGGTGGCTTCCCATCTTTCTTGGCCTGAGCAAGGTCAGCCTGCAGCCAGAGTACAGAGGGCC
AACACTGGTGTTCCTGAACAAGGGCCTTAGCAGGGCCTGAAGGCCCTCTCTGTAGTGTGAACCTCCTGGAGC
CAGGCCACATGTTCTCCTCATACCGCAGGYTAGYGATGGTGAAGTTGAGGGTGAATAGTATTMANGRAGATGG
CTGGCARACCTGCCCGGGCGGCCGCTCSAAATCC

Fig. 5

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AGCGTGGTCGCGGCCGAGGTGTCCTTCAGGGTCTGCTTATGCCCTTGTTCAAGAACACCAAGTGTGAGCTCTCTG
TACTCTGGTTGCAGACTGACCTTGCTCAGGCCTGAGAAGGATGGGGCAGCCACCAGAGTGGATGCTGTCTGCAC
CCATCGTCCTGACCCCAAAGCCCTGGACTGGACAGAGAGCGGCTGTACTGGAAGCTGAGCCAGCTGACCCACG
GCATCACTGAGCTGGGCCCTACACCTGGACAGGGACAGTCTCTATGTCAATGGTTTCACCCATCGGAGCTCT
GTACCCACCACCAGCACC GG GTGTCAGCGAGGAGCCATTCAACCTGCCCGGGCGGCCGCTCGA

Fig. 6

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TTGGGGNTTTMGAGCGGCGCCCGGGCAGGTACCGGGGTGGTCAGCGAGGAGCCATTCACTGAACTTCACCA
TCAACAACCTGCCGTATGAGGAGAACATGCAGCACCTGGCTCCAGGAAGTTCAACACCACGGAGAGGGTCCTT
CAGGGCCTGCTCAGGTCCCTGTTCAAGAGCACCAAGTGTGGCCCTCTGTACTCTGGCTGCAGACTGACTTTGCT
CAGACTTGAGAAACATGGGGCAGCCACTGGAGTGGACGCCATCTGCACCCTCCGCCTTGATCCCACTGGTCCTG
GACTGGACAGAGAGCGGCTATACTGGGAGCTGAGCCAGTCCTCTGGCGGNGACNCCNCTT

Fig. 7A

AGCGTGGTCGCGGCCGAGGTCCAGTCGCAGCATGCTCTTTCTCCTGCCCACTGGCACAGTGAGGAAGATCTCTG
CTGTCAGTGAGAAGGCTGTATCCACTGAGATGGCAGTCAAAAGTGCATTTAATACACCTAACGTATCGAACAT
CATAGCTTGGCCAGGTTATCTCATATGTGCTCAGAACACTTACAATAGCCTGCAGACCTGCCCGGGCGGCCGC
TCGA

Fig. 7B

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TGTGGTGTGAACCTCCTGGAGNCAGGGTGACCCATGTCCTCCCATACTGCAGGTTGGTGATGGTGAAGTTGA
GGGTGAATGGTACCAGGAGAGGGCCAGCAGCCATAATTGTSGRGCKGSMGMSSGAGGMWGGWGTYYCWGAGGTT
CYRARRTCCACTGTGGAGGTCCAGGAGTGCTGGTGGTGGGCACAGAGSTCYGATGGGTGAAACCATTGACATA
GAGACTGTTCTGTCCAGGGTGTAGGGGCCAGCTCTTYRATGYCATTGGYCAGTTKGCTYAGCTCCCAGTACA
GCCRCTCTCKGYYGWCCAGSGCTTTGGGGTCAAGATGATGGATGCAGATGGCATCCACTCCAGTGGCTGCT
CCATCCTTCTCGGACCTGAGAGAGGTCAGTCTGCAGCCAGAGTACAGAGGGCCAACACTGGTGTTCTTTGAATA

Fig. 8

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TCGAGCGGCCGCCGGGCAGGTCAGGAAGCACATTGGTCTTAGAGCCACTGCCTCCTGGATTCCACCTGTGCTG
CGGACATCTCCAGGGAGTGCAGAAGGSAAGCAGGTCAAACCTGCTCAGATCAGTCAGACTGGCTGTTCTCAGTTC
TCACCTGAGCAAGGTCAGTCTGCAGCCAGAGTACAGAGGGCCAACACTGGTGTCTTGAACAAGGGCTTGAGCA
GACCCTGCAGAACCTCTTCCGTGGTGTGAACCTCCTGGAAACCAGGGTGTTCATGTTTTCTCATAATGC
AAGGTTGGTGATGG

Fig. 9

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Gene Name	Probe 1 Seq Name	P1	P2 Name	Probe 2 Seq Name	Probe 1 Value	Probe 2 Value	Probe 1 S/B	Probe 2 S/B	Probe 1 AS	Probe 2 AS
42100188 (D3)	+10 205A Ovary T	C	270A Liver N	42200606	8620	1240	57.7	63	2.9	65
42100188 (D3)	+19 325A Ovary T	C	356 Spleen Card N	42200623	5894	1002	35.3	89	3.9	89
42100188 (D3)	+37 355A Ovary T	C	571 Testis Testis	42200607	12151	2121	54.3	73	2.8	73
42100188 (D3)	+51 426A Ovary T (test)	C	415A Adipose N	42200613	7487	1480	53.0	73	9.7	73
42100188 (D3)	+35 263A Ovary T	C	573 Uterus N	42200622	7802	2116	39.2	84	4.5	84
42100188 (D3)	+13 389A Ovary T (test)	C	11 Cerebrum N	42200609	3713	1113	20.4	83	2.6	83
42100188 (D3)	+19 393A Ovary T (SCF)	C	12 Spleen N	42200601	2435	314	12.1	75	2.1	75
42100188 (D3)	+26 344A Ovary T (test)	C	272A Dendritic cell	42200608	4576	1753	23.5	69	2.3	69
42100188 (D3)	+22 364A Ovary T	C	52 Pancreas N	42200629	7904	3596	34.5	81	5.4	81
42100188 (D3)	+20 315 Ovary T (test)	C	540 PBMC T-cell	42200605	2191	1081	14.0	80	2.5	80
42100188 (D3)	+20 265A Ovary T	C	3710 Small Intestine	42200604	1978	971	10.4	80	2.7	80
42100188 (D3)	+20 335A Ovary T	C	375 Heart N	42200624	1911	983	15.3	83	2.8	83
42100188 (D3)	+19 428A Ovary T (test)	C	57 Ovary N	42200626	1606	87	3.8	100	2.0	100
42100188 (D3)	+16 261A Ovary T	C	243A Esophagus N	42200612	1837	3480	14.4	97	9.5	97
42100188 (D3)	+16 265A Ovary T	C	310 Stomach muscle	42200611	5914	2653	30.4	88	6.0	88
42100188 (D3)	+16 521 Ovary T	C	527 Ovary N	42200603	2059	1274	11.9	50	2.4	50
42100188 (D3)	+13 945A Ovary T (SCF)	C	319 Kidney N	42200627	1735	1072	11.0	92	4.9	92
42100188 (D3)	+14 262A Ovary T	C	945A Qx 5A (SCF)	42200602	4204	3074	23.0	93	3.1	93
42100188 (D3)	+13 325 Ovary T	C	394A Large Intestine	42200623	3002	2101	16.6	89	4.0	89
42100188 (D3)	+12 429A Ovary T (test)	C	374 Bone Marrow	42200619	1053	1297	9.6	90	3.1	90
42100188 (D3)	+12 382A Ovary T	C	364A Ovary N	42200614	2521	3084	22.0	65	23.9	65
42100188 (D3)	+12 382A Ovary T	C	3719 Brain N	42200610	2072	1663	10.9	88	2.3	88
42100188 (D3)	+12 382A Ovary T	C	3712 Lung N	42200625	1840	1473	10.7	87	3.8	87
42100188 (D3)	+11 201A Ovary T	C	85 Spleen N	42200620	1329	1304	9.1	90	3.3	90

Fig. 10

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Gene Name	Hal Probe 1 Exp Name	Probe 1 P1 P2 Name	Probe 2 P1 P2 Name	GEN ID	Probe1 Value	Probe2 Value	Probe1 g/b	Probe2 g/b	Prob82 g/b	Prob82 %
421B0181 (C3)	+188 385A Ovary T	S91 Fetal tissue	S91 Fetal tissue	422X0607	26711	1424	103.3	54	2.0	64
421B0181 (C3)	+115 523 Ovary T	S16 Spinal Cord N	S16 Spinal Cord N	422G0628	19559	1779	65.3	68	3.9	68
421B0181 (C3)	+111 426A Ovary T (meas)	415A Aorta N	415A Aorta N	422X0611	14125	1273	67.3	61	5.6	61
421B0181 (C3)	+108 205A Ovary T	270A Liver N	270A Liver N	422Q0605	16121	1488	93.3	43	2.9	43
421B0181 (C3)	+51 263A Ovary T	S73 Breast N	S73 Breast N	422H0623	11326	2235	58.2	68	4.4	68
421B0181 (C3)	+46 264A Ovary T (meas)	272A Decidua cells	272A Decidua cells	422M0603	6583	1424	24.5	40	2.1	40
421B0181 (C3)	+44 264A Ovary T	S2 Punctate N	S2 Punctate N	422N0629	9865	2245	40.9	64	3.6	64
421B0181 (C3)	+44 429A Ovary T (meas)	364A Ovary N	364A Ovary N	422D0614	2803	638	22.6	60	7.6	60
421B0181 (C3)	+42 261A Ovary T	S10 Skeletal muscle	S10 Skeletal muscle	422J0621	8271	1940	39.5	68	3.6	68
421B0181 (C3)	+38 3115 Ovary T (meas)	C710 Small intestine	C710 Small intestine	422C0604	2281	607	11.6	60	2.1	60
421B0181 (C3)	+25 265A Ovary T	C73 Heart N	C73 Heart N	422O0624	1192	1793	19.2	68	4.0	68
421B0181 (C3)	+23 822 Ovary T	C19 Kidney N	C19 Kidney N	42290627	563	1276	3.6	70	3.9	70
421B0181 (C3)	+22 266A Ovary T	S17 Ovary N	S17 Ovary N	42230603	2774	1260	14.3	46	2.7	46
421B0181 (C3)	+21 5934 Ovary T (SCID)	1250a N	1250a N	422R0601	1774	837	8.4	56	2.1	56
421B0181 (C3)	+19 9483 OT 1-P (SCID)	P483 OT 1-P (SCID)	P483 OT 1-P (SCID)	422V0602	6967	3726	41.5	70	9.2	70
421B0181 (C3)	+16 288A Ovary T	C119 Brain N	C119 Brain N	422Q0610	2313	1471	6.2	50	1.5	50
421B0181 (C3)	+15 525 Ovary T	C112 Lipid N	C112 Lipid N	422V0625	1657	1054	9.7	60	2.9	60
421B0181 (C3)	+14 202A Ovary T	C74 Bone Marrow N	C74 Bone Marrow N	422H0619	746	1743	4.5	63	2.7	63
421B0181 (C3)	+12 386A Ovary T	234A Large intestine	234A Large intestine	422A0622	3711	2214	16.8	69	3.8	69
421B0181 (C3)	+12 385A Ovary T	S40 PEMC (retained)	S40 PEMC (retained)	422J0605	630	544	4.2	53	1.9	53
421B0181 (C3)	+10 201A Ovary T	S7 Ovary N	S7 Ovary N	422M0626	592	730	3.7	75	2.6	75
421B0181 (C3)	+10 428A Ovary T (meas)	S6 Spleen N	S6 Spleen N	422V0620	1197	1237	7.8	65	3.5	65
421B0181 (C3)	382A Ovary T (meas)	243A Esophagus N	243A Esophagus N	422A0612	783	797	4.5	95	2.4	95
421B0181 (C3)		11 Colon N	11 Colon N	422B0609	3470	862	8.9	24	1.7	24

Fig. 11

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Fig. 12

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Gene Name	Ref. Probe 1 Exp Name	P1	P2 Name	Probe 2 ID	Probe 1 Value	Probe 2 Value	Probe 1 S/B	Probe 2 S/B	Probe 1 A%	Probe 2 A%
421H0187 (B11)	+20.2 425A Ovary T (met)	1	415A Aorta N	422X0611	5441	270	36.3	2.3	50	50
421H0187 (B11)	+10.0 523 Ovary T	2	516 Spland Ovary N	422X0628	5318	573	27.1	2.3	56	56
421H0187 (B11)	+8.3 425A Ovary T (met)	3	354A Ovary N	422X0614	1252	150	10.1	2.3	58	58
421H0187 (B11)	+5.7 385A Ovary T	4	391 Fetal tissue	422X0607	9507	1683	33.8	2.1	45	45
421H0187 (B11)	+4.8 205A Ovary T	5	270A Liver N	422X0606	5456	1235	31.1	2.0	50	50
421H0187 (B11)	+4.2 265A Ovary T	6	CT5 Heart N	422X0624	1834	438	11.9	2.0	48	48
421H0187 (B11)	+3.6 281A Ovary T	7	CT19 Brain N	422X0610	309	1259	2.6	2.0	48	48
421H0187 (B11)	+3.4 263A Ovary T	8	510 Skeletal muscle	422X0621	9753	1016	17.7	2.0	55	55
421H0187 (B11)	+2.5 5115 Ovary T (met)	9	513 Breast N	422X0623	4163	1239	23.0	2.0	62	62
421H0187 (B11)	+2.1 264A Ovary T (met)	10	CT10 Small Intestine	422X0604	1565	627	8.8	2.1	47	47
421H0187 (B11)	+2.1 522A Ovary T	11	S2 Pancreas N	422X0629	3455	1630	14.9	2.0	60	60
421H0187 (B11)	+1.7 380A Ovary T	12	274A Dendritic cell	422X0608	2667	1270	13.4	1.9	44	44
421H0187 (B11)	+1.6 933A Ovary T (SCF)	13	CT9 Kidney N	422X0627	291	605	2.4	2.5	51	51
421H0187 (B11)	+1.5 262A Ovary T	14	340 PBMNC (adipocyte)	422X0605	410	687	3.2	2.0	47	47
421H0187 (B11)	+1.5 288A Ovary T	15	12 Skin N	422X0601	1622	984	7.9	2.2	44	44
421H0187 (B11)	+1.4 428A Ovary T (met)	16	334A Large Intestine	422X0622	1892	1245	10.1	2.6	50	50
421H0187 (B11)	+1.3 355A Ovary T	17	CT12 Lung N	422X0625	664	908	4.1	2.6	68	68
421H0187 (B11)	+1.2 201A Ovary T	18	243A Esophagus N	422X0612	236	923	2.7	1.9	78	78
421H0187 (B11)	+1.0 945 OT 1-P (SCID)	19	S7 Ovary N	422X0624	382	501	2.9	2.0	58	58
421H0187 (B11)	+1.0 266A Ovary T	20	S6 Spleen N	422X0620	358	677	4.2	2.3	58	58
421H0187 (B11)		21	945 OT 1-P (SCID)	422X0602	2582	2493	13.1	6.9	57	57
421H0187 (B11)		22	11 Colon N	422X0609	2261	562	12.5	1.7	38	38
421H0187 (B11)		23	S37 Ovary N	422X0603	1739	965	9.7	2.2	56	56
421H0187 (B11)		24	CT4 Bone Marrow	422X0619	283	843	2.3	2.2	44	44

Fig. 14

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11721-1

ACGGTTTCAATGGACACTTTTATTGTTTACTTAATGGATCATCAATTTTGTCTCACTACCTACAAATGGAATTT
CATCTTGTTTCCATGCTGAGTAGTGAAACAGTGACAAAGCTAATCATAATAACCTACATCAAAAGAGAACTAAG
CTAAACACTGCTCACTTTCTTTTAAACAGGCAAAATATAAATATATGCACTCTAXAATGCACAATGGTTTAGTCA
CTAAAAAATTCAAATGGGATCTTGAAGAATGTATGCAATCCAGGGTGCAAGATGAGCTGAGATGCTGTG
CAACTGTTTAAAGGGTTCTTGGCACTGCATCTCTTGGCCACTAGCTGAATCTTGACATGGAAGGTTTTAGCTAAT
GCCAAGTGGAGATGCAGAAAATGCTAAGTTGACTTAGGGGCTGTGCACAGGAACATAAAGGCAGGAAAGTACTA
AATATTGCTGAGAGCATCCACCCAGGAAGGACTTTACCTTCCAGGAGCTCCAACTGGCACCACCCCAAGTGC
TCACATGGCTGACTTTATCCTCCGTGTTCCATTTGGCACAGCAAGTGGCAGTG

11721-2

AAGGCTGGTGGGTTTTTGATCCTGCTGGAGAACCTCCGCTTTCATGTGGAGGAAGAAGGGAAGGGAAGATGC
TTCTGGGAACAAGTTAAAGCCGAGCCAGCCAAAATAGAAGCTTTCGAGCTTCACTTTCCAAGCTAGGGGATG
TCTATGTCAATGATGCTTTTGGCACTGCTCACAGAGCCACAGCTCCATGGTAGGAGTCAATCTGCCACAGAAG
GCTGGTGGGTTTTTGATGAAGAAGGAGCTGAACACTTTGCAAAGGCCCTGGAGAGCCAGAGCGACCTTCCT
GGCCATCCTGGGCGGAGCTAAAGTTGCAGACAAGATCCAGCTCATCAATAATATGCTGGACAAAGTCAATGAGA
TATTATTGGTGGTGAATGGCTTTTACCTTCTTAAAGGTGCTCAACAACATGGAGATTGGCACTTCTCTGTTT
GATGAAGAGGGAGCCAAGATTGTCAAAGACCTAATGTCCAAAGCTGAGAAGAATGGTGTGAAGATTACCTTGCC
GTGACTTTGTCACTGCTGACAAGTTTGATGA

11724-1

TTTGTTCCTTACATTTTCTAAAGAGTTACTTAAATCAGTCAACTGGTCTTTGAGACTCTTAAGTTCTGATTCC
AACTTAGCTAATTCATTCTGAGAACTGTGGTATAGGTGGCGTGTCTTCTAGCTGGGACAAAAGTTCTTTGTT
TTCCCTGTAGAGTATCACAGACCTTCTGCTGAAGCTGGACCTCTGTCTGGGCTTGGACTCCCAAATCTGCT
TGTCATGTTCAAGCCTGGAATGTTAATCTTTAATCTTCCATATGGATGGACATCTGTCTAAGTTGATCCTTT
AGAACACTGCAATTATCTTCTTGAAGTCAATTTCTTCTTCTTGTCTTGAATCGCATCACTAACTTCCTCTC
CCATTTCTTAGCTTCATCTATCACCTGTACAGATCATCTGGAGGGAAGACATGCTCTTAGTAAAGGCTGCAA
GCTGGGTACAGTACTGTCCAAGTTTCTGAAGTTGCTGAACCTCTTGTCTTTCTTGTTCAAAGTAACCTGA
ATCTCTCAAATTGTCTCTTCCAAGTGGACTTTTCTCTGCGCAAAGCATCCAG

11724-2

TCATTGCCTGTGATGGCATCTGGAATGTGATGAGCAGCCAGGAAGTTGTAGATTTCAATCAATCAAAGGATTCA
GCATGTGGTGAAGCTGTGAGGCAAGAGAAAACAAGAACTGTATGGCAAGTTAAGAAGCACAGAGGCAAAACAAGA
AGGAGACAGAAAAGCAGTTGCAGGAAGCTGAGCAAGAAATGGAGGAAATGAAAGAAAAGATGAGAAAGTTTGCT
AAATCTAAACAGCAGAAAATCCTAGAGCTGGAAGAAGAGAATGACCGGCTTAGGGCAGAGGTGCACCCTGCAGG
AGATACAGCTAAAGAGTGTATGGAACACTTCTTTCTTCCAATGCCAGCATGAAGGAAGAACTTGAAGGGTCA
AAATGGAGTATGAAACCCTTTCTAAGAAGTTTCAAGTCTTTAATGTCTGAGAAAGACTCTTAAGTGAAGAGTT
CAAGATTTAAAGCATCAGATAGAAGGTAAATGTATCTAAACAAGCTAACCTAGAGGCCACCGAGAAACATGATA
CCAAACGAATGTCACTGAAGAGGGAACACAGTCTATACCAGGT

Fig. 15A

SUBSTITUTE SHEET (RULE 26)

11725-32-1.2

AAGCCAATAATCACCATTATTACTTAATATATGCCAACCACTGTACTTGGCAGTTCACAAATTCTCACCGGT
CAACAACCCCATGAGGTATTATTCCCACTTATAGATAGGGAAACCACAGCTCAAGTAAGTTAGGAAACGTAG
CCAAGTATACAGAATACGAAGTGGCAAACTAGAAAGGAAGACTGACACTGCTATCTGCTGGCCTCCAGTGT
CCTGGCTCTTTTACACGGGTCAATGTCTCCAGCGCTGCTGCTGCTGCATTACCATGCCCTCATTGTTTT
TCTTCTCTGGTGTTCAACTGCATCCTTCAAGAAGTCTCACTCATTCCAGAGACCACTTATTCTTTCTCTCTT
TCTGAAATTACTTTTAATAATCTTCATGAGGGGGAAAAAGAAAGATGCCTGTTGGTAGTTTTGTTGTTTAAAGCTG
CTCAATTTGGGACTTAAACAATTTGTTTTCATCTTGACATCCTGTAAACAGCTGTGTTTTGCTAGAAAGATCAC
TCTCCCTCTCTTTTAGCATGGCTTCAACCTCTTCAATTCATTTTCTTTTCTTTCAACAACATCTCAAGTCT
TCAAAGTGTGATGCAGAAAGAGCCCTCTTCAAGTTATGTTGTGCTACTTCTGAACATGTGCTTTTAAAGATTC
ATTTTCTTCTGAAGATCCTGTAACCACTCCCTGTATTGGCTAGGTCTTTCTCTTTCTCTTCCAAAACAGCCT
CATGGTATTCATCTGTTTCTCTTTTCTTTTAAAGTTCAGGAGCTTCAGAAC

11726-1&2

CAAGCTTTTTTTTTTAAAAAGTGTTAGCATTAAATGTTTTATTGTACGCAGATGGCAACTGGGTTTATG
TCTTCATATTTTATATTTTTGTAATTAAAAAATTACAAGTTTAAATAGCCAATGGCTGGTTATATTTTCAG
AAAAATGATTAGACTAATTCATTAATGGTGGCTTCAAGCTTTTCTTATTGGCTCCAGAAAATTCACCCACCT
TTTGTCCCTTCTAAAAAACTGGAATGTTGGCATGCATTTGACTTCACACTCTGAAGCAACATCTGACAGTCA
TCCACATCTACTTCAAGGAATATCAGTGGG/MTACTTTTTCAGAGAGGGAATGAAAGAAAGGCTTGATCATTTT
GCAAGGCCACACCACTGGCTGAGAAGTCACTACTACAAGTTTATCACCTGCAGCGTCCAAGGCTTCTGAA
AAGCAGTCTTGCTCTCGATCTGCTTACCATCTTGGCTGCTGAGTCTGACGAGCGGCTGTAAGGACCGATGGA
AATGGATCCAAGCACCAACAGAGCTTCAAGACTCGCTGCTTGGCTGAATTCGGATCCGATATCGGCATGGC
CT

11727-1&2

AAGTGTAGCATTAACTGTTTATTGTACGCAGATGGCAACTGGGTTTATGTCTTCATATTTTATATTTTGTGTA
AATTAATAAAATMCAAGTTTTAAATAGCCAAATGGCTGGTTATATTTTCAAGAAACATGATTAGACTAATTTCAT
TAATGGTGGCTTCAAGCTTTTCTTATTGGCTCCAGAAAATTCACCCACCTTTTGTCCCTTCTTAAAAAACTGG
AATGTTGGCATGCATTTGACTTCACACTCTGAAGCAACACTCTGACAGTCATCCACATCTACTTCAAGGAATAT
CAGCTTGAATACTTTTCAAGAGGGAATGAAAGAAAGGCTTGATCATTTTGAAGGCCACACCACGTGGCTG
AGAAGTCAACTACTACAAGTTTATCACCCTGCAGCGTCTCAAGGCTTCTGAAAAGCAGTCTTGCTCTCGATCTGC
TTCACCATCTTGGCTGCTGGAGTCTGACGAGCGGTGTAAGGACCGATGGAAATGGATCCAAAGCACCACAAAG
AGCTTCAAGACTCGCTGCTTGGCATGAATTCGGATCCGA

Fig. 15B

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11728.1.40.19.19

TACAAACTTTATTGAAACGCACACGCGCACACACAAACACCCCTGTGGATAGGGAAAAGCACCTGGCCACAG
GGTCCACTGAAACGGGGAGGGGATGGCAGCTTGTAAATGTGGCTTTTGCCACAACCCCTTCTGACAGGGAAGGC
CTTAGATTGAGGCCACCTCCCATGGTGATGGGGAGCTCAGAATGGGGTCCAGGGAGAATTTGGTTAGGGGA
GGTGCTAGGGAGGCATGAGCAGAGGGCACCTCCGAGTGGGGTCCCGAGGGCTGCAGAGTCTTCAGTACTGTCC
CTCACAGCAGCTGTCTAAGGCTGGGTCCCTCAAAGGGGCGTCCAGCGCGGGGCTCCCTGCGCAAACTTG
GTACCCCTGGCTGCGCAGCGGAAGCCAGCAGGACAGCAGTGGCGCGGATCAGCACAAACAGAGCCCTGGCGGTA
GGGACAGCAGGCCAGCCCTGTGCGTTGTCTCGGCAGCAGGTGGTTATCATGGCAGAAGTGTCTTCCACA
CTTCACGTCTTACACCCACGTGAXGGCTACXGGCCAGGAAG

11728.2.40.19.19

CCCGTGGGTGCCATCCACGGAGTTGTTACCTGATCTTTGGAAGCAGGATCGCCCGTCTGCACTGCAGTGGAAGC
CCCGTGGGCAGCAGTGATGGCCATCCCGCATGCCAGGCCTCTGGGAAGGGGCAGCAACTGGAAGTCCCTGAG
ACGGTAAGATGCAGGAGTGGCCGGCAGAGCAGTGGGCATCAACCTGGCAGGGGCCACCCAGATGCCTGCTCAG
TGTGTGGGCCATTTGTCCAGAAGGGGACGGCAGCAGCTGTAGCTGGCTCCTCCGGGTCCAGGCAGCAGGCCA
CAGGGCAGAACTGACCATCTGGGCACCGGTTCCAGCCACCAGCCCTGCTGTAAAGGCCACCCAGCTCACCAGG
GTCCACATGGTCTGCTCGCTCCGACTCCGCGGTCTTGGGCCCTGATGGTTCTACCTGCTGTGAGCTGCCAG
TGGGAAGTATGGCTGCTGCCAATGCCAACGCCACCTGCTGCTCGATCACCTGCACTGCTGCCCCAAGACACT
GTGTGTGACCTGATCCAGAGTAAGTGCTCTCCAAGGAGAACG

11730-1

GAATCACCTTTCTGGTTTAGCTAGTACTTTGTACAGAACATGAGGTTTCCACAGCGGAGTCTCCCTGGGCTC
TGTTTGGCTCTCGTAAGGCAGGCCTACACCTTTTCTCTCTATGGAGAGGGGAATATGCATTAAGGTGAA
AAGTCACCTTCCAAAAGTGAGAAAGGGATTGATTGCTGCTTCAGGACTGTGGAATTATTTGGAATGTTTACA
AATGGTTGCTACAAAACAACAAAAAGGTAATTACAAATGTGTACATCACAACTGCTTTTTAAAGACATTAT
GCATTGTGCTCACATTCCTTAAATGTTGTTTCCAAAGGTGCTCAGCCTCTAGCCCAGCTGGATTCTCCGGGAA
GAGGCAGAGACAGTTTGGCGAAAAAGACACAGGGAAGGAGGGGGTGGTGAAGGAGAAAGCAGCCTTCAGTTA
AAGATCAGCCCTCAGTTAAAGGTCAGCTTCCCGCAXGCTGGCCTCAXGCGGAGTCTGGGTGAGAGGAGGAGCA
GCAGCAGGGTGGGACTGGGGCGT

11730-2

AACCGGAGCGCGAGCAGTAGCTGGGTGGGCACCATGGCTGGGATCACCACCATCGAGGCGGTGAAGCGCAAGAT
CCAGGTTCTGCAGCAGCAGGAGATGATGCAGAGGAGCGAGCTGAGCGCTCCAGCGAGAAGTTGAGGGAGAAA
GGCGGGCCCGGAAACAGGCTGAGGCTGAGGTGGCTCCTTGAACCGTAGGATCCAGCTGGTTGAAGAAGAGCTG
GACCGTGCTCAGGAGCGCTGGCCACTGCCCTGCAAAAGCTGGAAGAAGCTGAAAAAGCTGCTGATGAGAGTGA
GAGAGGTATGAAGGTTATTGAAAAACGGGCCCTTAAAGATGAAGAAAAGATGGAACCTCCAGGAAATCCAACCTCA
AAGAAGCTAAGCACATTGCAGAAGAGGCAGATAGGAAGTATGAAGAGGTGGCTCGTAAGTTGGTGATCATTGAA
GGAGACTTGAACGCACAGAGGAACGAGCTGAGCTGGCAGAGTCCCGTTGCCGAGAGATGGATGAGCAGATTAG
ACTGATGGACCAGAACCTGAAGTGTCTGAGTGC

Fig. 15C

SUBSTITUTE SHEET (RULE 26)

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11732.1contig

GAGAACTTGGCCTTTATTGTGGGCCAGGAGGGCACAAAGGTGAGGAGGCCAAGGGAGGGATCTGGTTTTCTG
GATAGCCAGGTCATAGCATGGGTATCAGTAGGAATCCGCTGTAGCTGCACAGGCCTCACTTGCTGCAGTTCCGG
GGAGAACACCTGCACTGCATGGCGTTGATGACCTCGTGGTACACGACAGGCCATTGGTGCAGTGCAAGGGCAC
GCGCATGGGCTCGCTCGAGGGCAGGCAGCAGGAGCATTGCTCCTGCACATCCTCGATGTCAATGGAGTACA
CAGCTTTGCTGGCACACTTTCCCTGGCAGTAATGAATGTCCACTTCTCTGGGACTTACAATCTCCACTTTG
ATGTAAGTGCACCTTGGCTGTGATGTCTTTGCAATCAGGCTCCTCACATGTGTACAGCAGGTGCCTGGAATTT
CACGATTTTGCCTCCTTCAGCCAGACACTTGTGTTTCATCAAATGGTGGGCAGCCCGTGACCCTCTCTCCAGA
TGTACTCTCCTCT

11732.2contig

GCCTGGACCTTGGCGGATCAGTGCCACACAGTGAAGTCTTGGCAAATGGCCAGACCTTGCTGCAGAGTCATCG
TGTCAATTGTGACCATGGACCCCGGCTTCATGTGCCAACAGCCAGTCTCCTGTTCCGGTGGAGGAGACGTGTG
GCTGCCGCTGGACCTGCCCTTGTGTGTGCACGGGCAGTCCACTCGGCACATCGTCACCTTCGATGGGCAGAAT
TTCAAGCTTACTGGTAGCTGCTCCTATGTATCTTTCAAACAAGGAGCAGGACCTGGAAGTGTCTCTCCACAA
TGGGGCCTGCAGCCCGGGGCAAAACAAGCCTGCATGAAGTCCATTGAGATTAAGCATGCTGGCGTCTCTGCTG
AGCTGCACAGTAACATGGAGATGGCAGTGGATGGGAGACTGGTCTTGGCCGTACGTTGGTGAACATGGAA
GTCAGCATCTACGGCGTATCATGTATGAAGTCAGGTTTACCCATCTTGGCCACATCCTCACATACCGCCXC
AAAACAACGAGTT

11735-1-2

AGATCAACCTCTGCTGGTCAGGAGGAATGCCTTCTTGTCTTGGATCTTTGCTTTGACGTTCTCGATAGTRWCA
aCTKKRYTSRAMSKMAAGKGYRATGRWMTTKSYWGWRSYKTMWMSGRARAYTTaGaCAYCCCMCCTCWgAG
aCGSAGKACCARGTGCAgAgTGGACTCTTTCTGGATGTTGTAGTCAGACAGGGTGGCTCCATCTTCCAGCTGT
TTCCAGCAAAGATCAACCTCTGCTGATCAGGAGGGATGCCTTCTTATCTTGGATCTTTGCCTTGACATTCTC
GATGGTGTCACTGGGCTCCACCTCGAGGGTGTGGTCTTACCAGTCAGGGTCTTACGAAGATYTGATCCAC
CTCTGAGACGGAGCACCAGGTGCAGGGTGAAGTCTTTCTGGATGTTGTAGTCAGACAGGGTGGCYCCATCTTCC
AGCTGCTTTCCSaGCAAAGATCAACCTCTGCTGGTCAGGAGGRATGCCTTCTTGTCTGTGATCTTTGCTTGA
CRTTCTCRATGGTGTCACTCGGCTCCACTTCGAGAGTGATGGTCTTACCAGTCAGGGTCTTACGAAGATCTGC
ATCCCACTCTAA

11740.2.contig

AAGTCAAAACAGACAAAGATTATTACCAGCTGCAAGCTATATTAGAAGCTGAACGAAGAGACAGAGGTCATGA
TTCTGAGATGATTGGAGACCTTCAAGCTCGAATTACATCTTTACAAGAGGAGGTGAAGCATCTCAAACATAATC
TCGAAAAAGTGGAAGGAGAAAGAAAGAGGCTCAAGACATGCTTAATCACTCAGAAAAGGAAAAGAATAATTA
GAGATAGATTTAACTACAACTTAAATCATTACAACAACGGTTAGAACAAGAGGTAATGAACACAAAGTAAC
CAAAGCTCGTTTAACTGACAAACATCAATCTATTGAAGAGGCAAAAGTCTGTGGCAATGTGTGAGATGGAAAAA
AGCTGAAAGAAGAAAGAGAAGCTCGAGAGAAGGCTGAAAATCGGGTTGTTGAGATTGAGAAACAGTGTTCATG
CTAGACGTTGATCTGAAGCAATCTCAGCAGAACTAGAACATTGACTGGAAATAAAGAAAGGATGGAGGATGA
AGTTAAGAATCTA

Fig. 15D

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11765.2&64.2.cont1g

CGCCTCCACCATGTCCATCAGGGTGACCCAGAAGTCTACAAGGTGTCCACCTCTGGCCCCGGGCCTTCAGCA
GCCGCTCTACACGAGTGGGCCCGGTTCCCGCATCAGCTCCTCGAGCTTCTCCGAGTGGGCAGCAGCAACTTT
CGCGGTGGCCTGGGCGGCGCTATGGTGGGGCCAGCGGCATGGGAGGCATCACCGCAGTTACGGTCAACCAGAG
CCTGCTGAGCCCECTTGCTCTGGAGGTGGACCCCAACATCCAGGCCGTGCGCACCCAGGAGAAGGAGCAGATCA
AGACCCTCAACAACAAGTTTGCCTCCTTCATAGACAAGGTACGGTTCCTGGAGCAGCAGAACAAGATGCTGGAG
ACCAAGTGGAGCCTCCTGCAGCAGCAGAAGACGGCTCGAAGCAACATGGACAACATGTTTCGAGAGCTACATCAA
CARCCTTAGGCGGCAGCTGGAGACTCTGGGCCAGGAGAAGCTGAAGCTGGAGCGGAGCTTGGAACATGCAGG
GGCTGGTGGAGACTTCAAGAACAAGTATGAGGATGAGATCAATAAGCGTACAGAGATGGAGAACGAATTTGTC
CTCATCAAGAAGGATGTGGATGAAGCTTACATGAACAAGGTAGAGCTGGAGTCTCGCCTGGAAGGGCTGACCGA
CGAGATCAACTTCTCAGGCAGCTGTATGAAGAGGAGATCCGGGAGCTGCAGTCCCAGATCTCGGACACATCTG
TGGTGTGTCCATGGACAACAGCCGCTCCCTGGACATGGACAGCATCATTGCTGAGGTCAAGGCACAGTACGAG
GATATTGCCAACCGCAGCCGGGCTGAGGCTGAGAGCATGTACCAGGTCAAGTATGAGGAGCTGCAGAGCCTGGC
TGGGAAGCACGGGGATGACCTGCGGGCACAAGACTGAGATCTCTGAGATGAACCGGAACATCAGCCCCGGCT
XCAGGCTGAGATTGAGGGCCTCAAAGGCCAGAXGGCTTXCCTGGAXGXCCGCCAT

11767.2.cont1g

CCCGGAGCCAGCCAACGAGCGGAAAATGGCAGACAATTTTCGCTCCATGATGCGTTATCTGGGTCTGGAACC
CAAACTCTCAAGGATGGCTGGCGCATGGGGGAACAGCCTGCTGGGGCAGGGGGCTACCCAGGGGCTTCTAT
CCTGGGGCTACCCGGGCAGGCACCCCAAGGGGCTTATCCTGGACAGGCACCTCCAGGCGCTACCTGGAGC
ACCTGGAGCTTATCCCGGAGCAGCTGCACCTGGAGTCTACCCAGGGCCACCCAGCGGCCCTGGGGCTACCCAT
CTTCTGGACAGCCAAGTGCCACCGGAGCCTACCTGCCACTGGCCCTATGGCGCCCTGCTGGGCCACTGATT
GTGCTTATAACCTGCTTTGCTGGGGGAGTGGTGCTCGCATGCTGATAACAATTCTGGGCACGGTGAAGCC
CAATGCAACAGAAATTGCTTTAGATTTCAAAGAGGGAATGATGTTGCCCTTCCACTTTAACCACGCTTCAATG
AGAACAAACAGGAGATCATTGGTTGAATACAAAGCTGGATAA

11768-1&2

GGGAATGCAACAACCTTTATTGAAAGGAAAGTGCAATGAAATTTGTTGAAACCTTAAAAGGGGAAACTTAGACAC
CCCCCTCRAgCGMAGKACCARGTGCARAgGTGGACTCTTCTGGATGTTGTAGTCAGACAGGGTRCGWCCATC
TTCCAGCTGTTTTYCCRGCAAAGATCAACCTCTGCTGATCAGGAGGRATGCCCTTCTTATCTTGGATCTTTGCCT
TGACATTCTCGATGGTGTCACTGGGCTCCACCTCGAGGGTGATGGTCTTACCAGTCAGGGTCTTCACGAAGATY
TGCATCCACCTCTGAGACGGAGCACCAGGTGCAGGGTRGACTCTTCTGGATGTTGTAGTCAGACAGGGTGCG
YCCATCTTCCAGCTGcTTTCCSaGCAAAGATCAACCTCTGCTGGTCAGGAGGRATGCCCTTCTTGTCTYGGATC
TTTGCTTTGACRTTCTCAATGGTGTCACTCGGCTCCACTTCGAGAGTGATGGTCTTACCAGTCAGGGTCTTCAC
GAAGATCTGCATCCACCTCTAAGACGGAGCACCAGGTGCAGGGTGGACTCTTCTGGATGgTTGTAGTCAGAC
AGGGTGCGTCCATCTTCCAGCTGTTTCCAGCAAAGATCAACCT

Fig. 15E

SUBSTITUTE SHEET (RULE 26)

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11768-1&2-11735-1&2

AGGTTGATCTTTGCTGGGAAACAGCTGGAAGATGGACGCACCCTGTCTGACTACAACCATCCAGAAAGAGTCCA
CCCTGCACCTGGTGCTCCGTCTTAGAGGTGGGATGCAGATCTTCGTGAAGACCCTGACTGGTAAGACCATCACT
CTCGAAGTGGAGCCGAGTGACACCATTTGAGAAYGTCAARGCAAAGATCCARGACAAGGAAGGCATYCCTCCTGA
CCAGCAGAGGTTGATCTTTGCTSGGAAAAGCAGCTGGAAGATGGRCGCACCCTGTCTGACTACAACATCCAGAAA
GAGTCYACCTGCACCTGGTGCTCCGTCTCAGAGGTGGGATGCARATCTTCGTGAAGACCCTGACTGGTAAGAC
CATCACCTCGAGGTGGAGCCAGTGACACCATCGAGAATGTCAAGGCAAAGATCCAAGATAAGGAAGGCATCC
CTCCTGATCAGCAGAGGTTGATCTTTGCTGGGAAACAGCTGGAAGATGGACGCACCCTGTCTGACTACAACATC
CAGAAAGAGTCCACCTYTGCACYTGGTMCCTBCGCTCTYAGAGGKGGGRTGcaaaTCTWMTKWagaCaCtCaCTK
KYAAGRYYaTCAMCMWtgAKKTCgAKYSCASTKWCaCTWTCRAAAMGTYRWGCAWagaTCCMAGACAAGGAA
GGCATTCTCCTGACCAGCAGAGGTTGATCT

11769.1.contig

ATGGAGTCTCACTCTGTGACACAGGCTGGAGCGCTGTGGTGCGATATCGGCTCACTGCAGTCTCCACTTCTGG
GTTCAAGCGATCCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCAAGCGTCACCATTAATTTTGTATT
TTTAGTAGAGACATGGTTTCGCCATGTTGGCTGGGCTGGTCTCGAACTCCTGACCTCAAGTGATCTGTCTGGC
CTCCCAAAGTGTTGGGATTACAGGCGAAAGCCAACGCTCCCGGCCAGGGAACAACCTTAGAATGAAGGAAATAT
GCAAAAGAACATCACATCAAGGATCAATTAATTACCATCTATTAATTACTATATGTGGGTAATTATGACTATTT
CCCAAGCATTCTACGTTGACTGCTTGAGAAGATGTTTGTCTGCATGGTGGAGAGTGGAGAAGGGCCAGGATTC
TTAGGTT

11769.2.contig

AGCGCGGTCTTCCGGCGGAGAAAGCTGAAGGTGATGTGGCCGCCCTCAACCGACGCATCCAGCTCGTTGAGGA
GGAGTTGGACAGGGCTCAGGAACGACTGGCCACGGCCCTGCAGAACTGGAGGAGGCAGAAAAGCTGCAGATG
AGAGTGAGAGAGGAATGAAGGTGATAGAAAACCGGGCCATGAAGGATGAGGAGAAGATGGAGATTGAGGAGATG
CAGCTCAAAGAGGCCAAGCACATTGCGGAAGAGGCTGACCGCAAATACGAGGAGGTAGCTCGTAAGCTGGTCAT
CCTGGAGGGTGAGCTGGAGAGGGCAGAGGAGCGTGCGGAGGTGTCTGAACTAAAATGTGGTGACCTGGAAGAAG
AACTCAAGAATGTTACTAACAATCTGAAATCTCTGGAGGCTGCATCTGAAAAGTATTCTGAAAAGGAGGACAAA
TATGAAGAAGAAATTAACCTTCTGTCTGACAACTGAAAGAGGCTGAGACCCGTGCTGAATTTGAGAGAGAAC
GGTTGCAAACTGGAAGACAATTGATGACCTGGAAGAGAACTTGCCAGC

11770.1.contig

GTGCACAGGTCCCATTTATTGTAGAAAATAATAAATTACAGTGATGAATAGCTCTTCTTAAATTACAAAACA
GAAACCACAAGAAGGAAGAGGAAAAACCCAGGACTTCAAGGGTGAAGCTGTCCCTCCTCCTGCCACCT
CCCAGGCTCATTAGTGCTTGGAAAGGGCAGAGGACTCAGAGGGGATCAGTCTCCAGGGGCCCTGGGCTGAAG
CGGGTGAGGCAGAGAGTCTGAGGCCACAGAGCTGGGCAACCTGAGCCGCTCTCTGGCCCCCTCCCCACCAC
TGCCCAAACCTGTTTACAGCACCTTCGCCCTCCCTCTAAACCCGTCCATCCACTCTGCACTTCCAGGCAGG
TGGGTGGGCCAGGCTCAGCCATACTCTGGGCGCGGGTTTCGGTGAGCAAGGCACAGTCCAGAGGTGATATC
AAGGCCT

Fig. 15F

SUBSTITUTE SHEET (RULE 26)

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11770.2.contig

GCAAGGAAC TGGTCTGCT CACACTTGCTGGCTTGC GCATCAGGACTGGCTTTATCTCCTGACTCACGGTGCAAA
GGTGCACTCTGCGAACGTTAAGTCCGTCCCAGCGCTTGAATCCTACGGCCCCACAGCCGGATCCCCCAGC
CTTCCAGGTCTCAACTCCCGTGGACGCTGAACAATGGCCTCCATGGGGCTACAGGTAATGGGCATCGCGCTGG
CCGTCTGGGCTGGCTGGCGGTATGCTGTGCTGCGCGCTGCCATGTGGCGGTGACGGGCTTCATCGGCAGC
AACATTGTACCTCGCAGACCATCTGGGAGGGCTATGGATGAACTGCGTGGTGACAGACACCGGCCAGATGCA
GTGCAAGGTGTACGACTCGCTGCTGGCACTGCCGAGGACCTGCAGGCGGCCCGCGCCCTCGTCATCATCA

11773.1.contig

TGCAAAAGGGACACAGGGTTCAAAAATAAAATTTCTCTTCCCCCTCCCCAAACCTGTACCCAGCTCCCCGA
CCACAACCCCTTCTCTCCCCGGGGAAGCAAGAAGGAGCAGGTGTGGCATCTGCAGCTGGGAAGAGAGAGGCC
GGGGAGGTGCCGAGCTCGGTGCTGGTCTTTCCAAATATAATACXTGTGTGAGAACTGGAAAATCCTCCAGC
ACCCACCACCAAGCACTCTCCGTTTCTGCCGTTGTTGGAGAGGGGCGGGGGCAGGGGCGCCAGGCACCGG
CTGGCTGCGGTCTACTGCATCCGTGGGTGTGACCCCGCGAGCCTCCTGCTGCTATTGTAGAAGAGATGACA
CTCGGGTCCCCCGGATGGTGGGGCTCCCTGGATCAGCTTCCCGTGTGGGGTTACACACCAGCACTCCC
CACGCTGCCGTTACAGACATCTTGCACTGTTGAGGTTGTACAGGCCATGCTTGTACAGTTG

11778.1.contig

GGGTGGAGGGACTGGTCTTTATTTCAAAAAGACACTTGTCAATATTCAGTATCAAAACAGTTGCACTATTGA
TTTCTCTTCTCCCAATCGGCCCAAGAGACCACATAAAAGGAGAGTACATTTTAAGCCAATAAGCTGCAGGA
TGACACCTAACAGACCTCCTAGAACTTACCAGAAAATGGGACTGGGTAGGGAAGGAACTTAAAGATCA
ACAACTGCCAGCCACGGACTGCAGAGGCTGTACAGCCAGATGGGGTGGCCAGGGTGCCACAAACCCAAAGC
AAAGTTTCAAAATAATATAAAATTTAAAAAGTTTGTACATAAGCTATTCAAGATTTCTCCAGCACTGACTGAT
ACAAAGCACAATTGAGATGGCACTTCTAGAGACAGCAGCTTCAAAACCAGAAAAGGTGATGAGATGAGTTTCA
CATGGCTAAATCAGTGGCAAAACACAGTCTTCTTTCTTTCTTTCAAGGAGGCAGGAAAGCAATTAAGTG
GTCACCTCAACATAAGGGGGACATGATCCATTCTGTAAGCAGTTGTGAAGGGG

11778-2&30-2

CAGGAACCGGAGCGCGAGCAGTAGCTGGGTGGGCACCATGGCTGGGATCACCACCATCGAGGCGGTGAAGCGCA
AGATCCAGGTTCTGCAGCAGCAGGCAGATGATGCAGAGGAGCGAGCTGAGCGCCTCCAGCGAGAAGTTGAGGGA
GAAAGGCGGGCCCGGAACAGGCTGAGGCTGAGGTGGCTCCTTGAACCGTAGGATCCAGCTGGTTGAAGAAGA
GCTGGACCGTGCTCAGGAGCGCTGGCCACTGCCCTGCAAAAGCTGGAAGAAGCTGAAAAGCTGCTGATGAGA
GTGAGAGAGGTATGAAGGTTATTGAAAACCGGGCTTAAAGATGAAGAAAAGATGGAATCCAGGAAATCCAA
CTCAAGAAGCTAAGCACATTGCAGAAGAGGCAGATAGGAAGTATGAAGAGGTGGCTCGTAAGTTGGTGATCAT
TGAAGGAGACTTGAACGCACAGAGGAACGAGCTGAGCTGGCAGAGTCCCGTTGCCGAGAGATGGATGAGCAGA
TTAGACTGATGGACCAGAACCTGAAGTGTCTGAGTGC

Fig. 15G

SUBSTITUTE SHEET (RULE 26)

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11782.1.contig

ATCTACGTCATCAATCAGGCTGGAGACACCATGTTCAATCGAGCTAAGCTGCTCAATATTGGCTTTCAAGAGGC
CTTGAAGGACTATGATTACAACCTGCTTTGTGTTCAAGTGATGTGGACCTCATTCCGATGGACGACCGTAATGCCT
ACAGGTGTTTTTCGCAGCCACGGCACATTTCTGTTGCAATGGACAAGTTCGGGTTTAGCCTGCCATATGTTTCAG
TATTTTGGAGGTGTCTCTGCTCTCAGTAAACAACAGTTTCTTGCCATCAATGGATTCCCTAATAATTATTGGGG
TTGGGGAGGAGAAGATGACGACATTTTAAACAGATTAGTTTCAAAAGGCATGTCTATATCACGTCCAAATGCTG
TAGTAGGGAGGTGTGCAATGATCCGGCATTCAAGAGACAAGAAAAATGAGCCCAATCCTCAGAGGTTTGACCGG
ATCGCACATACAAAGGAAACGATGCGCTTCGATGGTTTGAACCTACCTACCAAGGTGTTGGATGTCAGAGA
TACCGGTTATATACCCAAATCAC

11782.2.contig

CTAGACCTCTAATTAAAAGGCACAATCATGCTGGAGAATGAACAGTCTGACCCCGAGGGCCACAGCGAATTTTA
GGGAAGGAGGCAAGAGGTGAGAAGGGAAGGAAAGGAAGGAAGGAGAACAATAAGAACTGGAGACGTTGG
GTGGGTGAGGAGGTGTGGTGGAGGCTCGGAGAGATGGTAAACAAACCTGACTGCTATGAGTTTCAACCCATA
GTCTAGGGCCATGAGGGCGTCAGTTCTTGGTGGCTGAGGGTCCTTCCACCCAGCCACCTGGGGGAGTGGAGTG
GGGAGTTCTGCCAGGTAGCAGATGTTGTCTCCAAGTTCCTGACCCAGATGTCTGGCAGGATAACGCTGACCT
GTTCCCTCAACAAGGGACCTGAAAGTAATTTTGCTCTTTAC

11783-1 & 2

CCGAATTCAAGCGTCAACGATCCYTCCCTTACCATCAAATCAATTGGCCACCAATGGTACTGAACCTACGAGTA
CACCGACTACGGCGGACTAATCTTCAACTCCTACATACTTCCCCATTATTCTAGAACCCAGGCGACCTGCGA
CTCCTTGACGTTGACAATCGAGTAGTACTCCCGATTGAAGCCCCATTTCGTATAATAATTACATCACAAGACGT
CTTGCACTCATGAGCTGTCCCACTTAGGCTTAAAAACAGATGCAATTCCCGGACGTCTAAGCCAAACCACTT
TCACCGCTACACGACCGGGGTATACTACGGTCAATGCTCTGAAATCTGTGGAGCAAACACAGTTTCATGCCC
ATCGTCTAGAAATTAATCCCTAAAAATCTTGAATAGGGCCGTAATTTACCCTATAGCACCCCTCTACCC
CCTCTAG

11786.1.contig

GCTCTTCACACTTTTATTGTTAATTCTCTTCACATGGCAGATACAGAGCTGTGCTTGAAGACCACCACTGAC
CAGGAAATGCCACTTTTACAAAATCATCCCCCTTTTCATGATTGGAACAGTTTTCCTGACCGTCTGGGAGCGT
TGAAGGGTGACCAGCACATTTGCACATGCAAAAAAGGAGTGACCCCAAGGCCTCAACCACACTTCCAGAGCTC
ACCATGGGCTGCAGGTGACTTGCCAGGTTTGGGGTTCGTGAGCTTTCCTTGCTGCTGCGGTGGGGAGGCCCTCA
AGAACTGAGAGGCCGGGTATGCTTCATGAGTGTTAATTTACGGGACAAAAGCGCATCATTAGGATAAGGAA
CAGCCACAGCACTTCATGCTTGTGAGGGTAGCTGTAGGAGCGGGTGAAGGATTCCAGTTTATGAAAATTTAA
AGCAAACAACGGTTTTTATGCTGGGTGGGAAACAGGAAACTGTGATGTCGGCCAATGACCACCATTTTCTGCC
CATGTGAAGGTCCCATGAAACC

Fig. 15H

SUBSTITUTE SHEET (RULE 26)

43/101

11786.2.contig

CAAGCGCTTGGCGTTTGGACCCAGTTCAGTGAGGTTCTTGGGTTTTGTGCCTTTGGGGATTTTGGTTTGACCCA
GGGGTCAGCCTTAGGAAGGTCTTCAGGAGGAGGCCAGTTCCTTCAGTACCACCCCTCTCTCCCACTTTCC
CTCTCCCGGCAACATCTCTGGGAATCAACAGCATATTGACACGTTGGAGCCGAGCCTGAACATGCCCTCGGCC
CCAGCACATGGAACCCCTTCTTGCCTAAGGTGTCTGAGTTTCTGGCTCTTGAGGCATTTCCAGACTTGAA
ATTCTCATCAGTCCATTGCTCTTGAGTCTTTGCAGAGAACCTCAGATCAGGTGCACCTGGGAGAAAGACTTTGT
CCCCACTTACAGATCTATCTCCTCCCTTGGGAAGGGCAGGGAATGGGGACGGTGTATGGAGGGGAAGGSATCTC
CTGGGCCCTTCATTGCCACACTTGGTGGGACCATGAACATCTTTAGTGTCTGAGCTTCTCAAATTACTGCAATA
GGA

13691.1&2

AGCGTCAAATCAGAATGGAAGACTCAAAACCATCATCAACACCAAGATCAAAAGGACAAGRATCCTTCAAGA
AACAGGAAAAAAGTCTTAAACACCAAAAGGACCTAGTTCTGTAGAAGACATTAAAGCAAAATGCAAGCAAGT
ATAGAAAAAGGTGGTTCTCTTCCAAAGTGAAGCCAAATTCATCAATTATGTGAAGAATTGCTTCCGGATGAC
TGACCAAGAGGCTATTCAAGATCTCTGGCAGTGGAGGAAGTCTCTTAAAGAAATAGTTAAACAATTTGTAA
AAAAATTTCCGTCTTATTTTCAATTTCTGTAAACAGTTGATATCTGGCTGTCTTTTTATAATGCAGAGTGAGAACT
TTCCCTACCGTGTTTGATAAATGTTGTCCAGGTTCTATTGCCAAGAATGTGTGTCCAAATGCCTGTTTAGTT
TTTAAAGATGGAATCCACCCCTTGTCTGGTTTTAAGTATGTATGGAATGTTATGATAGGACATAGTAGTAGCG
GTGGTCAGACATGGAATGGTGGGSMGACAAAAATATACATGTGAAATAA

13692.1&2

TCCGAATCCAAGCGAATTATGGACAAACGATTCTTTTAGAGGATTACTTTTTCAATTTGGGTTTTAGTAAT
CTAGGCTTTGCCGTGTAAGAATACAACGATGGATTTTAAACTGTGTTGTGGAATGTGTTTAAAGGATTGATTC
TAGAACCTTTGTATATTTGATAGTATTTCTAACTTTCATTTCTTTACTGTTTGCAGTTAATGTTTATGTTCTGC
TATGCAATCGTTTATATGCAGTTTCTTTAATTTTTTAGATTTTCTGGATGTATAGTTTAAACAACAAAAAG
TCTATTTAAACTGTAGCAGTAGTTTACAGTTCTAGCAAAGAGGAAAGTTGTGGGGTTAACTTTGTATTTTCT
TTCTTATAGAGGCTTCTAAAAAGGTATTTTATATGTTCTTTTAACAAATATTGTGTACAACCTTTAAACAT
CAATGTTTGGATCAAACAAGACCCAGCTTATTTTCTGC

13693.2

TGTGGTGGCGGGCTGAGGTGGAGGCCAGGACTCTGACCCTGCCCTGCCTTCAGCAAGGCCCGGGCAGCG
CCGGCCACTACGAAGTCCGTTGGGTTGAAAAATATAGGCCAGTAAAGCTGAATGAAATTGTCGGGAATGAAGAC
ACCGTGAGCAGGCTAGAGGTCTTTGCAAGGGAAGGAAATGTGCCAACATCATCATTGCGGGCCCTCCAGGAAC
CGGCAAGACCACAAGCATTCTGTGCTTGGCCGGGCCCTGCTGGGCCAGCACTCAAAGATGCCATGTTGGAAC
TCAATGCTTCAAATGACAGGGGCATTGACGTTGTGAGGAATAAAATTTAAATGTTTGTCAACAAAAAGTCACT
CTTCCCAAAGGCCGACATAAGATCATCATTCTGGATGAAGCAGACAGCATGACCGACGGAGCCAGCAAGCCTT
GAGGAGAACCATGGAATCTACTCTAAACCACTCGTTGCCCTTGCTTGTAATGCTTCGGATAAGATCATCGA
GCC

Fig. 15I

SUBSTITUTE SHEET (RULE 26)

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13696.1-13744.1

CTTTGCAAAGCTTTTATTTTCATGTCTGCGGCATGGAATCCACCTGCACATGGCATCTTAGCTGTGAAGGAGAAA
GCAGTGCACGAGAAGGAATGAGTGGGCGGAACCAACGGCCTCCACAAGCTGCCTTCCAGCAGCCTGCCAAGGCC
ATGGCAGAGAGAGACTGCAACAAACACAAGCAACAGAGTCTCTTCACAGCTGGAGTCTGAAAGCTCATAGTG
GCATGTGTGAATCTGACAAAATTAAGTGTGCATAGTCCATTACATGCATAAAACACTAATAATAATCCTGTT
TACACGTGACTGCAGCAGGCAGGTCCAGTCCACCACTGCCCTCCTGCCACATCACATCAAGTGCCATGGTTTA
GAGGGTTTTTCATATGTAATTCCTTTATTCTGTAAAAGGTAACAAAATATACAGAACAAACTTCCCTTTTAA
AACTAATGTTACAAATCTGTATTATCACTTGGATATAAATAGTATATAAGCTGATC

13700.1

CAAGGGATATATGTTGAGGGTACRGRGTGACACTGAACAGATCACAAAGCAGGAGAAACATTAGTTCTCTCCCT
CCCAGCGTCTCCTTCGTCTCCCTGGTTTTCCGATGTCCACAGAGTGAGATTGTCCCTAAGTAAGTGCATGATC
AGAGTGTGKCTTTATAAGACTCTTCATTACGGTATCCAATTCAGCAATTGCTTCATCAAAATGCCGTTTTTGC
CAGGCTACAGGCCTTTTCAGGAGAGTTAGAAATCTCATAGTAAAAGACTGAGAAATTTAGTGCCAGACCAAGAC
GAATTGGGTGTGAGGCTGCATTNCTTTCTTACTAATTTCAAATGCTTCCTGTAAGCCTGTGGGAGTTCGAC
ACAAGTGGTTTTGTTTGTGCTCCAGATGCCACTTCAGAAAGATACCTAAAATAATCTCCTTTTCATTTCAAAGT
AGAACAC

13700.2

TCCGGAGCCGGGGTAGTCCGCCGCCGCCGCCGGTGACGCCACTGCAGGCACCGCTGCCGCCGCTGAGTAGT
GGGCTTAGGAAGGAAGAGGTATCTCGCTCGGAGCTTCGCTCGGAAGGGTCTTTGTTCCCTGCAGCCCTCCAC
GGGAATGACAATGGATAAAAGTGAGCTGGTACAGAAAGCCAAACTCGCTGAGCAGGCTGAGCGATATGATGATA
TGGCTGCAGCCATGAAGGCAGTCACAGAACAGGGGCATGAACCTCCAACGAAGAGAGAAATCTGCTCTCTGTT
GCCTACAAGAATGTGGTAAGGCCGCCGCCGCTCTTCTGCGGTGTCTCTCCAGCATTGAGCAGAAAACAGAG
AGGAATGAGAAGAAGCAGCAGATGGGCAAGAGTACCGTGAGAAGATAGAGGCAGAACTGCAGGACATCTGCAA
TGATGTTCTGGAGCTTGTGGACAAATATCTTATTCCAATGTACACAACCCAGAAA

13701.1

AAAAAGCAGCARGTTCAACACAAAATAGAAATCTCAAATGTAGGATAGAACAAAACCAAGTGTGTGAGGGGGGA
AGCAACAGCAAAAGGAAGAAATGAGATGTTGCAAAAAGATGGAGGAGGGTTCCTCTCTCTGAGGACTGAC
TCAAACTGATGTGGCAGTATACACATTCCAGAGTCAGGGGTGTTTATTCTTTTTGGGAGTAAGAAAAGGT
GGGGATTAAGAAGACGTTTCTGGAGGCTTAGGGACCAAGGCTGGTCTCTTCCCCCTCCCAACCCCTTGATC
CCTTTCTCTGATCAGGGGAAAGGAGCTCGAATGAGGGAGGTAGAGTTGGAAAGGGAAAGGATTCCACTTGACAG
AATGGGACAGACTCCTTCCCA

Fig. 15J

SUBSTITUTE SHEET (RULE 26)

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13701.2

TGGCAATAGCACAGCCATCCAGGAGCTCTTCARGCGCATCTCGGAGCAGTTCACTGCCATGTTCCGCCGGAAGG
CCTTCCTCCACTGGTACACAGGCGAGGGCATGGACGAGATGGAGTTCACCGAGGCTGAGAGCAACATGAACGAC
CTCGTCTCTGAGTATCAAGCAGTACCAGGATGCCACCGCAGAAGAGGAGGAGGATTCGGTGAGGAGGCCGAAG
AGGAGGCCCTAAGGCAGAGCCCCATCACCTCAGGCTTCTCAGTTCCTTAGCCGTCTTACTCAACTGCCCTTT
CCTCTCCCTCAGAAATTTGTGTTTGCTGCCTCTATCTGTTTTTGTGTTTTCTTCTGGGGGGGTCTAGAACAGT
GCCTGGCACATAGTAGGCGCTCAATAAATACTTGGTTGNTGAATGTCTCCT

13702.2

AGCTGGCGCTAGGGCTCGGTTGTGAAATACAGCGTRGTCAGCCCTTGCGCTCAGTGTAGAAACCCAGCCTGTA
AGGTCGGTCTTCGTCCATCTGCTTTTTCTGAAATACACTAAGAGCAGCCACAAAACCTGTAACTCAAGGAAAC
CATAAAGCTTGGAGTGCCTTAATTTTAACAGTTTCCAATAAAACGGTTTACTACCT

13704.2-13740.2

GGAGATGAAGATGAGGAAGCTGAGTCAGCTACGGGCARGCGGGCAGCTGAAGATGATGAGGATGACGATGTGCA
TACCAAGAAGCAGAAGACCGACGAGGATGACTAGACAGCAAAAAAGGAAAAGTTAAA

13706.1

GATGAAAATTAATACTTAAATTAATCAAAAGGCACTACGATACCACCTAAACCTACTGCCTCAGTGGCAGTA
KGCTAAKGAAGATCAAGCTACAGSACATYATCTAATATGAATGTTAGCAATTACATAKARGAAGCATGTTTGC
TTTCAGAAGACTATGGNACAATGGTCATTWGGCCCAAGAGGATATTTGGCCNGGAAAGGATCAAGATAGATN
AANGTAAAG

13706.2

GAGTAGCAACGCAAAGCGCTTGGTATTGAGTCTGTGGSGACTTCGGTTCGGTCTCTGCAGCAGCCGTGATCG
CTTAGTGGAGTGCTTAGGGTAGTTGGCCAGGATGCCGAATATCAAATCTTCAGCAGGCAGCTCCACCAAGGAC
TTATCTCASAAAATTGCTGACCGCTGGGCTGGAGCTAGGCAAGGTGGTGAATAAGAAATTCAGCAACCAGGA
GACCTGTGTGGAATTTGGTGAAAGGTACCGTGGAGAGGATGTCTACATTGTTGAGAGTGGNTGTGGCGAAATC
AATGACAATTTAATGGAGCTTTTGATCATGATTAATGCCCTGCAAGATTGCTTCAGCCAGCCGGGTTACTGCAAT
CATCCCATGCTTCCCTTATGCCCCGGCAGGATAAGAAAGATNAGAGCCGGGCCGCAATCTCAGCCAAGCTTGG
TGCAATATGCTATCTGTAGCAGTGCAGATCATATTATCACCATGGACCTACATGCTTCTCAAATTCANGGCTT
TTT

Fig. 15K

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13707.3

ATGCAAAAGGGGACACAGGGGGTTCAAAAATAAAATTTCTCTCCCCCTCCCCAAACCTGTACCCAGCTCCC
CGACCACAACCCCTTCTCCCCGGGGAAGCAAGAAGGAGCAGGTGTGGCATCTGCAGCTGGGAAGAGAGAG
GCCGGGGAGGTGCCGAGCTCGGTGCTGGTCTCTTTCAAATATAAATACGTGTGTGAGAACTGGAAATCCTCC
AGCACCCACCACCAAGCACTCTCGTTTTCTGCCGGTGTGAGAGAGGGGCGGNGGGCAGGGGCGCCAGGCAC
CGGTGGCTGCGGTCTACTGCATCCGCTGGGTGTCACCCCGCA

13710.2

AGGTTGGAGAAGGTCATGCAGGTGCAGATTGTCCAGGSKCAGCCACAGGGTCAAGCCCAACAGGCCAGAGTGG
CACTGGACAGACCATGCAGGTGATGCAGCAGATCATCAACACAGGAGAGATCCAGCAGATCCCGGTGCAGC
TGAATGCCGGCCAGCTGCAGTATATCCGCTTAGCCAGCCTGTATCAGGCACTCAAGTTGTGCAGGGACAGATC
CAGACACTTGCCACCAATGCTCAACAGATTACACAGACAGAGGTCCAGCAAGGACAGCAGCTTCAAGCCAGT
TCACAAGATGGACAGCAGCTCTACCAGATCCAGCAAGTCAACATGCCTGCGGGCCANGACCTCGCCAGCCCATG
TTCATCCAGTCAAGCCAACAGCCCTTCNACGGGCAGGCCCCCAGGTGACCGGCGACTGAAGGGCCTGAGCTG
GCAAGGCCAANGACACCAACACAATTTTGCCATACAGCCCCAGGCAATGGGCACAGCCTTTCTCCAGAG
GAC

13710-1

TGAGATTTATTGCATTTTCATGCAGCTTGAAGTCCATGCAAAGGGRGACTAGCACAGTTTTTAATGCATTTAAAAA
ATAAAAGGGAGGTGGGCAGCAACACACAAAGTCTAGTTTCTGGGTCCCTGGGAGAAAAGAGTGTGGCAATG
AATCCACCCACTCTCCACAGGGAATAAATCTGTCTCTTAAATGCAAAGAATGTTTCCATGGCCTCTGGATGCAA
ATACACAGAGCTCTGGGGTCAGAGCAAGGGATGGGAGAGGACCACGAGTGAAGGAGCAGCTACACACATTAC
CTAATTCATCTGAGGGCAAGAACAACGTGGCAAGTCTTGGGGTAGCAGCTGTT

13711.1

TCCAGACATGCTCCTGTCTAGGCGGGGAGCAGGAACCAGACCTGCTATGGGAAGCAGAAAGAGTTAAGGGAAG
GTTTCCTTTTCATTCTGTTCTCTTTTGTCTTTGAACAGTTTTTAAATATACTAATAGCTAAGTCATTTGC
CAGCCAGGTCCCGTGAACAGTAGAGAACAAAGGAGCTTGCTAAGAATTAATTTGCTGTTTTACCCCATTC
AACAGAGCTGCCCTGTTCCCTGATGGAGTTCCATTCTGCCAGGGCACGGCTGAGTAACAGGAAGCCATTCAAG
AAAGGCGGGTGTGAAATCACTGCCACCCCATGGACAGACCCCTCACTCTTCTTCTAGCCGACGCGCTACTTA
ATAAATATATTTATACTTTGAAATTATGATAACCGATTTTCCCATGCGGCATCCTAAGGGCACTTGCCAGCTC
TTATCCGGACAGTCAAGCACTGTTGTTGGACAACAGATAAAGGAAAAAGAAAAAGAAAAACAACCGCAACTTC
TGT

Fig. 15L

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13711.2

TGAGACGGACCACTGGCCTGGTCCCCCTCATKTGCTGTCTAGGACCTGACATGAAACGCAGATCTAGTGGCA
GAGAGGAAGATGATGAGGAACCTTGAGACGTCGGCAGCTTCAAGAAGAGCAATTAATGAAGCTTAACCTCAGGC
CTGGGACAGTTGATCTTGAAAGAAGAGATGGAGAAAGAGAGCCGGGAAAGGTCATCTCTGTTAGCCAGTGGCTA
CGATTCTCCCATCAACTCAGCTTCACATATTCATCATCTAAACTGCATCTCTCCCTGGCTATGGAAGAAATG
GGCTTCACCGGCTGTTTCTACCGACTTCGCTCAGTATAACAGCTATGGGGATGTCAGCGGGGAGTGCGAGAT
TACCAGACACTTCAGATGGCCACATGCCGCAATGAGAATGGACCGAGGAGTGTCTATGCCAACATGTTGGA
ACCAAAGATATTTCCATATGAAATGCTCATGGTGACCAACAGAGGGCCGAAACCAATCTCAGAGAGGTGGACA
GAA

13713.1&2

TCACTTTATTTTCTTGATATAAAACCCTATGTTGTAGCCACAGCTGGAGCCTGAGTCCGCTGCACGGAGACTC
TGGTGTGGGCTTGACGAGGTGGTCAGTGAATCCTGATAGGAGACTTGGTGAATACAGTCTCCTTCCAGAGG
TCGGGGGTGAGGTAGCTGTAGGTCTTAGAAATGGCATCAAAGGTGGCTTGGCGAAGTTGCCAGGCTGGCAGT
GCAGCCCCGGGCTGAGGTGTAGCAGTCATCGATACCAGCCATCATGAG

13715.4

CTGGAATATAGACCCGTGATCGACAAAACCTTTGAACGAGGCTGACTGTGCCACCGTCCCGCCAGCCATTCGCTC
CTACTGATGAGACAAGATGTGGTGATGACAGAATCAGCTTTTGTAAATATGTATAATAGCTCATGCATGTGTCC
ATGTCATAACTGTCTTCATACGCTTCTGCACTCTGGGGAAGAAGGAGTACATTGAAGGGAGATTGGCACCTAGT
GGCTGGGAGCTTGCCAGGAACCCAGTGCCAGGGAGCGTGGCACTTACCTTTGTCCCTTGCTTCATTCTTGTA
GATGATAAACTGGGCACAGCTCTTAAATAAAATATAAATGAACA

13717.1&2

TGAATGGGGAGGAGCTGACCCAGGAAATGGAGCTTGNGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAG
TGGGCATCTGTGGTGGTGCCTCTTGGGAAGGAGCAGAAGTACACATGCCATGTGGAACATGAGGGGCTGCCTGA
GCCCCCTCACCCTGAGATGGGGCAAGGAGGAGCCTCCTTCATCCACCAAGACTAACACAGTAATCATTGCTGTTTC
CGGTTGTCTTGGAGCTGTGGTCATCCTTGGAGCTGTGATGGCTTTTGTGATGAAGAGGAGGAGAAACACAGGT
GGAAAAGGAGGGGACTATGCTCTGGCTCCAGGCTCCAGAGCTCTGATATGTCTCTCCAGATTGTAAAGTGTG
AAGACAGCTGCCTGGTGTGGACTTGGTGACAGACAATGTCTTCACACATCTCCTGTGACATCCAGAGACCTCAG
TTCTCTTTAGTCAAGTGTCTGATGTTCCCTGTGAGTCTGCGGGCTCAAAGTGAAGAACTGTGGAGCCAGTCCA
CCCCTGCACACCAGGACCTATCCTGCACTGCCCTGTGTTCCCTTCCACAGCCAACCTTGCTGCTCCAGCCAA
ACATTGGTGGACATCTGCAGCCTGTGAGTCCATGCTACCCCTGACCTTCAACTCCTCACTTCCACACTGAGAAT
AATAATTTGAATGTGGGTGGCTGGAGAGATGGCTCAGCGCTGACTGCTCTTCAAAGGTCTGAGTTCAAATCC
CAGCAACCACATGGTGGCTCACAACCATCTGTAATGGGATCTAATACCCTCTTCTGCAGTGTCTGAAGACASCT
ACAGTGTACTTACATATAATAATAAATAAG

Fig. 15M

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13719.1&2

GGCCGGGCGCGCGCCCCGCCACACGCACGCCGGCGTGCCAGTTTATAAAGGGAGAGAGCAAGCAGCGAGT
CTTGAAGCTCTGTTTGGTGCTTTGGATCCATTTCCATCGGTCTTACAGCCGCTCGTCAGACTCCAGCAGCCAA
GATGGTGAAGCAGATCGAGAGCAAGACTGCTTTTCAGGAAGCCTTGGACGCTGCAGGTGATAAACTTGTAAGT
TTGACTTCTCAGCCAAGTGGTGTGGGCTTGCAAAATGATCAAGCCTTTCTTTCAATCCCTCTCTGAAAAGTAT
TCCAACGTGATATTCTTGAAGTAGATGTGGATGACTGTCAGGATGTTGCTTCAGAGTGTGAAGTCAAATGCAT
GCCAACATTCAGTTTTTTAAGAAGGGACAAAAGGTGGGTGAATTTTCTGGAGCCAATAAGGAAAAGCTTGAAG
CCACCATTAAATGAATTAGTCTAATCATGTTTTCTGAAAATATAACCAGCCATTGGCTATTTAAAACCTTGAATT
TTTTTAATTTACAAAAATATAAAATATGAAGACATAAACCCMGTTGCCATCTGCGTGACAATAAACATTAATG
CTAACACTT

13721.1

TCACATAAGAAATTTAAGCAAGTTACRCTATCTTAAAAACACAACGAATGCATTTTAATAGAGAAACCCTTCC
CTCCCTCCACCTCCCTCCCCACCCTCCTCATGAATTAAGAATCTAAGAGAAGAAGTAACCATAAAACCAAGTT
TTGTGGAATCCATCATCCAGAGTGCTTACATGGTGATTAGGTTAATATTGCCTTCTTACAAAATTTCTATTTTA
AAAAAATTATAACCTTGATTGCTTATTACAAAAAATTCAGTACAAAAGTTCAATATATTGAAAAATGCTTTT
CCCCTCCCTCAGACACCGTTTTATATATAGCAGAGAATAATGAAGAGATTGCTAGTCTAGATGGGGCAATCTT
CAAATTACACCAAGACGCACAGTGGTTATTTACCCTCCCTTCTCATAAG

13721.2

GGAAAGGATTCAAGAATTAGAGGACTTGCTTGCTRRAGAAAAAGACAACCTCTCGTCGCATGCTGACAGACAAAG
AGAGAGAGATGGCGGAAATAAGGGATCAAATGCAGCAACAGCTGAATGACTATGAACAGCTTCTTGATGTAAAG
TTAGCCCTGGACATGGAATCAGTGCTTACAGGAACTCTTAGAAGGCGAAGAAGAGAGGTTGAAGCTGTCTCC
AAGCCCTTCTCCCGTGTGACAGTATCCCGAGCATCCTCAAGTCGTAGTGTACCGTACAACCTAGAGGAAAGCGG
AAGAGGGTTGATGTGGAAGAATCAGAGGCGAAGTAGTAGTGTAGCATCTCTCATTCCGCTCAACCACTGGAA
ATGTTTGCATCGAAGAAATTGATGTTGATGGGAAATTTATCCCGCTTGAAGAACACTTCTGAACAGGATCAACC
AATGGGAAGGCTTGGGAGATGATCAGAAAAATTTGGAGACACATCAGTCAGTTATAAATATACCTCAA

13723.1

CATGGGTTTACCAGGTTGGCCAGGCTGCTCTTGAACSTGACCTCAGGTGATCCACCCGCTCGGCCTCCCA
AAGTGCTGGGATTACAGGCGTGAGCCACCAAGCCCGGCCCCAAAGCTGTTTCTTTGTCTTTAGCGTAAAGCT
CTCCTGCCATGCAGTATCTACATAACTGACGTGACTGCCAGCAAGCTCAGTCACTCCGTGGTCTTTTCTCTTT
CCAGTCTTCTCTCTCTTCAAGTTCTGCCTCAGTGAAAGCTGCAGGTCCCAGTTAAGTGATCAGGTGAGGG
TTCTTTGAACCTGGTTCTATCAGTCGAATTAATCCTTCATGATGG

Fig. 15N

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13723.2

GATGTGTTGGACCTCTGTGTCAAAAAAACCTCACAAGAATCCCCTGCTCATTACAGAAGAAGATGCATTTA
AAATATGGGTTATTTCAACTTTTATCTGAGGACAAGTATCCATTAATTATTGTGTGAGAAGAGATTGAATAC
CTGCTTAAGAAGCTTACAGAAGCTATGGGAGGAGGTTGGCAGCAAGAACAATTTGAACATTATAAAATCAACTT
TGATGACAGTAAAAATGGCCTTTCTGCATGGGAACCTTATTGAGCTTATTGGAATGGACAGTTTAGCAAAGGCA
TGGACCGGCAGACTGTGTCTATGGCAATTATGAAGTCTTATGAACCTATATTAGATGTGTTAAAGCAGGGT
TACATGATGAAAAAGGGCCACAGACGGAAAACTGGACTGAAAGATGGTTTGTACTAAAACCCACATAATTTCT
TACTATGTGAGTGAGGATCTGAAGGATAAGAAAGGAGACATTCTCTGGATGAAAATTGCTGTGTAGAAGTCC
TTGCCTGACAAAAGATGGAAGAAATGCCTTTT

13725.1

GACTGGTCTTTATTTCAAAAAGACACTTGTCAATATTCAGTRTCAAAACAGTTGCACTATTGATTTCTCTTTC
TCCCAATCGGCCCCAAAGAGACCACATAAAAGGAGAGTACATTTTAAGCCAATAAGCTGCAGGATGTACACCTA
ACAGACCTCCTAGAAACCTTACCAGAAAATGGGGACTGGGTAGGGAAGGAACTTAAAGATCAACAACTGCC
AGCCACGGGACTGCAGAGGCTGTACAGCCAGATGGGGTGGCCAGGGTGCCACAAACCCAAAGCAAAGTTTCAA
AATAATATAAAATTTAAAGTTTTGTACATAAGCTATTCAAGATTTCTCCAGCACTGACTGATACAAAGCACA
ATTGAGATGGCACTTCTAGAGACAGCAGCTTCAAACCCAGAAAAGGGTGATGAGATGAAGTTTCACATGGCTAA
ATCAGTGGCAAAAACAGTCTTCTTTCTTTCTTTCTTTCAAGGANGCAGGAAAGCAATTAAGTGGTCACCTTA
ACATAAGGGGGAC

13725.2

TGGGTGGGCACCATGGCTGGGATCACCACCATCGAGGCGGTGAAGCGCAAGATCCAGGTTCTGCAGCAGCAGGC
AGATGATGCAGAGGAGCGAGCTGAGCGCTCCAGCGAGAAGTTGAGGGAGAAAGGCGGGCCGGGAACAGGCTG
AGGCTGAGGTGGCTCCTTGAACCGTAGGATCCAGCTGGTTGAAGAAGAGCTGGACCGTCTCAGGAGCGCCTG
GCCACTGCCCTGCAAAAGCTGGAAGAAGCTGAAAAGCTGCTGATGAGAGTGAGAGAGGTATGAAGGTTATTGA
AAACCGGGCTTAAAGATGAAGAAAAGATGGAATCCAGGAAATCCAACCTCAAAGAAGCTAAGCACATTGCAG
AAGAGGCAGATAGGAAGTATGAAGAGGTGGCTCGTAAGTTGGTGATCATTGAAGGAGACTTGAACCGCACAGA
AGGAACGAGCTTGAGCTTGGCAAAAGTCCCGTTGCCAGAGATGGGATGAACCAGATTAGACTGATGGACCANA
ACC

13726.182

AGGGGCGNCGGGTGCGTGGGCCACTGGGTGACCGACTTAGCCTGGCCAGACTCTCAGCACCTGGAAGCGCCCCG
AGAGTGACAGCGTGAGGCTGGGAGGGAGGACTTGGCTTGAGCTTGTAAACTCTGCTCTGAGCCTCCTTGTCGC
CTGCATTTAGATGGCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAAGGGCCGTTCTGCCATCAACGAAGTGGTAA
CCCGAGAATACACCATCAACATTCAACAAGCGCATCCATGGAGTGGGCTTCAAGAAGCGTGCACCTCGGGCACTC
AAAGAGATTCGGAAATTTGCCATGAAGGAGATGGGAACTCCAGATGTGCGCATTGACACCAGGCTCAACAAAGC
TGTCTGGGCCAAAGGAATAAGGAATGTGCCATACGAATCCGGTGTGCGGCTGTCCAGAAAACGTAATGAGGAT
GAAGATTCACCAAATAAGCTATATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAGACAGT
CAATGTGGATGAGAACTAATCGCTGATCGTCAGATCAAATAAAGTTATAAAAT

Fig. 150

SUBSTITUTE SHEET (RULE 28)

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13727.1

TGGGAGCCACACTTGGCCCTCTTCTCTCCAAAGSGCCAGAACCTCCTTCTCTTTGGAGAATGGGAGGCCTC
TTGGAGACACAGAGGGTTTACCTTGGATGACCTCTAGAGAAATTGCCAAGAAGCCACCTTCTGGTCCCAAC
CTGCAGACCCACAGCAGTCAGTTGGTCAGGCCCTGCTGTAGAAGGTCACTTGGCTCCATTGCCTGCTTCCAAC
CAATGGGCAGGAGAGAAGGCCTTTATTTCTCGCCACCCATTCTCTGTACCAGCACCTCCGTTTTAGTCAG
TGTGTCCAGCAACGGTACCGTTTACACAGTCACCTCAGACACACCATTTACCTCCCTTGCCAAGCTGTTAGC
CTTAGAGTGATTGCAGTGAACACTGTTTACACACCGTGAATCCATTCCCATCAGTCCATTCCAGTTGGCACCAG
CCTGAACCATTTGGTACCTGGTGTAACTGGAGTCCTGTTACAAGGTGGAGTCGGGGCTTGCTGACTTCTCTT
CATTTGAGGGCAC

13727.2

ACCTAGACAGAAGGTGGGTGAGGGAGGACTGGTAGGAGGCTGAGGCAATTCCTTGGTAGTTTGTCTGAAACCC
TACTGGAGAAGTCAGCATGAGGCACCTACTGAGAGAAGTGCCAGAACTGCTGACTGCATCTGTTAAGAGTTA
ACAGTAAAGAGGTAGAAGTGTGTCTGAATCAGAGTGGAAAGCGTCTCAAGGGTCCACAGTGGAGGTCCCTGA
GCTACCTCCCTTCCGTGAGTGGGAAGAGTGAAGCCATGAAGAACTGAGATGAAGCAAGGATGGGGTTCCTGGG
CTCCAGGCAAGGGCTGTGCTCTCTGCAGCAGGGAGCCCCACGAGTCAGAAGAAAAGAACTAATCATTGTTGCA
AGAAACCTTGCCCGGATACTAGCGGAAACTGGAGGCGGNGGTGGGGGCACAGGAAAGTGAAGTGATTTGATG
GAGAGCAGAGAAGCCTATGCACAGTGGCGGAGTCCACTTGTAAGTG

13728.1&2

TCAAGCAATTGTAACAAGTATATGTAGATTAGAGTGAGCAAAATCATATACAATTTTCATTTCAGTTGCTAT
TTTCCAAATTGTTCTGTAATGTCGTTAAATTAATAAAGCCAAAAATTATTTATGACAAGA
AAGCCATCCCTACATTAATCTTACTTTTCCACTACCGGCCCATCTCCTTCTCTTTTCTAACTATGCCATT
AAACTGTTCTACTGGGCCGGGCGTGTGGCTCATGCCGTGAATCCAGCATTTTGGGAGGCCAAGGCAGGCGGA
TCATGAGGTCAAGAGATTGAGACCATCCTGGCCAACATGGTGAACCCCGCCTCGACTAAGAATACAAAAATTA
GCTGGGCATGGTGGCGCATGCCGTGAGTCTCAGCTACTCGGAGGCTGAGGCAGAAGATCGCTTGAACCCGGG
AGGCAGAGGATGCAGTGAGCCCCGATCGGCCACTGCACTTAGCCTGGGCGACAGACTGAGACTCTGCTC

13731.1&2

TGTGCCAGTCTACAGGCCTATCAGCAGCGACTCCTTCAGCAACAGATGGGGTCCCTGTTGAGCCCAACCCCAT
GAGCCCCCAGCAGCATATGCTCCCAATCAGGCCAGTCCCAACCTACAAGGCCAGCAGATCCCTAATTCTC
TCTCCAATCAAGTGCGCTCTCCCAGCCTGTCCCTTCTCCACGGCCACAGTCCAGCCCCCCTCCAGTCTCT
TCCCCAAGGATGCAGCCTCAGCCTTCTCCACACCAGTTTCCCCACAGACAAGTTCCCCACATCCTGGACTGGT
AGTTGCCCAGGCCAACCCCATGGAACAAGGCATTTTCCAGCC

Fig. 15P

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13734.1&2

TGTA AAAA CTG TTTT TA TTTT GTATA AAAA TAAAGGTGGTCCATGCCACGGGGGCTGTAGGAAATCCAAGCA
GACCAGCTGGGGTGGGGGATGTAGCCTACCTCGGGGACTGTCTGTCTCAAACGGGCTGAGAAGGCCCGTC
AGGGGCCAGGTCCACAGAGAGGCTGGGATACTCCCCAACCCGAGGGGCAGACTGGGCAGTGGGGAGCCCC
CATCGTCCCCAGAGGTGGCCACAGGCTGAAGGAGGGGCTGAGGCACCGCAGCCTGCAACCCCGAGGGCTGCA
GTCCACTAATTTTTACAGAATAAAAGGAACATGGGGATGGGGAAAAAGCACCAGGTCAAGGCAGGGCCGAGG
GCCCCAGATCCCAGGAGGGCCAGGACTCAGGATGCCAGCACCACCTAGCAGCTCCACAGTCTCTGGCACAGG
AGGCGCCACGGATTGGCACAGGCCGCTGCTGGCCATCACGCCACATTTGGAGAACTTGTCCGACAGAGGTCA
GCTCGGAGGAGCTCCTCGTGGGCACACACTGTACGAACACAGATCTCCTTGTTAATGACGTACACACGGCGGAG
GCTCGGGGACAGGGCACGGGAGGTCTCAGCCCCACTT

13736.2

ATGGCTGCTGGATTAGGTGGTAATAGGGGCTGTGGGCCATAAATCTGAAGCCTTGAGAACCTTGGGTCTGGAG
AGCCATGAAGAGGSAAGGAAAAGAGGGCAAGTCTGAACCTAACCAATGACCTGATGGATTGCTCGACCAAGAC
ACAGAAGTGAAGTCTGTGTCTGTGCACTTCCACAGACTGGAGTTTTGGTGTGAATAGAGCCAGTTGCTAAA
AAATTGGGGTTTGGTGAAGAAATCTGATTGTGTGTATTCAATGTGTGATTTAAAAATAAACAGCAACAA
CAATAAAACCCGACTGGCTGTTTTTCCCTGTATTTTACAACATTTTTTGACCTCTGAAAATTATTAT
ACTTCACCTAAATGGAAGACTGCTGTGTTGTGGAAATTTGTAATTTTTAATTTATTCTCTCTCTT
TTATTTTGCCTGCAGAAATCCGTTGAGAGACTAATAAGGCTTAATATTTAATTGATTGTTAATATGTATATA
AAT

13744.2-13696.2

GGCATGCGAGCGCACTCGGCGGACGCAAGGGCGGGGAGCACAGGAGCACTGCAGGCGCGGGTTGGGACA
GCGTCTTCGCTGCTGCTGGATAGTCTGTGTTTTCGGGATCGAGGATACTCACCAGAAACCGAAAATCCGAAAC
CAATCAATGTCCGAGTTACCACCATGGATGCAGAGCTGGAGTTTGCAATCCAGCCAAATACAACGAAAACAG
CTTTTGATCAGGTGGTAAAGACTATCGGCCCTCCGGGAAGTGTGGTACTTTGGCCTCCACTATGTGEATAATAA
AGGATTTCTACCTGGCTGAAGCTGGATAAGAAGGTGTCTGCCAGGAGGTCAAGGAAGGAGAAATCCCTCCAGT
TCAAGTTCGGGGCCAAAGTTCTACCCTGAAGATGTGGCTGAGGAGCTCATCCAGGACATCACCAGAAATTTT
CTTCCTTCAAGTGAAGGAAGGAATCCTTAGCGATGAGATCTACTGCCCCCTTGARACTGCCGTGCTCTGGGG
TCCTACGCTTGTGCATGCCAAGTTTGGGGACTACCACCAAGAAG

13746.1&2-13720.1&2

GAAGGAGTCGGGATACTCAGCATTGATGCACCCCAATTTCAAAGCGGCATTCTTCGGCAGGTCTCTGGGACAAT
CTCTAGGGTCACTACCTGGAACTCGTTAGGGTACAATGAATGCTGAAAGGAAAGAACACCTGCAGAACCGGA
CAGAAATTCACCCCGCGATCAGCTGATTGATCTCGGTGACAGAAATCATGGCTAAAGATGACGAGGACGTT
GTCAATTCCTGGGCTTTTGAAGTGAGTCCAGCAGCAGTCTGAGGTATTCGGGCCGGTTATGCACCTGGACCA
CCAGCACCAGTCCCGGGGGGCCAGGTGCCAGCCTTATCTACATTCCTCAGGGTCTGATCAAAGTTCAGCTGG
TACACCAGGGACCGGTACCGCAGCGTCAGGTTGTCCGCTCGGGCTGGGGACCGCCGGGACCAGGGAAGCCGCC
GACACGTTGGAGACCTGCGGATGCCACAGCCACAGAGGGTGTCCCAACCGCGGCCGCGGCACCCCGCGC
GGGTTCCGGCTCCAGCAACGGTGGGGCGAGGGCCTCGTTCTTCTTTGTGCGCCATTGCTGCTCCAGAGGACGA
AGCCGCGAGGCGGCCACACGAGCGTCAGGATTAGCACCTTCGGTTTGTAGATGCGGAACCTCATGGTCTCCAGG
GCCGGGAGCGCAGCTACAGCTCGAGCGTCGGCGCCGCGCTAGGAGCCGCGGCTCGGCTTCGTCTCGTCTCT
CCATTCAGCACCGGTCCTCGGAAAAAGCTCAGCCCGGTCCAACCGCACCTAGCTTCGTTACCTGCGCCT
CGCTTG

Fig. 15Q

SUBSTITUTE SHEET (RULE 26)

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14347.1

CAGATTTTATTTCAGTCGTCACTGGGGCCGTTTCTTGCTGCTTATTTGTCTGCTAGCCTGCTCTTCCAGCTG
CATGGCCAGGCGCAAGGCCTTGATGACATCTCGCAGGGCTGAGAAATGCTTGGCTTGTGGCCAGAGCAGATT
CCGCTTTGTTCAAAAGGTCTCCAGGTCATAGTCTGGCTGCTCGGTCTCATCTCAGAGAGCTCAAGCCAGTCTGGT
CCTTGCTGATGATCTCCTTGAGCTCTTCCATAGCCTTCTCCTCCAGCTCCCTGATCTGAGTCATGGCTTCGTT
AAAGCTGGACATCTGGGAAGACAGTTCCTCCTTCTCCTTGATAAATTGCCTGGAATCAGCGCCCGTTAGAGC
AGGCTTCCATCTCTTCTGTTTCAATTGAATCAACTGCTCTCCACTGGGCCCACTGTGGGGCTCAGCTCCTTG
ACCCTGCTGCATATCTTAAGGGTGTAAAGGATATTACAGGAGCTTATGCCTGGT

14347.2

CTCCTCTTGGTACATGAACCCAAGTTGAAAGTGGACTTAACAAAGTATCTGEAGAACCAAGCATTCTGCTTTGA
CTTTGCATTTGATGAAACAGCTTCGAATGAAGTTGTCTACAGGTTACAGCAAGGCCACTGGTACAGACAATCT
TTGAAGGTGGAAGCAACTTGTGTTTGCATATGGCCAGACAGGAAGTGGCAAGACATACTATGGGCGGAGAC
CTCTCTGGGAAAGCCAGAATGCATCCAAAGGGATCTATGCCATGGCCTTCGGGACGTCTTCTTGAAGAAT
CAACCTGTACCGGAAGTTGGGCCCTGGAAGTCTATGTGACATTCCTCGAGATCTACAATGGGAAGCTGTTTGA
CCTGCTCAACAAGAAGGCCAAGCTTGCGCGTGTGGAAGACGGCAAGCAACAGGTGCAAGTGGTGGGGCTTGC
AGGAACATCTGGNTAACTCTGCTTGATGATGGCANTCAAGATGATCGACATGGCAGCGCCTGCAGA

14348.2&14350.1&2

TCCGAATTCAAGCGACAAATTGGAWAGTGAAATGGAAGATGCCATATCATGAACATCAGGCAAACTTTTGGCG
CAAGATCTGATGAGACGACAGGAAGAATTAAGACGCATGGAAGAACTTCACAATCAAGAAATGCAGAAACGTAA
AGAAATGCAATTGAGGCAAGAGGAGGAACGACGTAGAAGAGAGGAAGAGATGATGATTTCGTCAACGTGAGATGG
AAGAACAATGAGGCGCCAAAGAGAGGAAAGTTACAGCCGAATGGGCTACATGGATCCACGGGAAAGAGACATG
CGAATGGGTGGCGGAGGAGCAATGAACATGGGAGATCCCTATGGTTCAGGAGGCCAGAAATTTCCACCTCTAGG
AGGTGGTGGTGGCATAGGTTATGAAGCTAATCCTGGCGTTCCACCAGCAACCATGAGTGGTTCATGATGGGAA
GTGACATGCGTACTGAGCGCTTTGGGCAGGGAGGTGCGGGCCCTGTGGGTGGACAGGGTCTAGAGGAATGGG
CCTGGAATCCAGCAGGATATGGTAGAGGGAGAGAAGGTACGAAGGC

14349.1&2

TTCTGTAAGACCCTGACTGGTAAGACCATCACTCTCGAAGTGGAGCCGAGTGACACCATGAGAATGTCAAGG
CAAAGATCCAAGACAAGGAAGGCATCCCTCCTGACCAGCAKAGGTTGATCTTTGCTGGGAAACAGCTGGAAGAT
GGAGCGACCCCTGTCTGACTACAACATCCAGAAAGAGTCCACCCTGCACCTGGTGCTCCGTCTCAGAGGTGGGAT
GCAAATCTTCGTGAAGACCCTGACTGGTAAGACCATCACCCTCGAGGTGGAGCCAGTGACACCATCGAGAATG
TCAAGGCAAAGATCCAAGATAAGGAAGGCATCCCTCCTGATCAGCAGAGGTTGATCTTTGCTGGGAAACAGCTG
GAAGATGGACGCACCCTGTCTGACTACAACATCCAGAAAGAGTCCACTCTGCACTTGGTCTCGCTTGAGGGG
GGGTGTCTAAGTTTCCCTTTAAGGTTTCAACAAATTCATTGCACTTTCCTTTCAATAAAGTTGTTGCATTCT

Fig. 15R

SUBSTITUTE SHEET (RULE 26)

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14352.1&2

GC GCGGGT GCGTGGGCCACTGGGTGACCGACTTAGCCTGGCCAGACTCTCAGCACCTGGAAGCGCCCCGAGAGT
GACAGCGTGAGGCTGGGAGGGAGGACTTGGCTTGAGCTTGTTAACTCTGCTCTGAGCCTCCTTGTCGCCTGCA
TTTAGATGGCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAGGCCGTTCTGCCATCAACGAAGTGGTAACCCGA
GAATACACCATCAACATTCACAAGCGCATCCATGGAGTGGGCTTCAAGAAGCGTGACCTCGGGCACTCAAAGA
GATTCGGAATTTGCCATGAAGGAGATGGGAACTCCAGATGTGCGCATTGACACCAGGCTCAACAAAGCTGTCT
GGGCCAAAGGAATAAGGAATGTGCCATACCGAATCCGTGTGCGGCTGTCCAGAAAACGTAATGAGGATGAAGAT
TCACCAAATAAGCTATATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAGACAGTCAATGT
GGATGAGAACTAATCGCTGATCGT

14353.1

AATTCCTTTATTTAAATCAACAACTCATCTTCTCAAGCCCCAGACCATGGTAGGCAGCCCTCCCTCTCCATCC
CCTCACCCACCCCTTAGCCACAGTGAAGGGAATGGAAAATGAGAAGCCACGAGGGCCCTGCCAGGGAAGGCT
GCCCCAGATGTGTGGTGAGCACAGTCAGTGCAGCTGTGGCTGGGGCAGCAGCTGCCACAGGCTCCTCCCTATAA
ATTAAGTTCCTGCAGCCACAGCTGTGGGAGAAGCATACTTGTAGAAGCAAGGCCAGTCCAGCATCAGAAGGCAG
AGGCAGCATCAGTACTCCAGCCATGGAATGAACGGAGGACACAGAGCTCAGAGACAGAACAGGCCAGGGGGA
AGAAGGAGAGACAGAATAGGCCAGGGCATGGCGGTGAGGGA

14353.2

TGATGAATCTGGGTGGGCTGGCAGTAGCCCGAGATGATGGGCTCTTCTCTGGGGATCCCACTGGTTCCTAAG
AAATCCAAGGAGAATCCTCGGAACCTCTCGGATAACCAGCTGCAAGAGGGCAAGAACGTGATCGGGTTACAGAT
GGGCACCAACCGCGGGGCGTCTCANGCAGGCATGACTGGCTACGGGATGCCACGCCAGATCCTCTGATCCACC
CCAGGCCCTTGCCCTGCCCTCCACGAATGGTTAATATATATGTAGATATATATTTAGCAGTGACATCCAG
AGAGCCCCAGAGCTCTCAAGCTCCTTTCTGTGAGGGTGGGGGTTCAAGCCTGTCTGTACCTCTGAAGTGCC
TGCTGGCATCCTCTCCCCATGCTTACTAATACATTCCTTCCCCATAGCC

17182.1&2

AGCGGAGCTCCCTCCCTGGTGGCTACAACCCACACAGCCAGGCTCAGGCATCGAGCAGAACTCCAGCGACTG
GGTAACCACTGACATTCAGGTGAAGGTGCGGGACACCTACCTGGATACACAGGTGGTGGGACAGACAGGTGTCA
TCCGCACTGTACGGGGGGCATGTGCTCTGTGTACCTGAAGGACAGTGAGAAGGTTGTCAGCATTTCCAGTGAG
CACCTGGAGCCTATCACCCCAAGAACAAAGGTGAAAGTGATCCTGGGCGAGGATCGGGAAGCCACGGG
CGTCTACTGAGCATTGATGGTGAGGATGGCATTGTCCGTATGGACCTTGATGAGCAGCTCAAGATCCTCAACC
TCCGCTTCTGGGGAAGCTCCTGGAAGCCTGAAGCAGGAGGGCCGGTGGACTTCGTGGATGAAGAGTGATCC
TCCTTCTTCCCTGGCCCTTGCTGTGACACAAGATCCTCCTGCAGGGCTAGGCGGATTGTTCTGGATTTCCTT
TTGTTTTCTTTAGGTTTCCATCTTTTCCCTCCCTGGTGCTCATTGGAATCTGAGTAGAGTCTGGGGGAGGG
TCCCCACCTTCTGTACCTCCTCCCCACAGCTTGCTTTTGTGTACCGTCTTCAATAAAAAGAAGCTGTTTGG
TCTA

Fig. 15S

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17183.2

GGTTCACAGCACTGCTGCTTGTGTGTTGCGGGCCAGGAATTCAGGCTCACAAGGCTATCTTAGCAGCTCGTTC
TCCGGTTTTTAGTGCCATGTTTGAACATGAAATGGAGGAGAGCAAAAAGAATCGAGTTGAAATCAATGATGTGG
AGCCTGAAGTTTTAAGGAAATGATGTGCTTCATTTACACGGGGAAGGCTCCAAACCTCGACAAAATGGCTGAT
GATTTGCTGGCAGCTGCTGACAAGTATGCCCTGGAGCGCTTAAAGGTCATGTGTAGGATGCCCTCTGCAGTAA
CCTGTCCGTGGAGAACGCTGCAGAAATTCATCCTGGCCGACCTCCACAGTGCAGATCAGTTGAAAACCTCAGG
CAGTGGATTTCATCAACTATCATGCTTCGGATGTCTTGAGACCTCTTGGG

17186.1&2

TCGTAGCCATTTTTCTGCTTCTTTGGAGAATGACGCCCACTGACTGCTCATTGTCGTTGGTTCCATGCCAATT
GGTGAAATAGAACCTCATCCGGTAGTGGAGCCGGAGGGACATCTTGTATCAACGGTGATGGTGGGATTTGGAG
CATACCAGAGCTTGGTGTCTCGCCATACAGGGCAAGAGGTTGTGACAAAGAGGAGAGATACGGCATGCCTGT
GCAGCCCTGATGCACAGTTCTCTGCTGTACTCTCCACTGCCAGCCGGAGGGGCTCCCTGTCCGACAGATA
GAAGATCACTCCACCCCTGGCTTG

17187.1&2

TGGCACACTGCTCTTAAGAACTATGAWGATCTGAGATTTTTTGTGTATGTTTTGACTCTTTGAGTGGTAA
TCATATGTGCTTTATAGATGTACATACCTCCTTGACAAATGGAGGGGAATTCATTTTCATCACTGGGAGTGT
CCTTAGTGATAAAAAACCATGCTGGTATATGGCTTCAAGTTGTAAAAATGAAAGTGACTTTAAAGAAAATAGG
GGATGGTCCAGGATCTCCACTGATAAGACTGTTTTAAGTAAGTAAAGGACCTTTGGGTCTACAAGTATATGTG
AAAAAATGAGACTTACTGGGTGAGGAAATTCATTGTTTAAAGATGGTCGTGTGTGTGTGTGTGTGTGTGTG
TTG
TYTGATAATGATTTGCTYTTTGVCMACATAAAATTAGGVCTGTATAAGTWTARATGCMTCCCTGGGKTTGATY
TTCCMAGATATTGATGATAMCCCTTAAATTTGAACCYGCCTTTTTCCCTTTGCTYTCMATTAAAGTCTATTCM
AAAG

17191.1&89.1

GGGGGTAGGCTCTTTATTAGACGGTTATTGCTGTACTACAGGGTCAGAGTGCAGTGAAGCAGTGTGAGAGGCC
CGGTTTCCAGCCCAAGAATGTGGATTTTCTCTCCCTATTGATCACAGTGGGTGGGTTCCTTCAGAAAAGCCCCAG
AGGCAGGGACCAAGTGAGCTCCAAGTTAGAAGTGGAACTGGAAGGCTTCAGTCACATGCTGCTTCCACGCTTCC
AGGCTGGGCAGCAAGGAGGAGATGCCCATGACGTGCCAGGTCTCCCATCTGACACCAGTGAAGTCTGGTAGGA
CAGCAGCCGCACGCCCTGCCTCTGCCAGGAGGCAATCATGGTAGGCAGCATTGCAGGGTCAGAGGTCTGAGTCC
GGAATAGGAGCAGGGGCAGGTCCCTGCGGAGAGGCACTTCTGGCCTGAAGACAGCTCCATTGAGCCCTGCAGT
ACAGGYGTAGTGCTTGGACCAAGCCACAGCCTGGTAAGGGGCGCTGCCAGGGCCACGGCCAGGAGGCA

Fig. 15T

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17192.1&2

TAATTTCTTAGTCGTTTGGAAATCCTTAAGCATGCAAAAGCTTTGAACAGAAGGGTTACAAAAGGAACCAGGGTT
GTCTTATGGCATCCAGTTAAGCCAGAGCTGGGAATGCCTCTGGGTATCCACATCAGGAGCAGAAGCACTTGAC
TTGTCGGTCTGTGCCACGGTTTGGGCGCCACCACGCCACGTCCACCTCGTCTCCCTGCCGCCACGTCC
TGGCGGCCAAGGTCTCCAAAATTGATCTCCAGCTGAGACGTTATATCATTGCTGGCTTCGGAAATGATGGT
CCATAACCGAATCTTCAGCATGAGCCTCTTCACTCTTTGATTTATGAAGAACAAATCCCTTCTTCCACTGCCCA
TCAGCACCTTCATTTGGTTTTCGGATATTAATTTACTTTTGGCCGGTCTTATTTGAATAGCCTTCCACTC
ATCCAAAGTCATCTCTTTGGACCTCCTCTTTTACCTCTTCAACTTCATTCTCCTTATTTTCAGTGTCTGCCA
CTGGATGATGTTCTTCACCTTCAGGTGTTTCTCAGTCACATTTGATTGATCCAAGTCAGTTAATTCGTCTTGG
ACAGTTCCCGAGTTGTGAGATCCGCTACCTCCACGTTTGTCTCGTGTTCAGGCCAGATCTATCACTTCCACT
ATGCCATCAAAATTCACGTTTGGCACGAGAATCAATCCATCTCTCGGCCATTCCACGTCCACGGCCCCCTC
GACCTCTTCAAGACCACCACGACCTCGAATAGGTGGTCAATAATCGGTCTATCAACTGAAAATTCGCTCCT
TCACCTTTTCTTCAAGTGGCTTTTCAATCTTCTGTTACGAGGTGGTGGCTTTCTGGTCTTCTATCAATTAT
TTCCCTTCACCTGAAGTTGTTGATCAGGTCTTCTTCAACTCGTGC

17193

AAGCGGATGGACCTGAGTCAGCCGAATCCTAGCCCCCTTCCCTTGGGCTGCTGTGGTGCTCGACATCAGTGACA
GACGGAAGCAGCAGACCATCAAGGCTACGGGAGGCCCGGGCGCTTGCGAAGATGAAGTTTGGCTGCCTCTCCT
TCCGGCAGCCTTATGCTGGCTTTGTCTTAAATGGAATCAAGACTGTGGAGACGCGTGGCGTCTGCTGAGC
AGCCAGCGGAACGTACCATCGCCGTCCACATTGCTCACAGGACTGGGAAGGCGATGCCTGTGGGAGCTGCT
GGTGGAGAGACTCGGGATGACTCCTGCTCAGATTCAAGCCTTGTCTAGGAAAGGGGAAAAGTTTGGTGGAGGAG
TGATAGCGGACTCGTTGACATTGGGGAACTTTGCAATGCCCGAAGACTTAACCTCCGATGAGGTTGTGGAA
CTAGAAAATCAAGCTGCACTGACCAACCTGAAGCAGAAGTACCTGACTGTGATTTCAAACCCAGGTGGTTACT
GGAGCCCATACCTAGGAAAGGAGGCAAGGATGTATTCCAGGTAGACATCCAGAGCACCTGATCCCTTTGGGGC
ATGAAGTGTGACAAGTGTGGGCTCCTGAAAGGAATGTTCCRGAGAAACCAGCTAAATCATGGCACCTTCAATTT
GCCATCGTGACGACACCTGTATAAATTAGGTTAAAGATGAATTTCACTGCTTTGGAGAGTCCCACCCACTAA
GCACTGTGCATGTAACAGGTTCTTTGCTCAGATGAAGGAAGTAGGGGGTGGGCTTTCTTGTGTGATGCCT
CCTTAGGCACACAGGCAATGTCTCAAGTACTTTGACCTTAGGCTAGAAGGCAAAGCTGCCAGTAAATGTCTCAG
CATTGCTGCTAATTTTGGTCTGCTAGTTTCTGGATTGTACAAATAAATGTGTTGTAGATGA

Fig. 15U

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16443.1.edit

TCGAGCGGCCGCCGGGCGAGGTGTCGGAGTCCAGCACGGGAGGCGTGGTCTTGTAGTTGTTCTCCGGCTGCCCA
TTGCTCTCCCACTCCACGGCGATGTCGCTGGGATAGAAGCCTTTGACCAGGCAGGTGAGGCTGACCTGGTTCTT
GGTCATCTCCTCCCGGATGGGGCAGGGGTACACCTGTGGTCTCGGGGCTGCCCTTTGGCTTTGGAGATGG
TTTTCTGATGGGGGCTGGGAGGGCTTTGTTGGAGACCTTGCACTTGTA CTCTTGCCATTCAACCAGTCCTGG
TGCANGACGGTGAGGACGCTNACCACACGGTACGNGCTGGTGTACTGCTCCTCCCGCGGCTTTGTCTTGGCATT
ATGCACCTCCACGCCGTCCACGTACCAATTGAACTTGACCTCAGGGTCTTCGTGGCTCACGTCCACCACCACGC
ATGTAACCTCAAANCTCGGNCGGANACGC

16443.2.edit

AGCGTGGTCGCGGCCGAGGTCTGAGGTTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT
TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
TACCGTGTGGTCAGCGTCTCACCCTCCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTC
CAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
ACACCCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTAT
CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCTCCCGTGC
TGGACTCCGACACCTGCCGGGCGGCCGCTCGA

16444.2.edit

AGCGTGGTTNCGGCCGAGGTCCCAACCAAGGCTGCANCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACT
GGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCAGAGAAGTGGTACATCAGCAAGAACCCCAAGGA
CAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACC
CTGCCGATGTGGACCTGCCGGGCGGNCGCTCGA

16445.1.edit

AGCGTGGTCGCGGCCGAGGTCAAGAACCCCGCCGACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAA
GAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGA
CTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCAGAGAAGTGGTACATCAGCAAGAACCCCAAG
GACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGA
CCCTGCCGATGTGGACCTGCCGGGCGGCCGCTCGA

Fig. 15V

SUBSTITUTE SHEET (RULE 26)

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16445.2.edit

TCGAGCGGTCGCCCCGGGCAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATC
GGNCATGCTCTCGCCGAACCAGACATGCCTCTTGNCCTTGGGGTTCTTGCTGATGTACCAGNTCTTCTGGGCCA
CACTGGGCTGAGTGGGGTACACGCAGGTCTCACCANTCTCCATGTTGCANAAGACTTTGATGGCATCCAGGTTG
CAGCCTTGGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGACAGAGTGGCACATCTTGAGGTCACGGCAGGT
GCGGGCGGGGTTCTTGACCTCGGTCGCGACCACGCT

16446.1.edit

TCGAGCGGCGCCCCGGGCAGGTCCCTCCTCAGAGCGGTAGCTGTTCTTATTGCCCGGCAGCCTCCATAGATNAA
GTTATTGCANGAGTTCTCTCCACGTCAAAGTACCAGCGTGGGAAGGATGCACGGCAAGGCCAGTGACTGCGT
TGCGGTCAGTATTCTTCATAGTTGAACATATCGCTGGAGTGGACTTCAGAATCCTGCCTTCTGGGAGCACTT
GGGACAGAGGAATCCGCTGCATTCTGCTGGTGGACCTCGGCCGCGACCACGCT

16446.2.edit

AGCGTGGTCGCGGCCGAGGTCCACCAGCAGGAATGCAGCGGATTCTCTGTCCCAAGTGCTCCAGAAGGCAGG
ATTCTGAAGACCACTCCAGCGATATGTTCAACTATGAAGAATACTGCACCGCCAACGCAGTCACTGGGCCTTGC
CGTGCATCCTTCCACGCTGGTACTTTGACGTGGAGAGGAATCCTGCAATAACTTCATCTATGGAGGCTGCCG
GGGCAATAAGAACAGCTACCGCTCTGAGGAGGACCTGCCCGGGCGGCCGCTCGA

16447.1.edit

TCGAGCGGCGCCCCGGGCAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATC
GGTCATGCTCTCGCCGAACCAGACATGCCTCTTGCTCTTGGGGTTCTTGCTGATGTACCAGTTCTTCTGGGCCA
CACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTG
CAGCCTTGGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGCCAGAATGGCACATCTTGAGGTCACGGCANGT
GCGGGCGGGGTTCTTGACCTCGGCCGCGACCACGCT

Fig. 15W

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16447.2.edit

AGCGTGGTCGCGGCCGAGGTCAAGAAACCCCGCCGACCTGCCGTGACCTCAAGATGTGCCACTCTGGCTGGA
AGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAG
ACTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCGAGAAGAACTGGTACATCAGCAAGAACCCCAA
GGACAAGAGGCATGTCTGGCTCGGCGAGAGCATACCGATGGATTCCAGTTCGAGTATGGCGCCAGGGCTCCG
ACCTGCCGATGTGGACCTGCCCGGGCGGCCGCTCGA

16449.1.edit

AGCGTGGTCGCGGCCGAGGTCTGTGTCAGAGTGGCACTGGTAGAAGNTCCAGGAACCTGAACTGTAAGGGTTCT
TCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGNAATGGGGCCCATGANATGGTTGN
CTGAGAGAGAGCTTCTTGTCTACATTGCGCGGGTATGGTCTTGCCCTATGCCCTTATGGGGGTGGCCGTTGNGG
GCGGTGNGGTCCGCTAAACCATGTTCTCAAAGATCATTGTTGCCCAACTGGGTTGCTGACCANAAGTG
CCAGGAAGCTGAATACCATTTCCAGTGTACATCCAGGGTGGGTGACGAAAGGGGTCTTTGAACTGTGGAAGG
AACATCCAAGATCTCTGNTCCATGAAGATTGGGGTGTGGAAGGGTTACCAGTTGGGAAGCTCGCTGTCTTTTT
CCTTCCAATCANGGGCTCGCTCTTCTGAATATTCTCAGGGCAATGACATAAATTGTATATTCGGTTCCTGGTT
CCAGGCCAG

16450.1.edit

TCGAGCGGCCGCCCGGGCAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGAT
TACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCTCCAGAGAAGTGGTCCCTCGGCCCGCCCTGGTG
TCACAGAGGCTACTATTACTGGCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAAT
CAGAAGAGCGAGCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCCTTCCACACCCCAA
TCTTCATGGACCAGAGATCTTGGATGTTCTTCCACAGTTCAAAAGACCCCTTTCGTACCCACCCTGGGTATG
ACACTGGAATGGTATTGAGCTTCTGGCACTTCTGGTCAGCAACCCAGTGTGGGCAAGAAATGATCTTTGAN
GAACATGGNTTTAGGCGGACCACACCGGCCACAACGGGCACCCCATAGGCATAGGCCAAGAACATACCCGNC
GAATGTAGGACAAGAAGCTCTNTCTCANACAANCATCTCATGGGCCCATTCANGACACTTCTGAGTACATCA
NTTCATGGCATCCTGGTGGCACTGATAAAACCCCTTACAGTTA

16450.2.edit

AGCGTGGTCGCGGCCGAGGTCTGTGTCAGAGTGGCACTGGTAGAAGTTCAGGAACCTGAACTGTAAGGGTTCT
TCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCCATGAGATGGTTGT
CTGAGAGAGAGCTTCTTGTCTACATTGCGCGGGTATGGTCTTGCCCTATGCCCTTATGGGGGTGGCCGTTGTGG
GCGGTGTGGTCCGCTAAACCATGTTCTCAAAGATCATTGTTGCCCAACTGGGTTGCTGACCAGAAGTG
CCAGGAAGCTGAATACCATTTCCAGTGTACATCCAGGGTGGGTGACGAAAGGGGTCTTTGAACTGTGGAAGG
AACATCCAAGATCTCTGGTCCATGAAGATTGGGGTGTGGAAGGGTTACCAGTTGGGAAGCTCGTCTGTCTTTT
TCCTTCCAATCANGGGCTCGCTCTTCTGATTATTCTCAGGGCAATGACATAAATTGTATATTCGGTTCCTGGG
TNCAGCCAATAATAAACCCTCTGTGACACANGGCGGGGCCGAAGGANCACT

Fig. 15X

SUBSTITUTE SHEET (RULE 26)

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16451.1.edit

AGCGTGGTCGCGGCCGAGGTCCTCACCAGAGGTACCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCA
GAGGCATAAGGTTTCGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATG
ACTCGTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGC
TTTAACTGTTGTGCCAGTGCTTANGCTTTGGAAGTGGTCATTTAGATGTGATTATCTAGATGGTGCCATGA
CAATGGTGTGAACATAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGACCTGCCCGGGGGCCGCTC
GA

16451.2.edit

TCGAGCGGCCGCGCGGCGAGGTCCATTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCAT
TGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTA
AAGCCTGATTCAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGA
GTGATCCGTAGGTTGGTTCAAGCCTTCGNTGACAGAGTTGCCACGGTAACAACCTCTTCCGAACCTTATGCC
TCTGCTGGTCTTTCAGTGCTCCACTATGATGTTGTAGGTGGTACCTCTGGTGAGGACCTCGGCCGCGACCAGC
CT

16452.1.edit

AGCGTGGCCGCGGCCGAGGTCCATTGGCTGGAACGGCATCAACTTGAAGCCAGTGATCGTCTCAGCCTTGTT
CTCCAGCTAATGGTGATGGNGGTCTCAGTAGCATCTGTACACGAGCCCTTCTTGGTGGGCTGACATTCTCCAG
AGTGGTGACAACACCCTGAGCTGGTCTGCTTGTCAAAGTGTCTTAAGAGCATAGACACTCACTTCATATTTGG
CGNCCACCATAAGTCCTGATACAACCACGGAATGACCTGTCAGGAAC

16452.2.edit

TCGAGCGGCCGCGCGGCGAGGTCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCCTTGACGATGAT
ATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCTGCACCAACTGACCTGAAGTTCACTCAGGT
CACACCCACAAGCCTGAGCGCCAGTGGACACCACCAATGTTTCAGCTCACTGGATATCGAGTGCGGGTGACCC
CCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTT
ATGGCGGCCACCAAATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT
TGTCAACACTCTGGAGAATGTGAGCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCACCA
TTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGCCAATGGACCTCGGCCG
CGACCACGCTT

Fig. 15Y

SUBSTITUTE SHEET (RULE 26)

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16453.1.edit

AGCGTGGTCGCGGCGAGGTCTGGCCGAAGTCCAGTGTACAGGGAAGATGTACATGTTATAGNTCTTCTCGAA
GTCCCGGGCCAGCAGCTCCACGGGTGGTCTCCTGCCTCCAGGCGCTTCTCATTCTCATGGATCTTCTTCACCC
GCAGCTTCTGCTTCTCAGTCAGAAGGTTGTTGCTCATCCCTCTCATACAGGGTGACCAGGACGTTCTTGAGC
CAGTCCCGCATGCGCAGGGGAATTGCGTCAGCTCAGAGTCCAGGCAAGGGGGGATGTATTTGCAAGGCCGAT
GTAGTCCAAGTGGAGCTTGTGGCCCTTCTTGGTGCCCTCCAAGGTGCACTTTGTGGCAAAGAAGTGGCAGGAAG
AGTCGAAGGTCTTGTGTCATTGCTGCACACCTTCTCAAAGTCCCAATGGGGGCTGGGCAGACCTGCCCGGGC
GGCCGCTCGA

16453.2.edit

TCGAGCGGCGCCCGGGCAGGTCTGCCAGCCCCATTGGCGAGTTTGAGAAGNGTGACGAATGACAACAAG
ACCTTCGACTCTTCTGCCACTTCTTTGCCACAAAGTGACCCCTGGAGGGCACCAGAAGGGCCACAAGCTCCA
CCTGGACTACATCGGGCCTTGCAAATACATCCCCCTTGCTGGACTCTGAGCTGACCGAATCCCCCTGCGCA
TGCGGGACTGGCTCAAGAACGTCCTGGTCACCTGTATGAGAGGGATGAGGACAACAACCTTCTGACTGAGAAG
CANAAGCTGCGGGTGAGAANATCCATGAGAATGANAAGCGCTGNAGGCANGAGACCACCCGTTGGAGCTGCT
GGCCCGGGACTTCGAGAAGAACTATAACATGTACATCTTCCCTGTACACTGECAGTTGGCCAGACCTCGGCCG
CGACCACGCT

16454.1.edit

AGCGTGGNTGCGGACGACGCCACAAAGCCATTGTATGTAGTTTTANTTCAGCTSCAAANAATACCNCAGCAT
CCACCTTACTAACCAGCATATGCAGACA

16454.2.edit

TCGAGCGGTGCGCCGGGCAGGTCTGGGCGGATAGCACCGGGCATATTTGGAATGGATGAGGTCTGSCACCCTG
AGCAGCCCAGCGAGGACTTGGTCTTAGTTGAGCAATTTGGCTAGGAGGATAGTATGCAGCAGGTTCTGAGTCT
GTGGGATAGCTGCCATGAAGNAACCTGAAGGAGGCGCTGGCTGGTANGGTTGATTACAGGCTGGGAACAGCT
CGTACACTTGCCATTCTCTGCATATACTGGNTAGTGAGGCGAGCCTGGCGCTCTTCTTTGCGCTGAGCTAAAGC
TACATACAATGGCTTTGNGGACCTCGGCCGCGACCACGCTT

Fig. 15Z

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16455.1.edit

TCGAGCGGCCGCCGGGCAGGTCCATTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCAT
TGTCATGACACCATCTAGATGAATCACATCTGAAATGACCACITCCAAAGCCTAAGCACTGGCACAACAGTTTA
AAGCCTGATTGAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGA
GTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAAGTTGCCACGGTAACAACCTCTTCCGAACCTTATGC
CTCTGCTGGTCTTTCAAGTGCCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTCGGCCGCGACCA
CGCT

16455.2.edit

AGCGTGGTTTGC GGCCGAGGTCTCACCANAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGC
AGAGGCATAAGGTTCCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGAT
GACTCGTGCTTTGACCCCTACACAGNTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGCTGAATCAGG
CTTTAAACTGTTGTGCCAGTGCTTANGCTTTGGAAGTGGTCATTTGAGATGTGATTCTANATGGTGTCTATG
ACAATGGTGNGAACTACAAGATTGGAGAGAAGTGGNACCGTCAGGGGANAAAATGGACCTGCCCGGGCGGCNCG
CTCGA

16456.1.edit

AGCGTGGTCCGGCCGAGGTCTGGCTTNGTCTCANGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCCGG
CTATGCCCTGNATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATC

16456.2.edit

TCGAGCGGCCGCCGGGCAGGTCCAATTGAAACAAACAGTTCTGAGACCGTTCTTCCACCACTGATTAAGAGTG
GGNGGGCGGTATTAGGGATAATATTCATTTAGCCTTCTGAGCTTTCTGGGCAGACTTGGTGACCTTGCCAGCT
CCAGCAGCCTTCTGGTCCACTGCTTTGATGACACCCACCGCAACTGTCTGTCTCATATCACGAACAGCAAAGCG
ACCCAAAGGTGGATAGTCTGAGAAGCTCTCAACACACATGGGCTTGCCAGGAACCATATCAACAATGGGCAGCA
TCACCAGACTTCAAGAATTTAAGGGCCATCTTCCAGCTTTTTACCAGAACGGCGATCAATCTTTTCTTCAGCT
CAGCAAACCTGCATGCAATGTGAGCCG

Fig. 15AA

SUBSTITUTE SHEET (RULE 26)

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16459.1.edit

TCGAGCGGCCGCCGGGCGAGGTCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTGGAGCCACTCCAATTGCT
GGCCGCTTCACTCCTGGAACCTTCACTAACCAGATCCAGGCAGCCTTCCGGGAGCCACGGCTTCTTGTTGNTAC
TGACCCAGGGGTGACCACCAGCCTCTCACGGAGGCATCTTATGTTAACCTACCTACCATTGCGTGTGTAACA
CAGATTCTCCTCTGCGCTATGTGGACATTGCCATCCCATGCAACAACAAGGGAGCTCACTCAGNGGGGTTTGAT
GTGGTGGATGCTGGCTCGGGAAGTTCTGCGCATGCGTGGCACCATTTCCTGTAACACCCATGGGANGNCATGC
CTGATCTGGACTTCTACAGAGATCCTGAAGAGATTGAAAAAGAAGAAGCAGGCTGNTTGCTGANAAGCAAGTGA
CCAAGGANGAAATTTCAAGGGTGAAANGGACTGCTCCCGCTCCTGAATTCAGTGTACTCAACCTGANGNTGCA
GACTGGTCTTGAAGGNAGCANGGGCCTCTGGGCTATTTAAGCANCCTCGGTGCGGAACACGNT

16459.2.edit

AGCGTGNGTCGCGGCCGAGGTGCTGAATAGGCACAGAGGGCACCTGTACACCTTCAGACCAGTCTGCAACCTCA
GGCTGAGTAGCAGTGAATCAGGAGCGGGAGCAGTCCATTACCCTGAAATTCCTCCTTGNCAGTGCCTTCTC
AGCAGCAGCCTGCTCTTCTTTTCAATCTCTTCAGGATCTCTGTAGAAGTACAGATCAGGCATGACCTCCCATG
GGTGTTCACGGGAAATGGTGCCACGCATGCGCAGAACTTCCGAGCCAGCATCCACCACATCAAAACCACTGAG
TGAGCTCCCTTGTGTGTCATGGGATGGGCAATGTCCACATAGCGCAGAGGAGAATCTGTGTTACACAGCGCAA
TGGTAGGTAGGTAAACATAAGATGCCTCCGCGAGAAGCTGGTGGTCAAGCCTGGGGTCAAGTAACCACAAGAAG
CCGTGGCTCCCGGAAGGCTGCCTGGATCTGGTTAGTGAAGGNTCCAGGAGTGAAGCGGCCAACAATTGGAGTGG
CTTCAGTGGCAAGCAGCAAACTTCAGCACAAGCCCTCTGGACCTGCCCGCGCGCTCGA

16460.1.edit

TCGAGCGGCCGCCGGGCGAGGTCCATTTTCTCCCTGACGGNCCCACTTCTCTCCAATCTTGTAGTTACACCAT
TGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCAAAGCCTAAGCACTGGCACAACAGTTTA
AAGCCTGATTGAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGA
GTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTCNTCCCGAACCTTATGC
CTCTGCTGGGCTTTCAGNGCCTCCACTATGATGNTGTAGGGGGGCACCTCTGGNGANGACCTCGGCCGCGACCA
CGCT

16460.2.ed1t

AGCGTGGTGGCGGCCGAGGTCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCA
GAGGCATAAGGCTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATG
ACTCGTGTCTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGC
TTTAAACTGTTGTGCCAGTGCTTANGCTTTGGAAGTGGGTCAATTCAGATGTGATTCATCTAGATGGTGCCATG
ACAATGGNGNGAACTACAAGATTGGAGAGAAGTGGNACCGNACGGGAGAAAATGGACCTGCCCGGGCGGCCGCT
CGA

Fig. 15BB

SUBSTITUTE SHEET (RULE 26)

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16461.1.edit

AGCGTGGTCGGCGCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG
TCATGCTCTCGCGAACCAGACATGCCTCTTGCTCTGGGGTTCTTGCTGATGTACCAGTTCTTCTGGGCCACA
CTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGNTGCA
ACCTTGCTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGCCAGAGTGGCACATCTTGAGGTCACGGCAGGTGC
GGNCGGGGNTTTTGGCGCTGCCCTCTGGNCTTCGGNTGTNCTCNATCTGCTGGCTCA

16461.2.edit

TCGAGCGGGCGCCCGGGCAGGTCTCGCGGTGCGACTGGTGATGCTGGTCTGTTGGTCCCCCGGCCCTCTGG
ACCTCTGGCCCCCTGGTCTCCAGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAGG
CTCAGGATGGTGGCGCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACC
ACCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCAGAGGGCAGNCGCAAGAACCCCGCCGCAC
CTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGCTGCAA
CCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCACTGTGG
CCAAAAGAAGTGGTACATCAGCAAGAACCCCAAGGACAAGAAGCATGTCTGGTTCGGCGAGAACATGACCGAT
GGATTCCAGTTCGAGTATGGCGGGCAGGGCTCCGACCCTGCCGATGGGGACCTTGGCCGCGAACACGCT

16463.1.edit

AGCGTGGNNGCGCGGAGGTATAAATATCCAGNCCATATCCTCCCTCCACACGCTGANAGATGAAGCTGTNCAA
AGATCTCAGGGTGGANAAAACCAT

16463.2.edit

TCGAGCGGGCGCCCGGGCAGGTCTTCAGACTTGGACTGTGTCACTGCCAGGCTTCAGGGCTCCAAGTTGC
AGACGGCCTGTTGTGGGACAGTCTCTGTAATCGCGAAAGCAACCATGGAAGACCTGGGGGAAAACACCATGGTT
TTATCCACCCTGAGATCTTTGAACAACTTCATCTCTCAGCGTGCGGAGGGAGGCTCTGGACTGGATTTCTAC
CTCGGCCGCGACCACGCT

Fig. 15CC

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16464.1.edit

CGAGCGGGCGACCGGGCAGGTNCAGACTCCAATCCANANAACCATCAAGCCAGATGTCAGAAGCTACACCATCA
CAGGTTTACAACCAGGCACTGACTACAAGANCTACCTGCACACCTTGAATGACAATGCTCGGAGCTCCCTGTG
GTCATCGACGCCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTCTGGCCACCACACCAATTCCTTGCT
GGTATCATGGCAGCCGCCAGTGCCAGGATTACCGGTACATCATCNAGTATGANAAGCCTGGGCTCCTCCAG
AGAAGNGGTCCCTCGGCCCGCCCTGNTGTCCANAGGNTACTATTACTGNGCCNGCAACCGGCAACCGATATC
NATTTTGNCATTGGCCTTCAACAATAATTA

16464.2.edit

AGCGTGGTTCGCGGCCGANGTCTGTGAGAGTGGCACTGGTAGAAGTTCAGGAACCTGAACTGTAAGGTTTC
TTCATCAGNGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCATGAGATGGTTG
TCTGAGAGAGAGCTTCTTGNCTGTCTTTTCTTCCAATCAGGGCTCGCTCTTCTGATTATTCCTCAGGGCA
ATGACATAAATGTATATTGGGTCCCGNTCCAGGCCAGTAATAGTANCTCTGTGACACCAGGGCGGNGCCG
AGGGACCACTTCTCTGGGAGGAGACCCAGGCTTCTCATACTTGATGATGTAACCGTAATCCTGGCACGTGGCG
GCTGCCATGATACCAGCAAGGAATTGGGGTGTGGTGGCCAGGAAACGCAGGTTGGATGGNGCATCAATGGCAGT
GGAGGCCGTGATGACCACAGGGGGAGCTCCGACATTGTCAATCAAGGTG

16465.1.edit

AGCGTGGNCGCGGCCGAGGTGCAGCGCGGGCTGTGCCACCTTCTGCTCTCTGCCCAACGATAAGGAGGGTNCCT
GCCCCCAGGAGAACATTAACTNTCCCCAGCTCGGCCTCTGCCGG

16465.2.edit

TCGAGCGGCGCCCGGGCAGGTTTTTTTTGCTGAAAGTGGNTACTTTATTGGNTGGGAAAGGAGAAGCTGTGG
TCAGCCCAAGAGGGAATACAGAGNCCGAAAAAGGGAGGGCAGGTGGGCTGGAACAGACGCAGGGCCAGGCA
GAACTTTCTCTCCTCACTGCTCAGCCTGGTGGTGGCTGGAGCTCANAAATTGGGAGTGACACAGGACACCTTC
CCACAGCCATTGCGGCGGCATTTTCATCTGGCCAGGACACTGGCTGTCCACCTGGCACTGGTCCCGACAGAAGCC
CGAGCTGGGAAAGTTAATGTTACCTGGGGCAGGAACCTCCTTATCATTGNGCAGAGAGCAGAAGGTGGCA
CAGCCCGCGCTGCACCTCGGCCGCGACACGCT

16466.2.edit

TCGAGCGGCGCCCGGGCAGGTCCACCATAAGTCTGTATACAACACGGATGAGCTGTGAGGAGCAAGGTTGAT
TTCTTTTCATTGGTCCGGNCTTCTCCTTGGGGGNCACCGCACTCGATATCCAGTGAGCTGAACATTGGGTGGCG
TCCACTGGGCGCTCAGGCT

16467.2.edit

TCGAGCGGTTGCGCCGGGCAGGTCCACCACACCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGA
TTACCGGTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCAGAGAAGCGGTCCCTCGGCCCGCCCTGGT
GTACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCAATATACAATTTATGTATTGNCCTGAAGAATAA
TCANNAANAGCGANCCCTGATTGGAAGGA

Fig. 15DD

SUBSTITUTE SHEET (RULE 26)

01 16469.edit.t

02 16469.edit

03 16470.edit

04_16470.edit

05 16471.edit

Fig. 15EE

66/101

06_16471.edit

AGCGTGGTCGCGGCCGAGGTCTGCTGCTTCAGCGAAGGGTTTCTGGCATAACCAATGATAAGGCTGCCAAAGAC
TGTTCCAATACCAGCACCAGAACCCAGCACTCTACTGTTGCAGCACCTGCACCAATAAATTTGGCAGCAGTAT
CAATGTCTCTGCTGATTGCACTGGTCTGAACTCCCTTTGGATTAGCTGAGACACACCATTCTGGGCCCTGATT
TTCCTAAGATAGAAGCTCAACTCTTTGCCCTCTAGCACATAGCCATCTGCTCGGTCACTGTCCGGCCCTTGA
AGCGATGCACGCAAGAAGCTTGCCCTGCTGGAAGTCTCTCCAGGAGACTGCTGATTTTGGCATTCTTTTTCC
TTTCATCATATTTCTTCTGAATTTTTTAGATCGTTTTTTGTTTAAATCTCTTCTTCTCAGGAGTCAGCTTG
GCCCCCGCCGATCCACACAGTCCGTGTGCGGGGAGGTAACAAGAAATACCGTGCCCTGAGGTTGGACGTGGGG
AATTTCTCCTGGGGCTCAGAGTGGTGTACTCGTAAACAAGGATCATCGATGGTGNCTACAATGCATCTAATAA
CGAGCTGGGTGGACCCAAAGAAGCTGGNGAANAATGGATCGNCTCATCGACAGGACACCGTACCCGACAGGG
GNACGANTCCCACTATGCGCTTGCCCTGGGCGCAANAAGGAAAAGTGGCCGGGCGGCCNTCGAAAGCCCAA
TTNTGGAAAAATCCATCACACTGGGNGGCCNGTCGAGCATGCATNTANAGGGGCCATTCCCCCTNANN

07_16472.edit

TCGAGCGGCCGCCCGGGCAGGTCCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAG
ACTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCGAGAAGAACTGGTACATCAGCAAGAACCCCAA
GGACAAGAGGCATGTCTGGTTGCGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCG
ACCTGCCGATGTGGACCTCGGCCGCGACCAGCT

08_16472.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG
TCATGCTCTCGCCGAACCAGACATGCCTCTTGTCTTGGGGTTCTTGCTGATGTACCAGTCTTCTGGGCCACA
CTGGGCTGAGTGGGTACACGAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTGCA
GCCTTGGTTGGGACCTGCCCGGGCGGCCGCTCGA

09_16473.edit

TCGAGCGGCCGCCCGGGCAGGTCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGAT
TACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCAGAGAAGTGGTCCCTCGGCCCGCCCTGGTG
TCACAGAGGCTACTATTACTGGCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAAT
CAGAAGAGCGAGCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCAACTGSTAACCCCTCCACACCCCAA
TCTTCATGGACCAGAGATCTTGGATGTTCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCCTGGGTATG
ACACTGGAATGGTATTAGCTTCTTGGCACITCTGGTCAGCAACCCAGTGTGGGCAACAAATGATCTTTGAG
GAACATGGNTTTAGGCGGACCACCGCCCAACCGGCCACCCCAATAAGGCATAGGCCAAGACCATAACCGCC
GAATGTAGGACAAGAAGCTNTNTNANACCATNTNATGGGCCCATTCAGGACACTTCTGAGTACATCAT
TTATGNCATCTGTGGCACTTGATGAAACCCCTTACAGTTTCAAGGTTCTGGAACCTTTACCAGGCCNTTACAGG
ACTNCGCCGGACNCCTTAAGCCNATTNACCCCTGGGGCGTTCTANGGTCCCACTCGNNCACTGGNGAAAAATGGC
TACTGTN

Fig. 15FF

SUBSTITUTE SHEET (RULE 26)

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11_16474.edit

AGCGTGGTCGCGGCCGAGGTCCACTAGAGGTCTGTGTGCCATTGCCAGGCAGAGTCTCTGCGTTACAACTCC
TAGGAGGGCTTGCTGTGCGGAGGGCCTGCTATGGTGTGCTGCGGTTTCATCATGGAGAGTGGGGCCAAAGGCTGC
GAGGTGTGGTGTCTGNGAACTCCNAGGACANGAGGGCTAAATTCATGAAGTTTGTGGATGGCCTGATGATC
CACAATCGGAGACCTGTAACTACTACCGTCTNACCNCCTGCTGTNCNCCCCNTTCTGCTNAANACATNGG
GNTNNTCTTGNCCTCCTTGGGTNGAANATNNAATNGCCTNCCNTTCTANCNCTACTNGNTCCANANTTGG
CCTTTAAANAATCCNCCTTGCTTNNNCACTGTTCAANTNTTNTCGTAAACCTATNANTTNNATTANATNN
TNNNNNCTCACCCCTCCTCATTNANCCNATANGCTNNNAANTCCTTNANNCCCTCCNCCNNTNCTCCT
ACTNANTNCTTCTNCCCATTAACNAGCTCTTTCNTTAAANATAATGNGCCNNGCTCTNCATNTCTACNATNT
GNNNAATNCCCCNCCCNANCGNNTTTTGACCTNNNAACCTCCTTTCCTCTCCCTNCNNAATTNCNNAN
TTCNCNTTCCNCGNTTTCGNTNNTCCCATNCTTCCANNCTTCANTCTANCNCNCTNCAACTTATTTTCCT
NTCATCCCTTNTTCTTACANNCCCCCTNNTCTACTCNCNNTTNCATTANATTTGAAACTNCCACNCTANTT
NCCTCCTCTACNNTTTATTTTNCGNTCCTCTACNTAATANTTTAATNANTTNTCN

12_16474.edit

TCGAGCGGCCCGCCGGGCAGGTCTGCCAAGGAGACCTGTTATGCTGTGGGACTGGCTGGGGCATGGCAGGCG
GCTCTGGCTTCCACCCCTTCTGTTCTGAGATGGGGTGGTGGGCAGTATCTCATCTTTGGGTTCCACAATGCTC
ACGTGGTACGGCAGGGGCTTCTTAGGGCCAATCTTACCAGTTGGGTCCAGGGCAGCATGATCTTACCTTGAT
GCCAGCACACCTGTCTGAGCAACAGTGGCGCACAGCAGTGTCAACGTAGTAAGTTAACAGGGTCTCCGCT
GTGGATCATCAGGCCATCCACAACTTCATGGATTTAGCCCTCTGTCTCGGAGTTTCCAGACACCACAACCT
CGCAGCCTTTGGCCCCACTCTCCATGATGAACCGCAGCACACCATAGCAGGCCCTCCGCACAAGCAAGCCCTCC
TAAGAAATTTGTAACGCANANACTCTGCTGGCAATGGCACACAAACCTCTAGTGGACCTCGGNCGCGACCACGC

13_16475.edit

TCGAGCGGCCCGCCGGGCAGGTCTGGTCCAGGATAGCCTGCGAGTCTCCTACTGCTACTCCAGACTTGACATC
ATATGAATCATACTGGGGAGAATAGTTCTGAGGACCACTAGGGCATGATTCACAGATTCAGGGGGGCCAGGAG
AACCAGGGGACCTGGTTGTCTGGAATACCAGGGTCACCATTTCTCCAGGAATACCAGGAGGGCCTGGATCT
CCCTTGGGGCCTTGAGGTCTTGACCATTAGGAGGGCGAGTAGGAGCAGTTGGAGGCTGTGGGCAAACTGCACA
ACATTCTCAAATGGAATTTCTGGGTGGGGCAGTCTAATCTTGATCGTCACATATTATGTATCGCAGAGA
ACGGATCCTGAGTCACAGACACATATTTGGCATGGTTCTGGCTTCCAGACATCTCTATCCGNCATAGGACTGAC
CAAGATGGGAACATCCTCCTTCAACAAGCTTNTGTTGTGCCCCAAAATAATAGTGGGATGAAGCAGACCGAGAA
GTANCCAGCTCCCCTTTTGCACAAAGCNTCATCATGTCTAAATATCAGACATGAGACTTCTTTGGGCAAAAA
GGAGAAAAAGAAAAAGCAGTTCAAAGTANCCNCCATCAAGTTGGTTCTTGGCCNTTCAGCACCCGGGGCCCTT
TATAAACACCTNNGGCGCGGACCCCTT

Fig. 15GG

SUBSTITUTE SHEET (RULE 26)

68/101

14_16475.edit

AGCGTGGTCGCGGCCGAGGTGTTTTATGACGGGCCCGGTGCTGAAGGGCAGGGAACAACCTTGATGGTGCTACTT
TGAAGTCTTTCTTTCTCCTTTTGCACAAAGAGTCTCATGTCTGATATTTAGACATGATGAGCTTTGTGCA
AAAGGGGAGCTGGCTACTTCTCGCTCTGCTTCATCCCACTATTATTTTGGCACAACAGGAAGCTGTTGAAGGAG
GATGTTCCCATCTTGGTCAGTCTATGCGGATAGAGATGTCTGGAAGCCAGAACCATGCCAAATATGTGTCTGT
GACTCAGGATCCGTTCTCTGCGATGACATAATATGTGACGATCAAGAATTAGACTGCCCAACCCAGAAATTC
ATTTGGAGAATGTTGTGCAGTTTGCCACAGCCTCCAACCTGCTCCTACTCGCCCTCCTAATGGTCAAGGACCTC
AAGGCCCAAGGGAGATCCAGGCCCTCCTGGTATTCTGGGAGAAATGGTGACCCTGGTATTCCAGGACAACCA
GGGTCCCCTGGTTCTCCTGGCCCCCTGGAATCNGGNGAATCATGCCCTACTGGTCTCAAACCTATTCTCCCAN
ATGATTCATATGATGTCAAGTCTGGGATAGCNAGTANGGANGGACTCGCAGGCTATTCTGGACCANACCTGCC
GGGGGGCGTTTCAAGGCCGAATCTGCANANTNCTTCACTGGCGGCCGTGAGCTGCTTTAAAGGGCCA
TTCNCCTTTAGNGNGGGGANTACAATTACNGCGCGGCTTTANANCGCGNGCTGGGAAAT

15_16476.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCG
TCATGCTCTCGCCGAACCAGACATGCCTCTTGTCTTGGGGTTCTTGCTGATGTACCAAGTTCTTCTGGGCCACA
CTGGGCTGAGTGGGGTACACGAGGTCTCACCAGTCTCATGTTGCAGAAGACTTTGATGGCATCCAGGTTGCA
GCCTTGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGTCAGAGTGGCACATCTTGAGGTCACGGCAGGTGC
GGGCGGGTCTTTCGGCTGCCCTCTGGGCTCCGGATGTTCTCGATCTGCTGGCTCAGGCTCTTGAGGGTGGTG
TCCACCTCGAGGTACGGTCACGAACCACATTGGCATCATCAGCCCGGTAGTAGCGGCCACCATCGTGAGCCTT
CTCTTGANGTGGCTGGGGCAGGAAGTGAAGTCGAAACCAGCGCTGGGAGGACCAGGGGGACCAANAGGTCCAG
AAGGGCCCGGGGGGACCAACAGGACCAGCATACCAAGTGCAGCCCGGAGAACCTGCCCGGCCGNCCTCG
AA

16_16476.edit

TCGAGCGNNGCCCCGGGCGAGGTCTCGCGGTGCGACTGGTGATGCTGGTCTGTTGGTCCCCCGGCCCTCCTGE
ACCTCCTGGTCCCCCTGGTCTCCAGCGCTGGTTTCGACTTCAGCTTCTGCCCGAGCCACCTCAAGAGAAGG
CTCAGGATGGTGGCCGCTACTACGGGCTGATGATGCCAATGTGGTTCTGTGACCGTGACCTCGAGGTGGACACC
ACCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCAGAGGGCAGCCGGAAGACCCCGCCGCAC
CTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCA
ACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTC
GCCAGAAAGTGGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGA
TGGATTCCAGTTCGAGTATGGCGCCAGGGCTCCACCTGCCGATGTGGACCTCCGGCCGCGACCACTT

Fig. 15HH

SUBSTITUTE SHEET (RULE 26)

69/101

17_16477.edit

TNGAGCGGCCCGGCCAGGNTGNNACGCTGGTCTGCTGGTCTCTGGCAAGGCTGGTGAAGATGGTCAC
CCTGGAAAACCCGGACGACCTGGTGAGAGAGGAGTTGTTGGACCACAGGGTGCTCGTGGTTTCCTGGAACTCC
TGGACTTCCTGGCTTCAAAGGCATTAGGGGACACAATGGTCTGGATGGATTGAAGGGACAGCCCGGTGCTCCTG
GTGTGAAGGGTGAACCTGGTGCCCTGGTGAAAATGGAATCCAGGTCAAACAGGAGCCCGTGGGCTTCCTGGT
GAGAGAGGACCGTGTGGTGCCCTGGCCANACCTCGGCCGCGACCAGGCTAAGCCGAATTTCCAGCACACT
GGNGCCGTTACTANTGGATCCGAGCTCGGTACCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGNGTGA
AATTGTTATCGGCTCACAAATTTACACANCATACGAAGCCGAAAGCATAAAGTGTAAAGCCTTGGGGTGCTAA
TGAGTGAGCTAACTCNCATTAAATTTGCGTTGCGCTCACTGCCCGCTTTTCCANNNGGAAACNTGGCNTNGCC
NGCTTGCTTAANTGAAATCCGCCNACCCCGGGGAAAGNCGGTTTGCNGTATTGGGCGNCTTTTCCCTTTC
CTCGGNTTACTTGANTTANTGGGCTTTGGNCGNTTCGGGTTGNGCGGANCNGGTTCAACNTCACNCCAAAGNG
GNAANACGGTTTTCCANAATCCGGGGGNTANCCAAANGNAAACATNNGNCNAANGGGCT

18_16477.edit

AGCGTGGTTNGCGGCCGAGGTCTGGGCCAGGGGACCAACACGTCTCTCTCACCAGGAAGCCACGGGCTCCT
GTTTGACCTGGAGTTCCATTTTACCAGGGGACCAAGGTTACCCCTTACACCAGGAGCACCAGGGCTGTCCCTT
CAATCCATNCAGACCATTGTGNCCTTAATGCCTTTGAAGCCAGGAAGTCCAGGAGTTCCAGGGAACCAACCGA
GCACCTGTGGTCCAACAACCTCTCTCACCAGGTGTCGGGTTTTCCAGGGTGACCATCTTACCAGCCTT
GCCAGGAGGACCAGGAGGACGCGTTACCAACCTGCCCGGGCGGCCGCTCGA

21_16479.edit

TCGAGCGGCCCGCCGGGCAGGTCCATTTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCAT
TGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTA
AAGCCTGATTCAGACATTGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGA
GTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTCTTCCGAACCTTATGCC
TCTGCTGGTCTTTCAGTGCCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTCGGCCGCGACACG
CT

22_16479.edit

AGCGTGGTCGCGGCCGAGGTCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCA
GAGGCATAAGGTTCCGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAAACCAACCTACGGATG
ACTCGTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGC
TTTAAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCATTTCAAGATGTGATTATCTAGATGGTGCCATG
ACAATGGTGTGAACATAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGACCTGCCCGGGCCGGCCGC
TCGA

Fig. 15II

SUBSTITUTE SHEET (RULE 26)

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24_16480.edit

TCGAGCGNCGCCCGGGCAGGTCCAGTAGTGCCTTCGGGACTGGGTTACCCCCAGGTCTGCGGCAGTTGTAC
AGCGCCAGCCCCGCTGGCTCCAAAGCATGTGCAGGAGCAAATGGCACCGAGATATCCTTCTGCCACTGTTCT
CCTACGTGGTATGTCTTCCCATCATCGTAACACGTTGCCTCATGAGGGTCACACTTGAATTCCTTTTCCGTT
CCCAAGACATGTGCAGCTCATTGGCTGGCTCTATAGTTTGGGAAAGTTTGTGAACTGTGCCACTGACCTT
TACTTCTCTTCTTACTGGAGCTTTCGTACCTTCCACTTCTGCTGTTGGTAAATGGTGGATCTTCTATCAA
TTTCATTGACAGTACCCACTTCTCCAAACATCCAGGGAATAGTGATTTAGAGCGATTAGGAGAACCAAAT
ATGGGGCAGAAATAAGGGGCTTTTCCACAGGTTTTCCTTGGAGGAAGATTTAGTGGTGACTTTAAAAGAATA
CTCAACAGTGTCTTCATCCCATAGCAAAAGAAACNGTAAATGATGGAANGCTTCTGGAGATGCCNNCATT
TAAGGGACNCCAGAACTTCACCATCTACAGGACCTACTTCAGTTTACANNAAGNCACATANTCTGACTCANAA
AGGACCCAGTAGCNCCATGGNCAGCACTTTNAGCCTTCCCTGGGGAAAANNTTACNTTCTTAAANCCTNGG
CCNNGACCCCTTAAGNCCAAATNTGGAAAANTTCNTNCTNCTGGGGGGCNGTTTACATGCNTTTNAAGGG
CCCAATTNCCCNCT

25_16481.edit

TCGAGCGGCGCCCGGGCAGGTGTCGGAGTCCAGCACGGGAGGCGTGGTCTTGTAGTTGTTCTCGGCTGCCCA
TTGCTCTCCCACTCCACGGCGATGTCGCTGGGATAGAAGCCTTTGACCAGGCAGGTGAGGCTGACCTGGTCTT
GGTCATCTCCTCCCGGATGGGGGAGGGGTACACCTGTGGTTCTCGGGGCTGCCCTTGGCTTTGGAGATGG
TTTTCTCGATGGGGCTGGGAGGGCTTTGTTGGAGACCTTGCACTTGTACTCCTTGCCATTGAGCAGTCCCTGG
TGCAGGACGGTGAGGACGCTGACCACACGGTACGTGCTGTTGTACTGCTCCTCCCGGGCTTTGTCTTGGCATT
ATGCACCTCCACGCGCTCCACGTACCACTTGAACCTGACCTEAGGGTCTTGTGGCTCACGTCCACCACACGCG
ATGTAACCTCAGACCTCGGCCGCGACACGCT

26_16481.edit

AGCGTGGTCCGCGCCGAGGTCTGAGGTTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGT
TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
TACCGTGTGGTCAGCGTCTCACCCTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTC
CAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAAGGSCAAGCCCGAGAACACAGGTG
TACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTA
TCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCTCCCGTGC
TGGACTCCGACACCTGCCCGGGCGGCGCTCGA

27_16482.edit

TCGAGCGGCGCCCGGGCAGGTTGAATGGCTCCTCGCTGACCACCCCGGTGCTGGTGGTGGGTACAGAGCTCCG
ATGGGTGAAACCATTGACATAGAGACTGTCCCTGTCCAGGGTGTAGGGGCCAGCTCAGTGATGCGTGGGTCA
GCTGGCTCAGCTTCCAGTACAGCCGCTCTCTGTCCAGTCCAGGGCTTTTGGGGTCAGGACGATGGGTGCAGACA
GCATCCACTCTGGTGGCTGCCCATCTTCTCAGGCTGAGCAAGGTGAGTCTGCAACCAGAGTACAGAGAGCT
GACACTGGTGTCTTGAACAAGGGCATAAGCAGACCTGAAGGACACCTCGGCCGCGACACGCT

Fig. 15JJ

SUBSTITUTE SHEET (RULE 26)

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28_16482.edit

AGCGTGGTCGCGGCCGAGGTGTCCTTCAGGGTCTGCTTATGCCCTTGTTCAAGAACACCAGTGTGAGCTCTCTG
TACTCTGGTTGCAGACTGACCTTGCTCAGGCCTGAGAAGGATGGGGCAGCCACCAGAGTGGATGCTGTCTGCAC
CCATCGTCTGACCCCAAAGCCCTGGAAGTGGACAGAGAGCGGCTGTAAGAGCTGAGCCAGCTGACCCACG
GCATCACTGAGCTGGGCCCTACACCCTGGACAGGACAGTCTCTATGTCAATGGTTTCACCCATCGGAGCTCT
GTACCCACCACCAGCACCAGGGGTGGTCAGCGAGGAGCCATTCAACCTGCCCGGGCGGCCGCTCGA

29_16483.edit

AGCGTGGTCGCGGCCGAGGTGTCCTGTGAGAGTGGCACTGGTAGAAGTTCCAGGAACCCTGAAGTGAAGGGTTCT
TCATCAGTGCCAAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCCATGAGATGGTTGT
CTGAGAGAGAGCTTCTTGCTTACATTCCGGCGGTATGGTCTTGGCCTATGCCCTATGGGGGTGGCCGTTGTGG
GCGGTGTGGTCCGCCTAAACCATGTTCTCAAGATCATTTGTTGCCCAACTGGGTTGCTGACCAGAAGTG
CCAGGAAGCTGAATACCATTTCCAGTGTACATCCAGGGTGGGTGACGAAAGGGTCTTTGAAGTGTGAAGG
AATCCAGATCTCTGGTCCATGAAGATTGGGGTGTGAAGGGTTACAGTTGGGGAAGCTCGTCTGTCTTTT
TCCTTCAATCAGGGGCTCGCTCTTGATTATTCTTCAGGGCAATGACATAAATTGTATATTGCGTCCCGGTT
CCAGGCCAGTAATAGTAGCCTCTGTGACACCAGGGCGGGGCGAGGGACCCTTCTNTTGAAGAGACCAGTTT
TCATACTTGATGATGAGNCCGTAATCCTGGCACGTGGNGGTTGCATGATNCCACCAAGGAAATNGGNGGGGN
GGACCTGCCCGGGCGGCTTCAAAAGCCCAATCCACACACTTGGNGGCGTACTATGGATCCCACTCNGTCCA
ACTTGGNGGAATATGGCATAACTTTT

31_16484.edit

TCGAGCGGCCGCGCCGGGCGAGGTCTTGACCTTTTCAGCAAGTGGGAAGGTGTAATCCGTCTCCACAGACAAGGC
CAGGACTCGTTTGATCCGTTGATGATAGAATGGGGTACTGATGCAACAGTTGGGTAGCCAATCTGCAGACAGA
CACTGGCAACATTGCGGACACCCTCCAGGAAGCGAGAATGCAGAGTTTCTCTGTGATATCAAGCACTTCAGGG
TTGTAGATGCTGCCATTGTGCAACACCTGCTGGATGACCAGCCAAAGGAGAAGGGGAGATGTTGAGCATGTT
CAGCAGCGTGGCTTCGCTGGCTCCCACTTTGTCTCCAGTCTTGATCAGACCTCGGCCGCGACCACGCT

37_16487.edit

AGCGTGGTCGCGGCCGAGGTCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCT
CCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCAGCAACACCAAGGTGGACAAGAGA
GTTGAGCCCAAATCTTGAGCAAACTCACACATGCCACCGTGCCAGCACCTGAATCCTGGGGGACCGTC
AGTCTTCTCTTCCCCGCATCCCCCTTCAAACCTGCCCGGGCGGCCGCTCG

Fig. 15KK

SUBSTITUTE SHEET (RULE 26)

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38_16487.edit

CGAGCGGCCGCCGGGCAGGTTTGAAGGGGGATGCGGGGAAGAGGAAGACTGACGGTCCCCCAGGAGTTCA
GGTGCTGGGCACGSGTGGGCATGTGTGAGTTTGTGACAAGATTTGGGCTCAACTCTCTTGTCACCTTGGTGTT
GCTGGGCTTGTGATCTACGTTGCAGGTGTAGGTCTGGGTGCCGAAGTTGCTGGAGGGCACGGTCACCACGCTGC
TGAGGGAGTAGAGTCTGAGGACTGTAGGACAGACCTCGGCCGCGACACGCT

39_16488.edit

NGGNNGGTCCGGNCNGNCAGGACCACTCNTCTTCGAAATA

41_16489.edit

AGCGTGGTCGCGGCCGAGGTCCTCACTTGCCCTCTGCAAAGCACCGATAGCTGCGCTCTGGAAGCGCAGATCTG
TTTTAAAGTCCTGAGCAATTTCTCGCACCAGACGCTGGAAGGGAAGTTTGCGAATCAGAAGTTCAGTGGACTTC
TGATAACGTCTAATTTACGGAGCGCCACAGTACCAGGACCTGCCCGGGCGGCCGCTCGA

42_16489.edit

TCGAGCGGCCGCCGGGCAGGTCCTGGTACTGNGGGCGCTCCGTGAAATTAGACGTTATCAGAAGTCCACTGAAC
TCTGATTCGCAAACTTCCCTTCCAGCGTCTGGTGCGAGAAATTGCTCAGGACTTTAAACAGATCTGCGCTTC
CAGAGCGCAGCTATCGGTGCTTTCAGGAGGCAAGTGAGGACCTCGGCCGCGACACGCT

45_16491.edit

TCGAGCGGCCGCCGGGCAGGTCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATC
GGTCATGCTCTCGCCGAACCAGACATGCCTCTTGTCTTGGGGTTCTTGCTGATGTACCAGTTCTTCTGGGCCA
CACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTCCAGAAGACTTTGATGGCATCCAGGTTG
CAGCCTTGGTTGGGGTCAATCCAGTACTCTCCACTTTCCAGTCAGAGTGGCACATCTTGAGGTACGGCAGGT
GCGGGCGGGGTTCTTGACCTCGGCCGCGACACGCT

Fig. 15LL

SUBSTITUTE SHEET (RULE 26)

73/101

46_16491.edit

GTGGGNTTGAACCCNTTTNANCTCCGCTTGGTACCGAGCTCGGATCCACTAGTAACGGCCGCCAGTGTGCTGGA
ATTCGGCTTAGCGTGGTCGCGGCCGAGGTCAAGAACCCCGCCGCACCTGCCGTGACCTCAAGATGTGCCACTC
TGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCA
ACATGGAGACTGGTGAGACCTGCGTGTACCCACTCAGCCAGTGTGGCCAGAGAAGTGGTACATCAGCAAG
AACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCA
GGGCTCCGACCCTGCCGATGTGGACCTGCCCGGGCGGCCGCTCGA

47_16492.edit

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGCTGTACAGTGAGATATTACAGGATCACTTACGGAGAAAC
AGGAGGAAATAGCCCTGTCCAGGAGTTCACTGTGCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAAC
CTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCGCAAGCAGCAAGCCAATT
TCCATTAATTACCGAACAGAAATTGACAAACCATCCAGATGCAAGTGACCGATGTTCAAGACAACAGCATTAG
TGTCAGTGGCTGCCTTCAAGTTCCTGTTACTGGTTACAGAGTAACCACTCCCAAAATGGACCAGGAC
CAACAAAACTAAACTGCAGGTCCAGATCAACAGAAATGACTATTGAAGGCTTGACGCCACAGTGGAGTAT
GTGGTTAAGTGTCTATGCTCAGAATCAAGCGGAGAGAAAGTCAAGCTCTGGTTCACTGNAAGTAACCAACAT
TGATCGCCTAAAGGACTGGCATTCACTGATGNGGATGCCGATTCCATCAAAATTGNTTGGGAAAACCCACAGGG
GCAAGTTTNCANGTCNAGGNGGACCTACTCGAGCCCTGAGGATGGAATCCTTGACTNTTCTTNNCTGATGGG
GAAAAAAACCTTNAAACTTGAAGGACCTGCCCGGGCGGCCGTNCAAAACCAATTCCACCCCTTGGGGGCG
TTCTATGGGNCCCACTCGGACCAAACTTGGGGTAAN

48_16492.edit

TCGAGCGGCCGCCCGGGCAGGTCTTGCACTCTGCAGTGTCTTCTTACCATCAGGTGCAGGGAATAGCTCAT
GGATTCCATCCTCAGGGCTCGAGTAGGTCAACCTGTACCTGGAACTTGCCCTGTGGGCTTTCCAAGCAATT
TTGATGGAATCGGCATCCACATCAGTGAATGCCAGTCTTTAGGGCGATCAATGTTGGTTACTGCAGTCTGAAC
CAGAGGCTGACTCTCTCGCTTGGATTCTGAGCATAGACACTAACCACATACTCCACTGTGGGCTGCAAGCCTT
CAATAGTCATTTCTGTTTGTCTGGACCTGCAGTTTTAGTTTTGTTGGTCTGGTCCATTTTGGGAGTGGTG
GTTACTCTGTAACAGTAACAGGGGAACCTGAAGGCAGCCACTTGACACTAATGCTGTTGCTGCTGAACATCGGT
CACTTGCACTCTGGGATGGTTTGTCAATTTCTGTTCCGTAATTAATGGAAATGGCTTGCTGCTTGCGGGCTTG
TCTCCAGGCCAGTGACAGCATACACAGTGATGGTATAATCAACTCCAGGTTTAAGCCGCTGATGGTAGCTGAA
ACTTTGCTCCAGGCACAAGTGAACCTCTGACAGGGCTATTTCTNCTGTTCTCCGTAAGTGATCCTGTAATATC
TCACTGGGACAGCAGGANGCATTCCAAAACCTCGGGCGNGACCCCTAAGCCGAATTNTGCAATATNCATCACA
CTGGCGGGCGCTCGANCATTCATTAAGGCCCAATCNCCTATAGGGAGTNTANTACAATTNG

Fig. 15MM

SUBSTITUTE SHEET (RULE 28)

74/101

49_16493.edit

TCGAGCGGCCGCCCGGGCAGGTCACTTTTGGTTTTGGTCATGTTCCGTTGGTCAAAGATAAAACTAAGTTTG
AGAGATGAATGCAAAGGAAAAAATATTTCCAAAGTCCATGTGAAATTGTCTCCCATTTTTTGGCTTTTGAG
GGGGTTCAAGTTTGGGTTGCTTGTCTGTTCCGGGTTGGGGGAAAGTTGGTTGGGTGGGAGGGAGCCAGGTGG
GATGGAGGGAGTTTACAGGAAGCAGACAGGGCCAACGTCG

55_16496.edit

AGCGTGGTCGCGGCCGAGGTCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCA
GAGGCATAAGGTTCCGGGAAGAGGTTGTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATG
ACTCGTGCTTTGACCCCTACACAGTTTCCCATATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGC
TTTAAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCATTTAGATGTGATTATCTAGATGGTGCCATGA
CAATGGTGTGAACATAAGATTGGAGAGAAGTGGACCGTCAGGGAGAAAATGGACCTGCCCGGGCGGCCGCTC
GA

56_16496.edit

TCGAGCGGCCGCCCGGGCAGGTCCATTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCAT
TGTCATGGCACCCTAGATGAATCACATCTGAAATGACCACTTCAAAGCCTAAGCACTGGCACAACAGTTTA
AAGCCTGATTAGACATTCGTTCCCACTCATCTCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGA
GTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTCTCCCGAACCTTATGCC
CTGCTGGTCTTTCAGTGCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTCGGCCGCGACCAG
CT

59_16498.edit

TCGAGCGGCCGCCCGGGCAGGTCCACCATAAGTCCTGATACAACCACGGATGAGCTGTCAGGAGCAAGGTTGAT
TTCTTTTATTGGTCCGGTCTTCTCCTTGGGGGTCACCCGCACTCGATATCCAGTGAGCTGAACATTGGGTGGTG
TCCACTGGGCGCTCAGGCTTGTGGGTGTGACCTGAGTGAACCTCAGGTCAAGTTGGTGCAGGAATAGTGGTTACT
GCAGTCTGAACCAGAGGCTGACTCTCTCCGCTGGATTCTGAGCATAGACACTAACCACATACTCCACTGTGGG
CTGCAAGCCTTCAATAGTCATTTCTGTTTGATCTGGACCTGCAGTTTGTAGTTTTGTTGGTCTGGTCCATTTT
TGGGAGTGGTGGTTACTCTGTAACCAAGTAACAGGGGAACCTGAAGGCAGCCACTTGACACTAATGCTGTTGTCC
TGAACATCGGTCACTTGCACTCTGGGATGGTTGNCAATTTCTGTTCCGTAATTAATGGAATTTGGCTTGCTGCT
TGCGGGGCTGTCTCCACGGCCAGTGACAGCATACACAGNGATGGNATNATCAACTCCAAGTTTAAGGCCCTGAT
GGTAACCTTTAACTTGCTCCAGCCAGNGAACTTCCGACAGGGTATTTCTTCTGGTTTTCCGAAAGNGANCCT
GGAAATNNTCTCCTTGGANCAGAAGGANCNTCCAAACTTGGGCCGGAACCCCTT

Fig. 15NN

75/101

60_16473.edit

AGCGTGGTCGCGGCCGAGGTCTGTGAGAGTGGCACTGGTAGAAGTTCAGGAACCCTGAACTGTAAGGGTTCT
TCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGCTGGAATGGGGCCCATGAGATGGTTGT
CTGAGAGAGAGCTTCTTGCTACATTCGGCGGGTATGGTCTTGGCCTATGCCCTTATGGGGGTGGCCGTGTGG
GCGGTGTGGTCCGCCTAAACCATGTTCTCAAAGATCATTTGTTGCCAACACTGGGTGCTGACCAGAAGTG
CCAGGAAGCTGAATACCATTTCCAGTGTACATCCAGGGTGGGTGACGAAAGGGGTCTTTGAACTGTGGAAGG
AACATCCAAGATCTCTGGTCCATGAAGATTGGGGTGTGGAAGGGTACCAGTTGGGGAAGCTCGTCTGTCTTTT
TCCTTCCAATCAGGGGCTCGCTCTTCTGATTATCTTCAGGGCAATGACATAAATTGTATATTCGGTTCGCGGT
TCCAGGCCAGTAATAGTAGCCTCTTGTGACACCAGGCGGGGCCANGGACCACTTCTCTGGGANGAGACCCAGC
TTCTCATACTTGATGATGTAACCCGGTAATCTGCACGTGGCGGCTGNCATGATACCANCAAGGAATTGGGTGN
GNGGACCTGCCCGCGGGCCCTCNA

60_16498.edit

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCTGCTGTGACAGTGAGATATTACAGGATCACTTACGGAGAAAC
AGGAGGAAATAGCCTGTCCAGGAGTTCACTGTGCTGGGAGCAAGTCTACAGCTACCATCAGCGGCTTAAAC
CTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCGCAAGCAGCAAGCCAATT
TCCATTAATTACCGAACAGAAATTGACAAACCATCCAGATGCAAGTGACCGATGTTGAGGACAACAGCATTAG
TGTCAGTGGCTGCCCTCAAGTCCCCTGTTACTGGTTACAGAGTAACCACTCCCAAAAATGGACCAGGAC
CAACAAAACATAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGCTTGACGCCACAGTGGAGTAT
GTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAAGCTCTGGTTGAGTGCAGTAACCACTATTCC
TGCAACCACTGACCTGAAGTTCACTCAGGTACACCCACAAGCCTGAGCCGCCAGTGGACACCACCAATGTTT
ACTCACTGGATATCGAGTGCAGGTGACCCCAAGGAGAAGACCGGACCCATGAAAGAAATCAACCTTGTCTCT
GACAGCTCATCCNGGGTGTATCAGGACTTATGGGGGACTGCCCGCGCGGCGNTCGAAANCGAATTNTGAA
TTTCTTCTNCACTGGGNGGCGNTTCGAGCTTNTNTANANGGCCAATTCNCCTNTAGNGGGTCTGN

61_16499.edit

AGCGTGGTCGCGGCCGAGGTGTCNAGGA

62_16483.edit

TCGAGCGGCCGCCCGGGCAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGAT
TACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCTCCAGAGAAGTGGTCCCTCGGCCCCGCGCTGGT
TCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAAT
CAGAAGAGCGAGCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCAACTGGTAACCTTCCACACCCCAA
TCTTCATGGACCAGAGATCTTGATGTTCTTCCACAGTTCAAAGACCCCTTTCGTACCCACCCCTGGGTATG
ACACTGGAAATGGTATTGAGCTTCTGGCACTTCTGGTCAGCAACCCAGTGTGGGCAACAAATGATCTTTGAG
GAACATGGTTTATAGCGGACCAACCGCCACAACGGGCACCCCATAGGNAATAGGCCAAGACCATACCCCGC
CGAATGTAGGACAAGAAGCTCTNTCTCAACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAETACATCA
TTTCATGTCATCTGGTGGGCACTTGATGAANAACCTTACAGTTCAGGGTCTCTGGAATCTTACCAGNGCCA
CTTCTGACAGGANCTTGGGCGNGACCACT

Fig. 1500

SUBSTITUTE SHEET (RULE 26)

76/101

63_16500.edit

AGCGTGGTCGCGGCCGAGGTCCATTTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCATTG
TCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTAAA
GCCTGATTCAGACATTGTTCCCACTCATCTCCAACGGCATAATGGGAAACTGTGTAGGGTCAAAGCAGGAGT
CATCCGTAGGTTGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTTTCGGAACCTTATGCCTC
TGCTGGTCTTTCAGTGCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTGCCGGGGCGCCCGCT
CGA

64_16493.edit

AGCGTGGTCGCGGCCGAGGTGTGCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCTGTAAA
CTCCCTCCATCCCAACCTGGCTCCCTCCCAACCAACCACTTCCCCCAACCCGAAACAGACAAGCAACCCA
AACTGAACCCCTCAAAAGCCAAAAAATGGGAGACAATTCACATGGACTTTGGAAAAATTTTTTCTTTG
CATTATCTCTCAAACTTAGTTTTATCTTTGACCAACCGAACATGACCAAAACCAAAAGTGACCTGCCGGG
CGGCCGCTCGA

64_16500.edit

TCGAGCGGCCGCCGGGCAGGTCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAG
CAGAGGCATAAGGTTCCGGAAGAGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGA
TGACTCGTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAG
GCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCATTTAGATGTGATTATCTAGATGGTGCCAT
GACAATGGTGTGAACCTACAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGACCTCGGCCGCGACCACG
CT

Fig. 15PP

SUBSTITUTE SHEET (RULE 26)

77/101

16501.edit

TCGAGCGGCCGCCCGGGCAGGTACCGGGGTGGTCAGCGAGGAGCCATTCACTGAACCTCACCATCAACAACC
TGCGGTATGAGGAGAACATGCAGCACCTGGCTCCAGGAAGTTCAACACCACGGAGAGGGTCCTTCAGGGCCTG
CTCAGGTCCCTGTTCAAGAGCACAGTGTGGCCCTCTGTACTCTGGCTGCAGACTGACTTTGCTCAGACCTGA
GAAACATGGGGCAGCCACTGGAGTGGACGCCATCTGCACCCTCGCCTTGATCCCACTGGTNCCTGGACTGGACA
NANAGCGGCTATACTTGGGAGCTGANCCNAACCTTTGGCGGNGACNCCNCTT

16501.2.edit

GAGGACTGGCTCAGCTCCAGTATAGCGCTCTCTGTCCAGTCCAGGACCAGTGGGATCAAGGCGGAGGGTGCA
GATGGCGTCCACTCCAGTGGCTGCCCCATGTTTCTCAAGTCTGAGCAAAGNCAGTCTGCAGCCAGAGTACAGAG
GGCCAACACTGGTGCTCTTGAACAGGGACCTGAGCAGGCCCTGAAGGACCCTCTCCGTGGTGTGAACCTCCTG
GAGCCAGGGTGCTGCATGTTCTCCTCATACCGCAGGTTGTTGATGGTGAAGTTCAGTGTGAATGGCTCCTCGCT
GACCAACC

16502.1.edit

AGCGTGGTGGCGGCCGAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCGCCACGTGCCAGGATTA
CCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCTCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGGTGTC
ACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATAAATTTATGTCATTGCCCTGAAGAATAATCA
GAAGAGCGAGCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCTTCCACACCCAATC
TTCATGGACCANANANCTTGGATNGTCTTTACNGGTTNAAAAAACCTTTTCGCCCCCCCACCTTGGGGATT
AACCTTGGGAAANGGGGATTTNACNNTTCC

16502.2.edit

TCGAGCGGCCGCCCGGGCAGGTCTGTGAGAGTGGCACTGGTAGAAGTTCCAGGAACCCTGAACTGTAAGGGTT
CTTCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCCATGAGATGGTT
GTCTGAGAGAGAGCTTCTTGTCTACATTGGCGGGTATGGTCTTGGCCTATGCCTTATGGGGGTGGCCGTTGT
GGGCGGTGTGGTCCGCCTAAACCATGTTCTCAAGATCATTTGTTGCCCAACACTGGGTGCTGACCAGAAG
TGCCAGGAAGCTGAATACCATTTCCAGTGTATACCCAGGGNGGGTGACCAAAGGGGTCNTTTNGACCTGGNG
AAAGGAACCATCCAAAANCTCTGNCCCATG

Fig. 15QQ

SUBSTITUTE SHEET (RULE 26)

78/101

16503.1.edit

AGCGTGGNCGCGCCGAGGTCTGAGGATGTAACTCTTCCCAGGGGAAGGCTGAAGTGTGACCATGGTGCTAC
TGGGTCCTTCTGAGTCAGATATGTGACTGATGNGAACTGAAGTAGGTACTGTAGATGGTGAAGTCTGGGTGTCC
CTAAATGCTGCATCTCCAGAGCCTTCCATCATTACCGTTTCTTCTTTGCTATGGGATGAGACACTGTTGAGTA
TTCTCTAAAGTCACCACTGAAATCTTCTCCAAAGGAAAACCTGTGGAAAAGCCCCCTATTTCTGCCCCATAAT
TTGGTTCTCCTAATCNCCTGAAATCACTATTTCCCTGGAANGTTTGGGAAAAANNGGGCNACCTGNCANTGGA
AANTGGATANAAAGATCCCACCATTTTACCCAACNAGCAGAAAGTGGGAANGGTACCGAAAAGCTCCAAGTAAN
AAAAAGGAGGGGAAGTAAAGGTCAAGTGGGCACCAAGTTTCAAACAAAACCTTTCCCCAACTATANAACCCA

16503.2.edit

AAGCGGCCGCCCGGGCAGGNNCAGNAGTGCCCTCGGGACTGGGNTCAGGCTCTGCGGCAGTTGTCACAG
CGCCAGCCCGCTGGCCTCAAAGCATGTGCAGGAGCAAAATGGCACCAGATATTCCTTCTGCCACTGTTCTCC
TACGTGGTATGTCTTCCCATCATCGTAACAGTTGCCTCATGAGGGTCACACTTGAATTCTCCTTTCCGTTC
CAAGACATGTGCAGCTCATTGGCTGGCTCTATAGTTTGGGAAAAGTTTGTGAACTGTGCCACTGACCTTTA
CTTCTCCTTCTCTACTGGAGCTTTCCGTACCTTCCACTTCTGCTGNTGGNAAAAAGGGNGGAACNTCTTATCA
ATTTATTGGACAGTANCCNCTTTCTNCCAAAACATNCAAGGAAAATATTGATTNCNAGAGCGGATTAAGG
AACAACCCNAATTATGGGGGCCAGAAATAAAGGGGGCTTTTCCACAGGTNTTTCTCT

16504.1.edit

TCGAGCGGCCGCCCGGGCAGGTCTGCAGGCTATTGTAAGTGTCTGAGCACATATGAGATAACCTGGGCCAAGC
TATGATGTTGATACGTTAGGTGTATTAATGCACCTTTTGACTGCCATCTCAGTGGATGACAGCCTTCTCACTG
ACAGCAGAGATCTTCTCACTGTGCCAGTGGGCAGGAGAAAGAGCATGCTGCGACTGGACCTCGGCCGCGACCA
CGCT

16504.2.edit

AGCGTGGTCCGGGCCGAGGTCCAGTCGCAGCATGCTCTTCTCTGCCCAGTGGCACAGTGAGGAAGATCTCTG
CTGTCACTGAGAAGGCTGTCACTGAGATGGCAGTCAAAAGTGCAATTAATACACCTAACGTATCGAACAT
CATAGCTTGGCCAGGTTATCTCATATGTGCTCAGAACACTTACAATAGCCTGCAGACCTGCCGGGCGGCCGC
TCGA

Fig. 15RR

SUBSTITUTE SHEET (RULE 26)

79/101

16505.1.edit

CGAGCGGCCGCCGGGCAGGTCCAGACTCCAATCCAGAGAACCACCAAGCCAGATGTCAGAAGCTACACCATCA
CAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGGAGCTCCCCGTG
GTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTCCTGGCCACCACACCAATTCCTTGCT
GGTATCATGGCAGCCGCCAGTGCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCA
GAGAAGTGGTCCCTCGGCCCGCCCTGGTGNACAGAAGCTACTATTACTGGCCTGGAACCGGGAACCGAATAT
ACAATTTATGTCATTGCCCTGAAGAATAATCANAAGAGCGAGCCCTGATTGGAAGG

16505.2.edit

AGCGTGGTCGCGGCCGAGGTCTGTGAGAGTGGCACTGGTAGAAGTTCAGGAACCCTGAAGTGTAAAGGTTCT
TCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCCATGAGATGGTTGT
CTGAGAGAGAGCTTCTTGCTGTCTTTTCCTTCCAATCAGGGGCTCGCTCTTCTGATTATTCCTCAGGGCAA
TGACATAAATTGTATATTCGGFTCCCGGTTCCAGGCCAGTAATAGTAGCCTCTGTGACACCAGGGCGGGCCGA
GGGACCACTTCTCTGGGAGGAGACCAGGCTTCTCATACTTGATGATGTANCCGGTAATCCTGGCACCGTGGCG
GCTGCCATGATACCAGCAAGGAATTGGGTGTGGTGGCAAGAAACGCAGGTTGGATGTTGCATCAATGGCAGTG
GAGGCGTCGATNACCACAGGGGAGCTCCGANCATTGTCAATCAAGGTGGACAGGTAGAATCTTGTAATCAGGTG
CCTGGTTTGTAAACCTG

16506.1.edit

TCGAGCGGCCGCCGGGCAGGTTTCGTGACCGTGACCTCGAGGTGGACACCACCCTCAAGAGCCTGAGCCAGCA
GATCGAGAACATCCGGAGCCAGAGGGCAGCCGCAAGAACCCGCGCCGACCTGCCGTGACCTCAAGATGTGCC
ACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAGTCTTC
TGCAACATGGAGACTGGTGAGACCTGCGTGACCCCACTCAGCCAGTGTGGCCAGAAGAACTGGTACATCAG
CAAGAACCCCAAGGACAAGAAGCATGTCTGGTTCCGGGAAAGCATGACCGATGGATTCCAGTTCGAGTATGGCG
GCCAGGGCTCCGACCCTGCCGATGTGGACCTCGGCCGCGACACGCTAAGCCCGAATTCAGCACACTGGCGGC
CGTTACTAGTGGGATCCGAGCTTCGGTACCAAGCTTGGCGTAATCATGGGNCATAGCTGTTCTGNGTGAAAA
TGGTATTCGCTTCACAATTTCCAC

16506.2.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG
TCATGCTCTCGCCGAACAGACATGCCTCTTGCTTGGGGTTCTTGCTGATGTACCAGTCTTCTGGGCCACA
CTGGGCTGAGTGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTGCA
GCCTTGGTTGGGTCAATCCAGTACTCTCCACTCTTCCAGTCAGAGTGGCACATCTTGAGGTCACGGCAGGTGC
GGGCGGGGTTCTTGCGGCTGCCCTCTGGGCTCCGGATGTTCTCGATCTGCTGGCTCAAGCTCTTGAAGGGTGGT
GTCCACCTCGAGGTCACGGTCACGAAACCTGCCCGGGCGGCCGCTCGA

Fig. 15SS

SUBSTITUTE SHEET (RULE 26)

80/101

16507.1.edit

AGCGTGGTCGCGGCCGAGGTCAAGAACCCGCGCCGACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAA
GAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGA
CTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCAGAGAAGTGGTACATCAGCAAGAACCCCAAG
GACAAGAGGCATGTCTGGTTCGCGGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCGA
CCCTGCCGATGTGGACCTGCCCGNGCCGNCCTCGAAAAAGCCNAATTTCCAGNCACACTTGCGCGGCCGTT
ACTACTG

16507.2.edit

TCGAGCGGCCGCGCGGCAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATC
GGTCATGCTCTCGCGAACCAGACATGCCTCTTGCTTGGGGTCTTGCTGATGTACCAGTCTTCTGGGCCA
CACTGGGCTGAGTGGGGTACAGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTG
CAGCCTTGGTGGGGTCAATCCAGTACTCTCCACTCTTCCAGTCAGAGTGGCACATCTTGAGGTCACGGCAGGT
GCGGGCGGGGTTCTTGACCTCGGCCGCGACCAAGCT

16508.1.edit

CGAGCGGCCGCGCGGCAGGTCCCCCCTTT
TTTTTTTTTTTTTTTTTTTT

16508.2.edit

AGCGTGGTCGCGGCCGAGGTCTGGCATTCTTCGACTTCTCTCCAGCCGAGCTTCCAGAACATCACATATCAC
TGCAAAAATAGCATTGCATACATGGATCAGGCCAGTGGAAATGTAAAGAAGGCCCTGAAGCTGATGGGGTCAAA
TGAAGGTGAATTAAGGCTGAAGGAAATAGCAAAATCACCTACACAGTCTTGGAGGATGGTTGCACGAAACACA
CTGGGGAATGGAGCAAAACAGTCTTTGAATATCGAACACGCAAGGCTGTGAGACTACCTATTGTAGATATTGCA
CCCTATGACATTGGTGGTCCTGATCAAGAATTTGGTGTGGACGTTGGCCCTGTTTGCTTTTATAAACCAAACT
CTATCTGAAATCCCAACAAAAAAATTTAACTCCATATGTGNTCCTCTTGTCTAATCTTGGCAACCAGTGCAA
GTGACCGACAAAATCCAGTTATTTATTTCCAAAATGTTTGAAAACAGTATAATTTGACAAAGAAAAAGGATA
CTTCTCTTTTTTGGCTGGTCCACCAATAACAATTCAAAAGGCTTTTGGTTTTATTTTTTANCCAATTCCAA
TTTCAAATGTCTCAATGGNGCTTATAATAAAATAAACCTTCACCCTTTTTTTTNGAT

Fig. 15TT

SUBSTITUTE SHEET (RULE 26)

81/101

16509.1.edit

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAAC
AGGAGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAAC
CTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGCAAGCCAATT
TCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACCGATGTTCAAGACAACAGCATTAG
TGTCAGTGGCTGCCCTTCAAGTTCCTGTTACTGGTTACAGAAGTAACCACCACTCCAAAAATGGACCAGGA
CCAACAAAACTAAAACTGCAGGTCCAGATCAAAACAGAAAAATGGACTATTGAAGGCTTGACGCCACAGTGGAA
GTATGTGGNTAGGNGTCTATGCTCAGAATCCCAAGCCGGAGAAAGTCAGCCTTCTGGTTTAGACTGCAGTAACC
AACATTGATCGCCCTAAAGGACTGGNCATTCACTTGGATGGTGGATGTCCAATTC

16509.2.edit

TCGAGCGGCCGCCCGGGCAGGTCTTGACAGTCTGCAGNGTCTTCTTACCATCAGGTGCAGGAATAGCTCAT
GGATTCCATCCTCAGGGCTCGAGTAGGTACCCCTGTACCTGGAAACTTGCCCTGTGGGCTTTCCCAAGCAATT
TTGATGGAATCGACATCCACATCAGNGAATGCCAGTCTTTAGGGCGATCAATGTTGGTTACTGCAGTCTGAAC
CAGAGGCTGACTCTCTCCGCTTGGATTCTGAGCATAGACACTAACCACATACTCCACTGTGGGCTGCAAGCCTT
CAATAGTCATTTCTGTTTGATCTGGACCTGCAGTTTTAAGTTTTTGGTGGTCTGNCCATTTTTGGGAAGTGG
GGGTTACTCTGTAACAGTAACAGGGGAACCTGAAGGCAGCCACTTGACACTAATGCTGTTGCTCCTGAACATC
GGTCACTTGATCTGGGGATGGTTTTGACAATTTCTGGTTCGGCAAATTAATGGAAATTGGCTTGCTGCTTGGC
GGGGCTGNCTCCACGGGCCAGTGACAGCATAC

16510.1.edit

TCGAGCGGCCGCCCGGGCAGGTCTTGACAGTCTGCAGTGTCTTCTTACCATCAGGTGCAGGAATAGCTCAT
GGATTCCATCCTCAGGGCTCGAGTAGGTACCCCTGTACCTGGAAACTTGCCCTGTGGGCTTTCCCAAGCAATT
TTGATGGAATCGACATCCACATCAGTGAATGCCAGTCTTTAGGGCGATCAATGTTGGTTACTGCAGTCTGAAC
CAGAGGCTGACTCTCTCCGCTTGGATTCTGAGCATAGACACTAACCACATACTCCACTGTGGGCTGCAAGCCTT
CAATAGTCATTTCTGTTTGATCTGGACCTGCAGTTTTAAGTTTTTGGTGGTCTGNCCATTTTTGGGAAGGG
GTGGTTACTCTTGTAACAGTAACAGGGGAACCTGAAGGCAGCCACTTGACACTAATGCTGGTGGCTGAACATC
GGTCACTTGATCTGGGGATGGTTTTGGTCAATTTCTGTTCCGTAATTAATGGGAAATTGGCTTACTGGCTTGGC
GGGCTGTCTCCACGGNCAGTGACAAGCATACACAGGNGATGGGTATAATCAACTCCAGGTTAAGGCCNCTGAT
GGTA

16510.2.edit

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAAC
AGGAGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAAC
CTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGTAAGCCAATT
TCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACCGATGTTCAAGACAACAGCATTAG
TGTCAGTGGCTGCCCTTCAAGTTCCTGTTACTGGTTACAGAGTAACCACCACTCCAAAAATGGGACCAGGA
CCAACAAAACTAAAACTGCANGGTCCAGATCAAAACAGAAATGACTATTGAAGGCTTGACGCCACAGTGGAG
TATGTGGGTTAGTGTCTATGCTCAGAATNCCAAGCGGAGAGAGTCAGCCTCTGGTTCAAGT

Fig. 15UU

SUBSTITUTE SHEET (RULE 26)

82/101

16511.1.edit

TCGAGCGGCCGCCCGGGCAGGTCTCAGGAGCTCACCACCATGGCCTGGGCTCTGCTCCTCCTCACCC
TCTCACTCAGGGCACAGGGTCTGGGCCAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCTGGA
CAGTCAGTCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGCTTATGAATTTGTCTCTGGTACCAACA
ACACCCAGGCAAGGCCCCAACTCATGATTTCTGAGGTCACTAAGCGGCCCTCAGGGGTCCCTGATCGCTTCT
CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGCTCCANGCTGAGGATGANGCTGATTATTAC
TGGAAGCTCATATGCAGGCAACAACAATTGGGTGTTCCGGCGGAAGGGACCAAGCTGACCGTNCTAAGGTCAAGC
CCAAGGCTTGCCCCCTCGGTCACTCTGTTCCACCTCCTCTGAAGAAGCTTCAAGCCAACAANGNCACACT
GGGTGTGTCTCATAAGTGGAAGTTCTACCC

16511.2.edit

AGCGTGGTCGCGGCCGAGGTCTGTAGCTTCTGTGGGACTTCCACTGCTCAGGCGTCAGGCTCAGGTAGCTGCTG
GCCGCGTACTTGTGTGCTTGTGNTTGGAGGGTGTGGTGGTCTCCACTCCCGCTTGACGGGGTGTCTATCTGC
CTTCCAGGCCACTGTCAAGGCTCCCGGTAGAAGTCACTTATGAGACACACCAAGTGTGGCTTGTGGCTTGAA
GCTCCTCAGAGGAGGGTGGGAACAGAGTGACCGAGGGGGCAGCCTTGGGCTGACCTAGGACGGTCAGCTTGGTC
CCTCCGCCGAACACCCAATTGTTGTTGCCTGCATATGAGCTGCAGTAATAATCAGCCTCATCTCAGCCTGGAG
CCCAGAGACNGTCAAGGGAGGCCCGTGTGTTGCCAAGACTTGAAGCCAGANAAGCGATCAGGGACCCCTGAGGG
CCGCTTTACNGACCTCAAAAAATCATGAATTTGGGGGGCCTTTCCTGGNGTTGGTTGGTNACCAGNAAAACA
AAATTTCATAAAGCACCAACGTCACTGCTGGTTCCAGTGCANGAANATGGTGAAGTGAANTGTCC

16512.1.edit

AGCGTGGTCGCGGCCGAGGTCCAGCATCAGGAGCCCCGCTTGCCGGCTCTGGTCATCGCCTTTCTTTTGTGG
CCTGAAACGATGTCATCAATTCGAGTAGCAGAACTGCCGTCTCCACTGCTGCTTATAAGTCTGCAGCTTCAC
AGCCAATGGCTCCCATATGCCAGTTCCTTCATGTCCACCAAAGTACCGTCTCACCATTTACACCCAGGTCT
CACAGTTCTCCTGGGTGTGCTTGGCCGAAGGGAGGTAAGTANACGGATGGTCTGGTCCCACAGTTCTGGATC
AGGGTACGAGGAATGACCTCTAGGGCTGGGCNACAAGCCCTGTATGGACCTGCCCGGGCGGGCCGCTCGA

16512.2.edit

TCGAGCGGCCGCCCGGGCAGGTCCATACAGGGCTGTTGCCAGGGCCCTAGAGGNCATTCTTGATACCTGATCC
AGAACTGTGGGACCAGCACCATCCGTCTACTTACCTCCCTTCGGGCCAAGCACACCCAGGAGAACTGTGAGACC
TGGGGTGTAAATGGNGAGACGGGTACTTTGGTGGACATGAAGGAAGTGGGCATATGGGAGCCATTGGCTGNGAA
GCTGCANACTTATAAGACAGCAGTGGAGACGGCAGTTCTGCTACTGCGAATTGATGACATCGTTTCAGGCCACA
AAAAGAAAGCGATGACCANAGCCGGCAAGGGGGCTTCTGATGCTGGACCTCGGCCGCCGACCACGCTT

Fig. 15VV

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16514.1.edit

AGCGTGGTCGCGGCCGAGGTCCACTAGAGGTCTGTGTGCCATTGCCAGGCAGAGTCTCTGCGTTACAACTCC
TAGGAGGGCTTGCTGTGCGGAGGGCCTGCTATGGTGTGCTGCGGTTTCATCATGGAGAGTGGGGCCAAAGGCTGC
GAGGTTGTGGTGTCTGGGAACTCCGAGGACAGAGGGCTAAATCCATGAAGTTTGTGGATGGCCTGATGATCCA
CAGCGGAGACCCCTGTTAACTACTACGTTGACACTGCTGTGCCACAGTGTGCTCANACAGGGTGTGCTGGGCA
TCAAGGTGAAGATCATGCTGCCCTGGGACCCANCTGGCAAAAATGGCCCTTAAAAACCCCTTGCCNTGACCAG
TGAACCATTTGTGNGAACCCCAAGATGAANATACTTGCCACCACCCCCATT

16514.2.edit

TCGAGCGGCGCCCGGGCAGGTCTGCCAAGGAGACCCTGTTATGCTGTGGGGACTGGCTGGGGCATGGCAGGCG
GCTCTGGCTTCCACCCCTTCTGTTCTGAGATGGGGTGGTGGGCAGTATCTCATCTTTGGGTTCCACAATGCTC
ACGTGGTCAGGCAGGGGCTTCTTAGGGCCAATCTTACCAGTTGGGTCAGGGCAGCATGATCTTACCTTGAT
GCCAGCACACCCTGTCTGAGCAACACGTGGCGCACAGCAGTGTCAACGTAGTAGTTAACAGGGTCTCCGCTGT
GGATCATCAGGCCATCCACAACTTCATGGATTTAGCCCTCTGTCCTCGGAGTTTCCAAAACACCACAACCTC
GCCAGCCTTTGGGCCCCACTTCTTCATGAATGAAACCGCAGCACACCATTANCAAGGCCCTTCCGCACAGGNAA
GCCCTTCTTAAGGAGTTTTGTAAACGCAAAAACTCTTGCCCTGGGGCAAATGGGCACACAGACCTNTANTNGGA
CCTTGGNCCGGAACACCGCTT

16515.1.edit

AGCGTGGTCGCGGCCGAGGTCTGGCCCTCCTGGCAAGGCTGGTGAAGATGGTCACCCTGGAAAACCCGGACGAC
CTGGTGAGAGAGGAGTTGTTGGACCACAGGGTGCTCGTGGTTTCCCTGGAACTCCTGGACTTCTGGCTTCAAA
GGCATTAGGGGACACAATGGTCTGGATGGATTGAAGGGACAGCCCGGTGCTCCTGGTGTGAAGGGTGAACCTGG
NGCCCTGGTGAATGGAATCCAGGTCAAACAGGAGCCCGNGGGCTTCTGGNGAGAGAGGACGTGTTGGTG
CCCCTGGCCANACCTGCCCGGGCGGCCGCTCNAAGCCGAAATCCAGNACACTGGCGGCCGNTACTANTGGA
ATCCGAACCTTCGGTACCAAAGCTTGGCCGTAATCATGGCCATAGCTTGTTCCCTGGGGNGGAAATTGGTATTCC
GCTNCCAATTCACACAACATACCGAACCCGGAAGCATTAAAGTGTAAGGCCCTGGGGGGGCTAAATGANG
TGAGCNTAACTCNCATTTAATTGGCGTTGCGCTTCACTGCCCCGCTTTTCCAGTCCGGGNA

16515.2.edit

TCGAGCGGCGCCCGGGCAGGTCTGGGCCAGGGGCACCAACACGTCTCTCTCACCAGGAAGCCACGGGCTCC
TGTTTGACCTGGAGTTCATTTTACCAGGGGCACAGGTTACCCCTTACACCAGGAGCACCGGGCTGTCCCT
TCAATCCATCCAGACCATTTGTGNCCCTAATGCCCTTGAAGCCAGGAAGTCCAGGAGTTCAGGGAAACCACGA
GCACCTGTGGTCCAACAACCTCTCTCTCACCAGGTGCTCCGGGTTTCCAGGGTGACCATCTTACCAGCCTT
GCCAGGAGGGCCAGACCTCGGCCGCGACCACGCT

Fig. 15WW

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16516.1.edit

ANCGTGGTCGCGGCCGAGGTCTCACCAGAGGTGNCACCTACAACATCATAGTGGAGGCACTGAAAGACCANCA
GAGGCATAAGGTTCCGGGAAGAGG

16516.2.edit

TCGAGCGGCCGCCCGGGCAGGTCCATTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCAT
TGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTA
AAGCCTGATTCAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGA
GTCATCCGTAGGTGGTTCAAGCCTTCGTTGACAGAGTTGTCCACGGTAACAACCTCTTCCCGAACCTTATGCC
TCTGCTGGTCTTTCAGTGCCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTCNGNCCNGAACAAC
GCTTAAGCCCGNATTCTGCAGAATAATCCCATCACACTTGGCGGCCGCTTCGANCATGCATCNTAAAAGGGGCC
CCAATTTCCCTTATAAGNGAANCCGTATTNCCAATTTCACTGGNCCCGCGNTTTTACAAACGNCGGTGAA
CTGGGGAAAAACCTGGCGGTTACCCAACCTTTAATCGCCNTTGGCAGCACAAATCCCCCTTTTCGNCCANCNTG
GGCGTAAATAACCGAAAA

16517.1.edit

ANCGNGGTGCGGCCGGANGTNTTTTTCTNTTTTTTT

16518.1.edit

AGCGTGGTCGCGGCCGAGGTCTGAGGTTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT
TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
TACCGGGNGGTGAGCGTCTCACCCTCTGCACCAGAATTGGTTGAATGGCAAGGAGTACAAGNGCAAGTTTC
CAACAAAGCCNTCCAGCCCCNTCGAAAAAACCATTTCCAAAGCCAAAGGGCAGCCCCGAGAACCAAGGTGT
ACACCTGCCCCCATCCGGGGAGGAAAAGANCAANAACCGTTGAGCCTTAACCTTGCTTGGTCNAANGCTTTT
TATCCCAACGNACTTCCCCNTGGAANTGGGAAAAACCAATGGGCCAANCCGAAAAACAATTACAANAACCCC

16518.2.edit

TCGAGCGGCCGCCCGGGCAGGTGTGCGAGTCCAGCACGGGAGGCGTGGTCTTGTAGTTGTTCTCCGGCTGCCCA
TTGCTCTCCCACTCCACGGCGATGTCGCTGGGATAGAAGCCTTGACCAGGCAGGTGAGGCTGACCTGGTTCTT
GGTCATCTCTCCCGGATGGGGCAGGGTGAACACCTGGGGTCTCGGGCTTGCCCTTTGGTTTTGAANATG
GTTTTCTCGATGGGGGTGGAAGGGCTTTGTTGNAACCTTGCACTTGACTCCTTGCCATTACCCAGNCCTGG
NGCAGGACGGNGAGGACNCTNACCACACGGAACCGGGCTGGTGGACTGCTCC

Fig. 15XX

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16519.1.edit

AGCGTGGTCGCGGACGANGTCCTGTCAGAGTGGNACTGGTAGAAGTTCCANGAACCTGAACTGTAAGGGTTCT
TCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGNGNCCTGGAATGGGGCCCATGANATGGTTGC
C

16519.2.edit

TCGAGCGGCCGCCCGGGCAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGAT
TACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGGTG
TCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACGAATATACAATTTATGTCATTGCCCTGAAGAATAAT
CAGAAGAGCGAGCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCAACTGGTAACCCCTCCACACCCCAA
TCTTCATGGACCAGAGATCTTGGATGTTCTTCCACAGTTCAAAGACCCCTTTCGGCACCCCCCTGGGTATG
AACCTGGGAAAANGGNANTTAANCTTCTGGCA

16520.1.edit

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGCTGTACAGTGAGATATTACAGGATCACTTACGGAGAAAC
AGGAGGAAATAGCCCTGTCCAGGAGTTCAGTGTGCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAAC
CTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGAAGCAGCAAGCCAATT
TCCATTAATTACCGAACAGAAATTGACAAACCATCCAGATGCAAGTGACCGATGTTCAGGACAACAGCATTAG
TGTCAGTGGCTGCCTTCAAGGTNCCCTGGTACTGGGTTACAGANTAACCACCACTCCAAAAATGGACCAGGA
ACCACAAAACCTTAAACTGCAGGTCAGATCAAAACAGAAATGACTATTGAANGCTTGAGCCACAGTGGGA
GTATGNGGGTAGTGNCTATGCTTCAGAATCCAAGCGGAAAAANGTCAAGCCTTNTGGGTTCAA

16520.2.edit

TCGAGCGGCCGCCCGGGCAGGTCTTGCACTCTGCAGTGTCTTCTTCACCATCAGGTGCAGGGAATAGCTCAT
GGATTCATCCTCAGGGCTCGAGTAGGTACCCCTGTACCTGGAACTTGCCCTGTGGGCTTTCCAAGCAATT
TTGATGGAATCGACATCCACATCAGTGAATGCCAGTCTTTAGGGCGATCAATGTTGGTTACTGCAGNCTGAAC
CAGAGGCTGACTCTCTCGCTTGGATTCTGAGCATAGACCTAACCACATACTCCACTGTGGGCTGCAANCCTT
CAATAANNCATTTCTGTTTGATCTGGACC

16521.2.edit

TCGAGCGGCCGCCCGGGCAGGTCTGGTGGGGTCTGGCACACGCACATGGGGGNGTTGNTCTNATCCAGCTGCC
CAGCCCCCAATTGGCGAGTTTGAGAAGGTGTGCAGCAATGACAACAANACCTTCGACTCTTCTGCCACTTCTTT
GCCACAAAGTGACCCCTGGAGGGCACCAAGAAGGGCCACAAGCTCCACCTGGAATACATCGGGCCTTGCAAATA
CATCCCCCTTGCTGGACTCTGAGCTGACCGAATCCCCCTTGGCATGCGGGACTGGCTCAAGAACCGTCTT
GGCACCTTGTATGANAGGGATGAAGACACNACC

Fig. 15YY

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16522.1.edit

AGCGTGGTCGCGGCCGAGGTCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCT
CCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGAGA
GTTGAGCCCAAATCTTGTGACAAAACCTACACATGCCACCGTGCCAGCACCTGAACTCTGGGGGGACCGTC
AGTCTTCTCTTCCCCCGCATCCCCCTTCAAACCTGCCCGGGGGCCGCTCGAAAGCCGAATTCAGCACACT
GGCGGCCGGTACTAGTGGANCCNAACCTGGNANCCAACCTGGNGGAANTAAATGGGCATAANCTGTTTCTGGGGG
GAAATTGGTATCCNGTTTACAATTCCNCACAACATACGAGCCGGAAGCATAAAAGNGTAAAAGCCTGGGGGNG
GCCTANTGAAGTGAAGCTAAACTCACATTAATTNGCGTTGCCGCTCACTGGCCCGCTTTTCCAGC

16522.2.edit

TCGAGCGGCCGCGCCGGGCAGGTTTGGAAAGGGGGATGCGGGGGAAGAGGAAGACTGACGGTCCCCCAGGAGTTC
AGGTGCTGGGCACGGTGGGCATGTGTGAGTTTTGTCAAGATTGGGCTCAACTCTTGTCCACCTTGGTGT
TGCTGGGCTTGTGATCTACGTTGCAGGTGTAGGTCTGGGNGCCGAAGTTGCTGGAGGGCACGGTCACCACGCTG
CTGAGGGAGTAGAGTCTGAGGACTGTANGACAGACCTCGGCCGNGACCACGCTAAGCCGAATTCGCAGATAT
CCATCACACTGGCGGCCGCTCCGAGCATGCATTTTAGAGG

16523.1.edit

AGCGTGGNCGCGGACGANGACAACAACCCC

16523.2.edit

TCGAGCGGCCGCGCCGGGCAGGNCCACATCGGCAGGGTGGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATC
GGTCATGCTCTTGCCGAACCAGACATGCCTCTTGTCTTGGGGTTCTTGCTGATGNACCAGTTCTTCTGGGCCA
CACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGTTG
CAGCCTTGGTTGGGGTCAATCCAGTACTCTCCACTCTTCAGTCAGAGTGGCACATCTTGAGGTACGGCAGGT
GCGGGCGGGGTTCTTGACCT

16524.1.edit

AGCGTGGTCGCGGCCGAGGTCCAGCCTGGAGATAANGGTGAAGGTGGTGCCCCGGGACTTCAGGTATAGCTGG
ACCTCGTGGTAGCCCTGGTGAGAGAGGTGAACTGGCCCTCCAGGACCTGCTGGTTTCCCTGGTGCTCCTGGAC
AGAATGGTGAACCTGGNGGTAAAGGAGAAAGAGGGGCTCCGGNTGANAAGGTGAAGGAGGCCCTCCTGNATTG
GCAGGGGCCCCANGACTTAGAGGTGGAGCTGGCCCCCTGGCCCCGAAGGAGGAAAGGGTGCTGCTGGTCTCC
TGGGCCACCTGG

Fig. 15ZZ

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16524.2.edit

TCGAGCGGCCGCCCGGGCAGGTCTGGGCCAGGAGGACCAATAGGACCAGTAGGACCCCTTGGGCCATCTTTCCC
TGGGACACCATCAGCACCTGGACCGCCTGGTTCACCCCTTGTACCCCTTTGGACCAGGACTTCCAAGACCTCCTC
TTTCTCCAGGCATTCTTGCAGACCAGGAGTACCANCAGCACCAGGTGGCCAGGAGGACCAGCAGCACCCCTT
CCTCCTTCGGGACCAGGGGACCAGCTCCACCTTAAGTCCTGGGGCCCTGCCAATCCAGGAGGGCCTCCTTC
ACCTTTCTACCCGGAGCCCTCTTCT

16526.1.edit

TCGAGCGGCCGCCCGGGCAGGTCCACCGGATATTCGGGGTCTGGCAGGAATGGGAGGCATCCAGAACGAGAA
GGAGACCATGCAAGCCTGAACGACCGCCTGGCCTTTACCTGGACAGAGTGAGGAGCCTGGAGACCGACAACC
GGAGGCTGGAGAGCAAAATCCGGGAGCACTTGAGAGAAGGAGCCAGGTGAGAGCTGGAGCCATTACTTC
AAGATCATCGAGGACCTGAGGGCTCANATCTTCGAAATACTGCNGACAATGCCCG

16526.2.edit

ATGCGNGGTCGCGGCCGANGACCANCTCTGGCTCATACTTGACTCTAAAGNCNTACCAGNANTTACGGNCATT
GCCAATCTGCAGAACGATGCGGGCATTGTCCGCANTATTTGCGAAGATCTGAGCCCTCAGGNCCTCGATGATCT
TGAAGTAANGGCTCCAGTCTCTGACCTGGGGTCCCTTCTTCTCCAAGTGCTCCCGGATTTTGCTCTCCAGCCTC
CGGTTCTCGGTCTCCAAGNCTTCTCACTCTGTCCAGGAAAAGAGGCCAGGCGGNCGATCAGGGCTTTTGCATGG
ACT

16527.1.edit

AGCGTGGTCGCGGCCGAGGTTGTACAAGCTTT
TT

16527.2.edit

TCGAGCGGCCGCCCGGGCAGGTCTGCCAACACCAAGATTGGCCCCGCCGCATCCACACAGTTNGTGTGCGGGG
AGGTAACAAGAAATACCGTGCCCTGAGGNTGGACGNNGGGAATTTCTCCTGGGGCTCAGAGTGTTGTACTCGTA
AAACAAGGATCATCGATGTTGTCTACAATGCATCTAATAACGAGCTGGTTCGTACCAAGACCCTGGTGAAGAAT
TGCATCGTGCTCATNGACAGCACACCGTACCGACAGTGGGTACCGAAGTCCCACTATGCNCCT

Fig. 15AAA

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16528.1.edit

TCGAGCGGCCGCCGGGCAGGTCCACCACCCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGAT
TACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCAGAGAAGTGGTCCCTCGGCCCGCCCTGGTG
TCACAGAGGCTACTATTACTGGCCTGGAACCGGAACCGAATATACAATTTATGTCATTGCCCTGAAG

16528.2.edit

AGCGTGNTCNCGGCCGAGGATGGGGAAGCTCGNCTGTCTTTTTCTTCCAATCAGGGGCTNNNTCTTCTGATTA
TTCTTCAGGGCAANGACATAAATTGTATATTCGGNTCCCGGTTCCAGNCCAGTAATAGTAGCCTCTGTGACACC
AGGGCGGGGCCGAGGGACCACTTCTCTGGGAGGAGACCCAGGCTTCTCATACTTGATGATGAAGCCGGTAATCC
TGGCAGGTGGGCGGCTGCCATGATACCACCAANGAATTGGGTGTGGTGGACCTGCCCGGGCGGCGCTCGAAA
ANCCGAATTCNTGCAAGAATATCCATCACACTTGGGCGGGCGNTCGAACCATGCATNTAAAAGGGCCCAAT
TTCCCCCTATTAGNGAAGCCNCAATTAACAAATTCACCTGG

16529.1.edit

TCGAGCGGCCGCCCGGGCAGGTCTCGCGGTGCGACTGGTGATGCTGGTCCGTGTTGGTCCCCCGGCCCTCTGG
ACCTCCTGGTCCCCCTGGTCTCCAGCGTGTTTCGACTTCAGCTTCTGCCCCAGCCACCTCAAGAGAAGG
CTCACGATGGTGGCGCTACTACGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACC
ACCCTCAAGAGCCTTGAGCCAGCAGAATCGAAAACATTGGAACCCAAGAAGGGCAAGCCGCAAGAAACCCC
GCCCGCACCTGGCCGNGAACCTCAAGAANGTGGCCACNTCTTGACTGGGAAAAAAGGGAAAANTACTTGGAA
TTGGAC

16529.2.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG
TCATGCTCTCGCGAACCAGACATGCCTCTTGCTCTGGGGTCTTGCTGATGTACCAGTTCTTCTGGGCCACA
CTGGGCTGAGTGGGGTACACGAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTGCA
GCCTTGGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGTCAGAAGTGGCACATCTTGAGGTCACGGCAGGGT
GCGGGCGGGGTTCTTGCGGCTGCCCTTCTGGGCTCCCGAATGTTCTNNGAACTTGCTGG

Fig. 15BBB

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16530.1.edit

AGCGTGGTCGCGGCCGAGGTCCACTAGAGGTCTGTGTGCCATTGCCAGGCAGAGTCTCTGCGTTACAACTCC
TAGGAGGGCTTGCTGTGCGGAGGGCCTGCTATGGTGTGCTGCGGTTTCATCATGGAGAGTGGGGCCAAAGGCTGC
GAGGTTGTGGTGTCTGGGAACTCCGAGGACAGAGGGCTAAATCCATGAAGTTTGTGGATGGCCTGATGATCCA
CAGCGGAGACCTGTTAATACTACGTTGACACTTGCTTGTGCGCCACGTGTTGCTCANACANGGGTGGGCTGG
GCATCAAGGNG

16530.2.edit

TCGAGCGGCCGCCCGGGCAGGTCTGCCAAGGAGACCTGTTATGCTGTGGGGACTGGCTGGGGCATGGCAGGCG
GCTCTGGCTTCCACCTTCTGTTCTGAGATGGGGGTGGTGGGCAGTATCTCATCTTTGGGTTCCACAATGCTC
ACGTGGTCAGGCAGGGCTTCTTAGGGCCAATCTTACCAGTTGGGTCCAGGGCAGCATGATCTTCACTTGAT
GCCCAGCACACCTGTCTGAGCAACAGTGGCGCACAGCAAGTGTCAACGTAAGTAAGTTAACAGGGTCTCCGC
TGTGGATCATCAGGCCATCCACAACTTCATGGATTTAACCTCTGTCTCGGAG

16531.1.edit

TCGAGCGGCCGCCCGGGCAGGTGTTTCAGAGGTTCCAAGGTCCACTGTGGAGGTCCAGGAGTGCTGGTGGTGG
GCACAGAGGTCCGATGGGTGAAACCATTTGACATAGAGACTGTTCTGTCCAGGGTGTAGGGGCCAGTCTTTG
ATGCCATTGGCCAGTTGGCTCAGCTCCAGTACAGCCGCTCTCTGTTGAGTCCAGGGCTTTTGGGGTCAAGATG
ATGGATGCAGATGGCATCCACTCCAGTGGCTGCTCCATCCTTCTCGGACCTGAGAGAGGTCACTCTGCAGCCAG
AGTACAGAGGGCCAACTGCTGTTCTTTGAATA

16531.2.edit

AGCGTGGTCGCGGCCGAGGTCTGTACTGGGAGCTAAGCAAAGTACCAATGACATTGAAGAGCTGGGCCCTAC
ACCCTGGACAGGAACAGTCTCTATGTCAATGGTTTCACCCATCAGAGCTCTGTGNCACCACCAGCACTCCTGG
GACCTCCAGTGGATTTAGAACCTCAGGGACTCCATCCTCCTCTCCAGCCCCACAATTATGGCTGCTGGCC
CTCTCCTGGTACCATTACCCTCAACTTCACCATCACCACCTGCAGTATGGGGAGGACATGGGTCAACCTGNC
TCCAGGAAGTTCAACACCACA

16532.1.edit

TCGAGCGGCCGCCCGGACAGGTCTGGGCGGATAGCACCGGGCATATTTGGAATGGATGAGGTCTGGCACCTG
AGCAGTCCAGCGAGGACTTGGTCTTAGTTGAGCAATTTGGCTAGGAGGATAGTATGCAGCACGNTCTGAGNCT
GTGGGATAGCTGCCATGAAGTAACCTGAAGGAGGTGCTGGCTGGTANGGGTTGATTACAGGGTTGGGAACAGCT
CGTACACTTGCCATTCTCTGCATATACTGGTTAGTGAGGTGAGCCTGGCCCTCTCTTTTG

Fig. 15CCC

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01_16558.3.edit

AGCGTGGTCGCGGCCGAGGTGAGCCACAGGTGACCGGGGCTGAAGCTGGGGCTGCTGGNCCTGCTGGTCTCTG

02_16558.4.edit

CAGCNGCTCCNACGGGGCCTGNGGGACCAACAACACGTTTTACCCTTAGGCCCTTTGGCTCCTCTTTCTCCT
TTAGCACCAGGTTGACCAGCAGCNCANCAGGACCAGCAAATCCATTGGGGCCAGCAGGACCGACCTACCCACG
TTCACCAGGGCTTCCCCGAGGACCAGCAGGACCAGCAGGACCAGCAGCCCCAGCTTCGCCCCGCTCACCTGTGG
CTCACCTCGGCCGCGACCAAGCT

03_16535.1.edit

TCGAGCGGTGCCCCGGGCAGGTCCACCGGGATAGCCGGGGTCTGGCAGGAATGGGAGGCATCCAGAACGAGAA
GGAGACCATGCAAAGCCTGAACGACCGCCTGGCCTTTACCTGGACAGAGTGAGGAGCCTGGAGACCGANAACC
GGAGGCTGGANAGCAAAATCCGGGAGCACTTGGAGAAGAAGGGACCCAGGTCAAGAGACTGGAGCCATTACTT
CAAGATCATCGAGGGACCTGAGG

04_16535.2.edit

AGCGNGGTGCGGCCGAGGTCCAGCTCTGTCTCATACTTGACTCTAAAGTCATCAGCAGCAAGACGGGCATTGT
CAATCTGCAGAACGATGCGGGCATTGTCCGAGTATTTGCGAAGATCTGAGCCCTCAGGTCTCGATGATCTTG
AAGTAATGGTCCAGTCTCTGACCTGGGTCCCTTCTTCTCAAGTGCTCCCGGATTTGCTCTCCAGCCTCCG
GTTCTCGGTCTCCAGGCTCCTCACTCTGTCCAGGTAAGAAGGCCAGGCGGTGTTGAGGCTTTGCATGGTCTC
CTTCTCGTTCTGGATGCCTCCATTCTGCCAGACCC

05_16536.1.edit

TCGAGCGGCCGCCCCGGGCAGGTGAGGAAGCACATTGGTCTTAGAGCCACTGCCTCCTGGATTCCAACCTGTGCTG
CGGACATCTCCAGGGAGTGAGAAAGGAAGCAGGTCAAACCTGCTCAGATCAGTCAGACTGGCTGTTCTCAGTTC
TCACCTGAGCAAGGTGAGTCTGCAGCCAGAGTACAGAGGGCCAACACTGGTGTCTTGAACAAGGGCTTGAGCA
GACCCTGCAGAACCTCTTCCGTGGTGTGAACCTCCTGGAACACAGGGTGTTCATGTTTTCTCATATATGC
AAGGTTGGTGATGG

Fig. 15DDD

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07_16537.1.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG
TCATGCTCTCGCCGAACCAGACATGCCTCTTGTCCTTGGGGTTCTTGCTGATGTACCAGTTCTTCTGGGCCACA
CTGGGCTGAGTGGGGTACACCGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTGC
AGCCTTGGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGTCAGAAGTGGGCACATCTTGAGGTCAACCGGCAG
GTGCCGGGCCGGGGTTCTTGCGGCTTGCCCTCTGGGCTCCGGATGTTCTCGATCTGCTTGGCTCAGGCTCTTG
AGGGTGGGTGTCCACCTCGAGGTACGGTCACCGAAACCTGCCCGGGCGGCCCGCTCGA

08_16537.2.edit

TCGAGCGGTGCGCCGGGCAGGTTTCGTGACCGTGACCTCGAGGTGGACACCACCCTCAAGAGCCTGAGCCAGCA
GATCGAGAACATCCGGAGCCAGAGGGCAGCCGCAAGAACCCGCGCCGACCTGCCGTGACCTCAAGATGTGCC
ACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTC
TGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGGCCCAGAAGAACTGGTACATC
AGCAAGGAACCCCAAGGACAAGAGCATTGTCTTGGTTGGCGAGNAGCATGACCCGATGGATTCCAGTTTCGA
GTATTGGCGGCCAGGGCTTCCCGACCTTGCCGATGTGGACCTCGGCCGCGACCACCGCT

Fig. 15EEE

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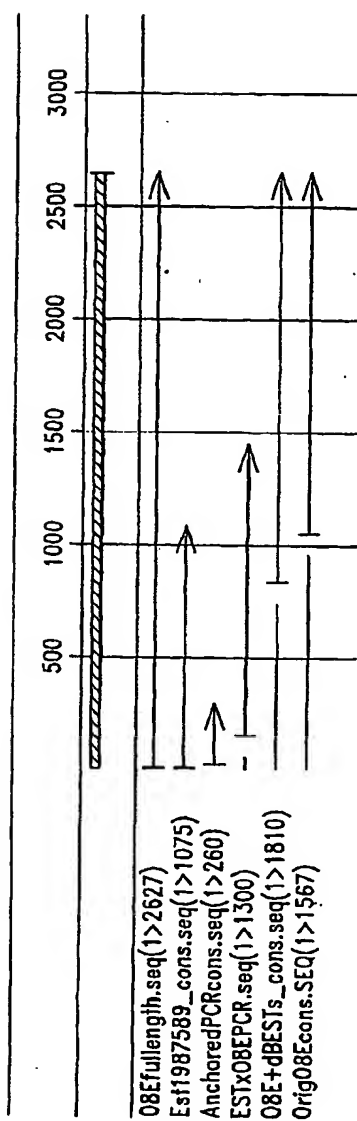


Fig. 16

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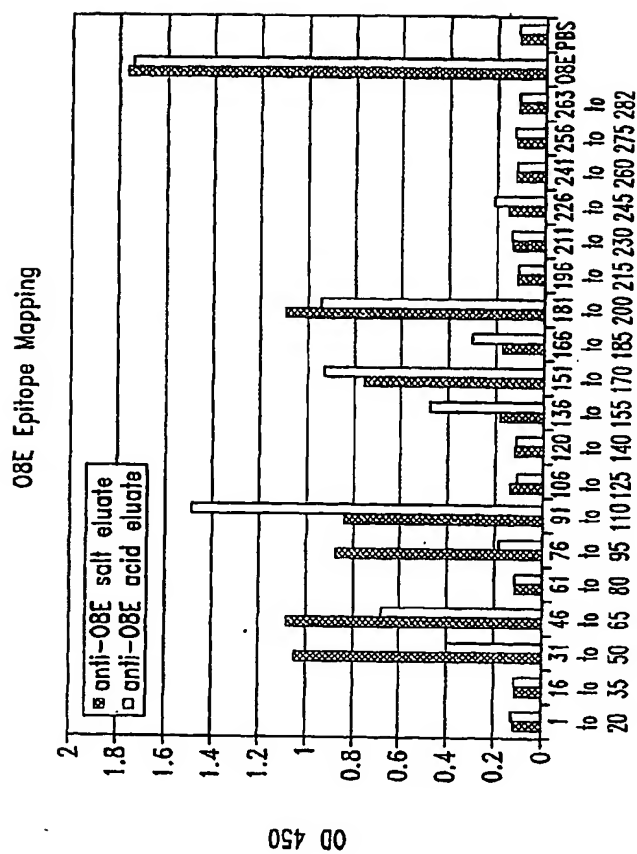
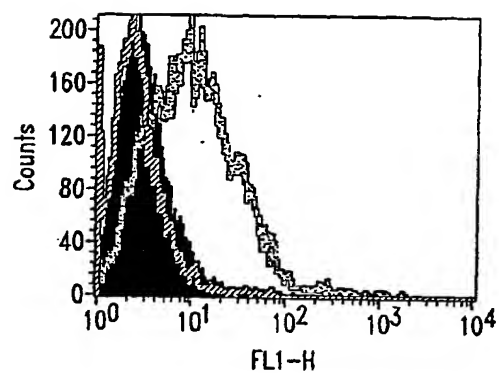


Fig. 17

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O8E Surface Expression



- B305D/HEK stained with anti-O8E antibody
- - - O8E/HEK stained with anti-O8E antibody
- ... O8E/HEK stained with an irrelevant antibody

Fig. 18

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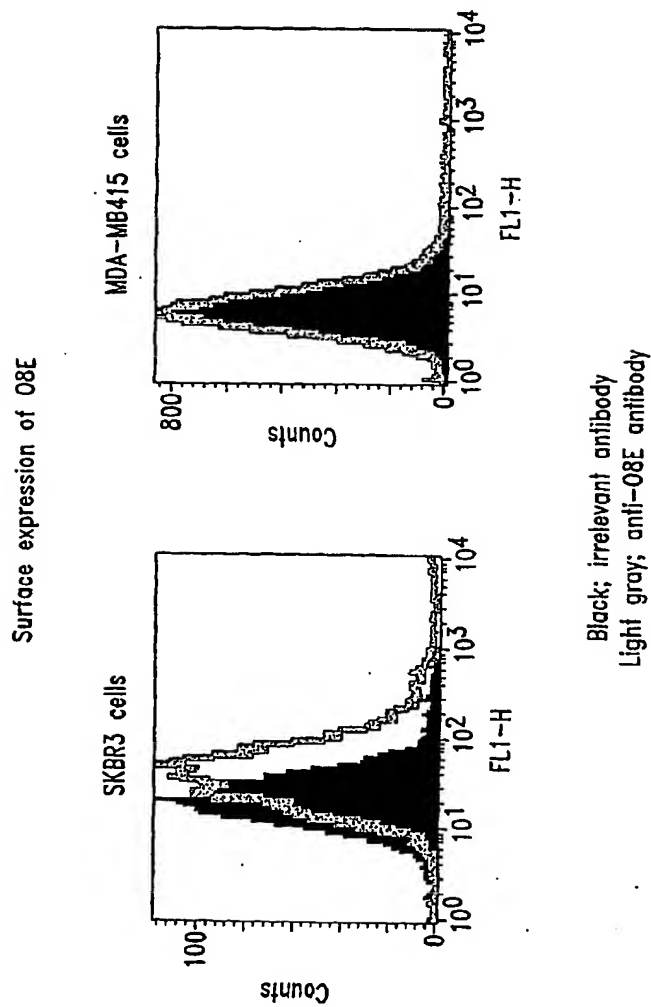
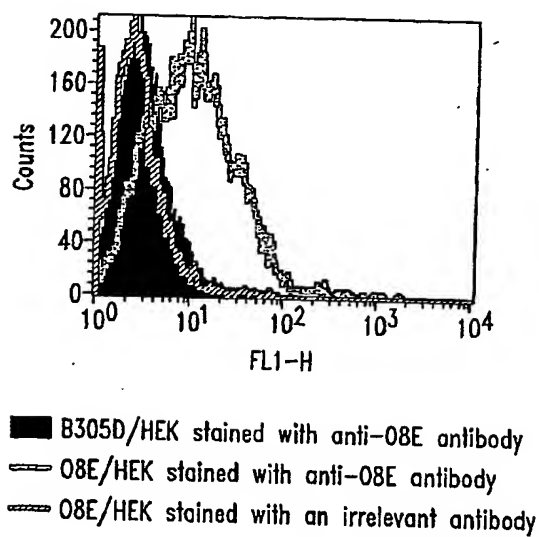


Fig. 19

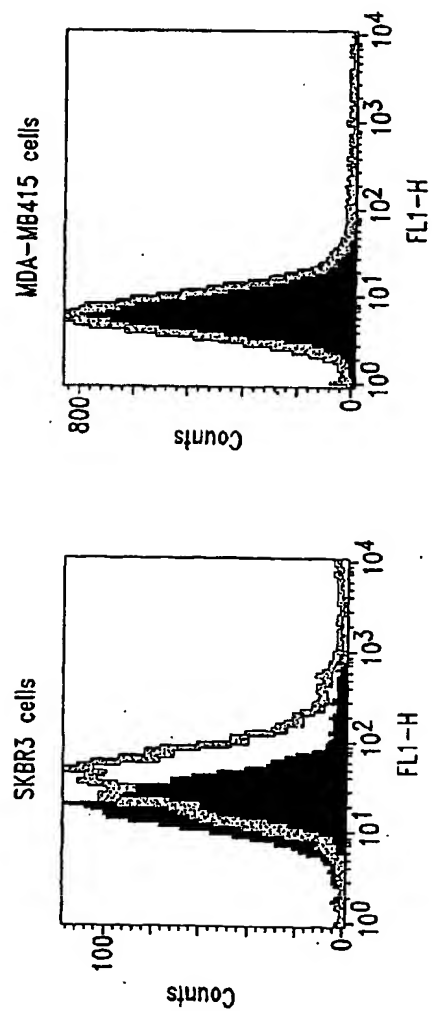
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O8E Surface Expression

*Fig. 20*

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Surface expression of O8E

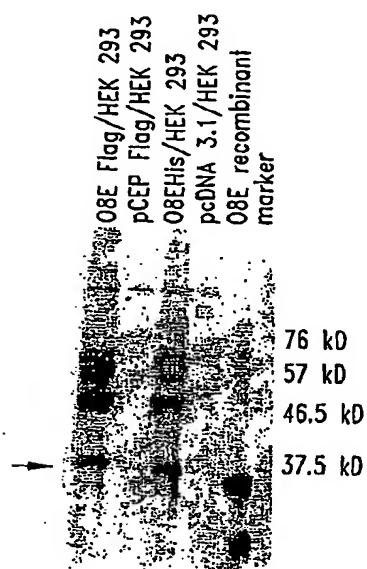


Black; Irrelevant antibody
Light Grey; Anti-O8E antibody

Fig. 21

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O8E expression in HEK293 Cells
(probed with anti-O8E rabbit polyclonal sera #2333L)

*Fig. 22*

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08E Rabbits 01212000

Date: 1/21/99

Antigen on Plate	Sera Sample	Antibody Dilutions											
		1:1000	1:2000	1:4000	1:8000	1:16000	1:32000	1:64000	1:128000	1:256000	1:512000	1:1024000	1:2048000
08E (#632-24)	Preimmune sera (#2576L):11/10/99	0.13	0.09	0.08	0.07	0.07	0.07	0.07	0.05	0.07	0.07	0.07	0.07
	Average	0.10	0.08	0.07	0.07	0.07	0.07	0.07	0.05	0.06	0.07	0.06	0.07
	α -08E (#2576K):11/11/2000	0.11	0.08	0.07	0.07	0.07	0.07	0.07	0.05	0.07	0.07	0.06	0.07
	Average	2.92	2.81	2.74	2.70	2.58	2.08	1.51	1.01	0.58	0.40	0.24	0.15
	Preimmune sera (#2333L):11/10/99	2.93	2.77	2.74	2.69	2.48	2.08	1.57	1.00	0.56	0.40	0.23	0.16
	Average	2.93	2.79	2.74	2.69	2.53	2.08	1.59	1.00	0.57	0.40	0.23	0.16
	Preimmune sera (#2333L):11/10/99	0.09	0.07	0.06	0.05	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07
	Average	0.08	0.07	0.06	0.07	0.10	0.07	0.07	0.07	0.07	0.07	0.07	0.07
	α -08E (#2333L):11/11/2000	0.08	0.07	0.06	0.05	0.08	0.07	0.07	0.07	0.07	0.07	0.07	0.07
	Average	2.73	2.75	2.64	2.48	2.30	1.78	1.41	0.92	0.58	0.32	0.20	0.14
Average		2.73	2.76	2.51	2.50	2.37	1.93	1.44	0.88	0.58	0.35	0.20	0.14
		2.73	2.76	2.57	2.54	2.33	1.85	1.43	0.90	0.58	0.33	0.20	0.14

Fig. 23

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affi-pure O8E #2576L 739.87A&B

Date: 5/2/2000	
Antibody Name	O8E polyclonal
Rabbit #, Bleed Date	2576L, 1/11/2000
Purification Method	affinity
Buffer	PBS
Notebook	#705, p150
lot #	739.87A
Antibody Concentration	1.4mg/ml
Initial Amount	18mg
	739.87B
	1.7mg/ml
	3mg

Antigen on Plate	Sera Sample	Antibody Dilutions											
		1:1000	1:2000	1:4000	1:8000	1:16000	1:32000	1:64000	1:128000	1:256000	1:512000	1:1024000	1:2048000
#632-24	preimmune sera (2576L)	0.15	0.11	0.09	0.08	0.08	0.07	0.07	0.07	0.07	0.08	0.07	0.08
	Average	0.14	0.10	0.09	0.08	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07
	α -O8E (2576K):2/8/2000	2.74	2.71	2.63	2.49	2.29	1.87	1.39	0.92	0.57	0.35	0.20	0.14
	Average	2.72	2.68	2.64	2.47	2.26	1.93	1.42	0.94	0.57	0.34	0.21	0.14
	affinity pure α -O8E poly	2.73	2.70	2.63	2.48	2.27	1.90	1.41	0.93	0.57	0.34	0.21	0.14
	salt peak 739-87A	2.69	2.60	2.50	2.21	1.83	1.34	0.99	0.64	0.38	0.22	0.15	0.11
	Average	2.59	2.48	2.38	2.21	1.82	1.33	1.00	0.62	0.37	0.22	0.14	0.11
	affinity pure α -O8E poly	2.64	2.54	2.44	2.21	1.83	1.34	1.00	0.63	0.37	0.22	0.15	0.11
	acid peak 739-67B	2.46	2.39	2.40	2.34	2.08	1.73	1.29	0.81	0.49	0.29	0.19	0.13
	Average	2.65	2.66	2.61	2.45	2.14	1.76	1.30	0.82	0.48	0.29	0.19	0.13
	Average	2.56	2.53	2.51	2.39	2.11	1.74	1.30	0.81	0.49	0.29	0.19	0.13

Fig. 24

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Anti-O8E mAb Binding to O8E Amino Acids
61-80 Induces Ligand Internalization

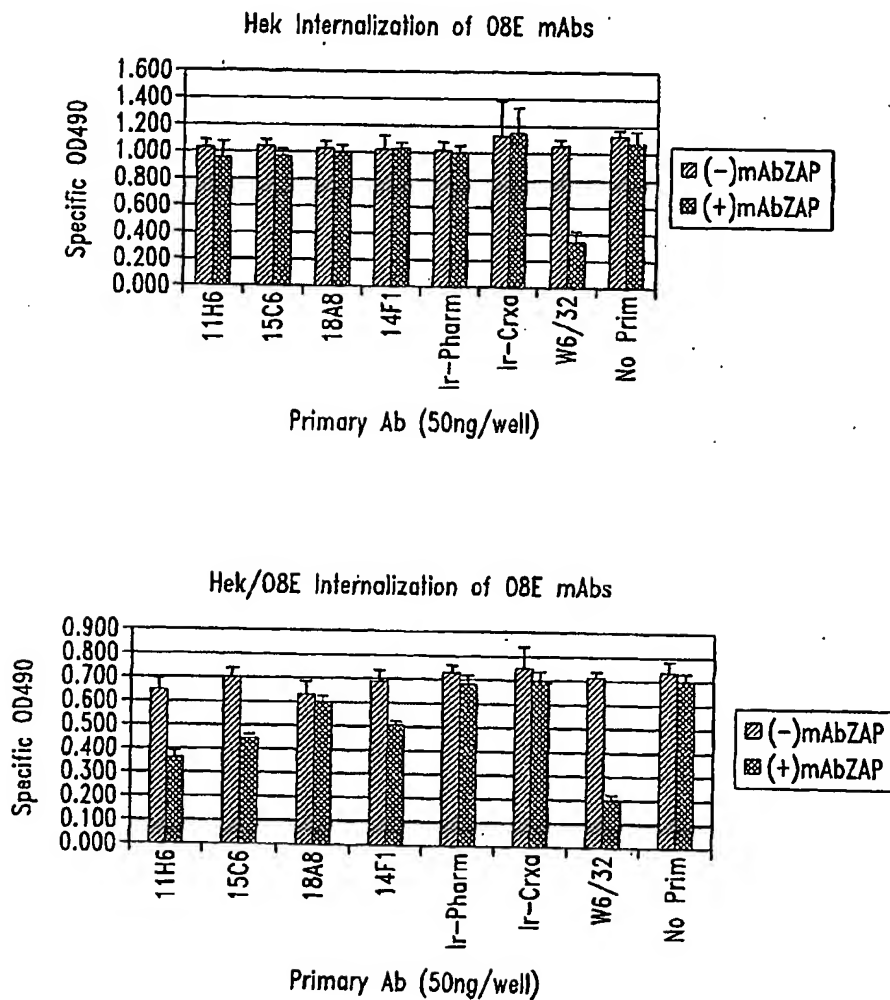


Fig. 25

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<110> Corixa Corporation
 Mitcham, Jennifer L.
 King, Gordon E.
 Algate, Paul A.
 Fling, Steven P.
 Retter, Marc W.
 Fanger, Gary Richard
 Reed, Steven G.
 Vedvick, Thomas S.
 Carter, Darrick
 Hill, Paul
 Albone, Earl

<120> COMPOSITIONS AND METHODS FOR THE THERAPY
 AND DIAGNOSIS OF OVARIAN CANCER

<130> 210121.46201PC

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<223> n = A,T,C or G

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<213> Homo sapiens

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<223> n = A,T,C or G

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cagcagggcc tcatcacact gggctggatt cactactcacc ccacacagac cgcgtttctc 180
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ttaggcaagt cagaaagaga acatggtcac ccaaaagcaa ctgtaactca gaaattaagt 660
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ctctctaatt tcaatttgtt tatatttacc tctgggtcga ataagggcat ctgtgcagaa 840
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agcttattac tgggtgagg gacagcttac tccatttgac cagattgttt ggctaacaca 960
tcccgaagaa tgattttgtc aggaattatt gttatttaat aaatatttca ggatattttt 1020
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1041

<210> 19

<211> 1043

<212> DNA

<213> Homo sapiens

<400> 19

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ctctgtggaa aactgatgag gaatgaattt accattaccc atgttctcat ccccaagcaa 60
agtgtgggt ctgattactg caacacagag aacgaagaag aacttttcct catacaggat 120
cagcagggcc tcatcacact gggctggatt cactactcacc ccacacagac cgcgtttctc 180
tccagtgtcg acctacacac tcaactgtct taccagatga tgttgccaga gtcagtagcc 240
attgtttgct cccccaagtt ccaggaaact ggattcttta aactaactga ccatggacta 300
gaggagattt cttcctgtcg ccagaaagga ttcatccac acagcaagga tccacctctg 360
ttctgtagct gcagccacgt gactgttggt gacagagcag tgaccatcac agaccttoga 420
tgagcgtttg agtccaacac cttccaagaa caacaaaacc atatcagtgt actgtagccc 480
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agcttattac tgggtgagg gacagcttac tccatttgac cagattgttt ggctaacaca 960
tcccgaagaa tgattttgtc aggaattatt gttatttaat aaatatttca ggatattttt 1020
cctctacaat aaagtaacaa tta

```

1043

<210> 20

<211> 448

<212> DNA

<213> Homo sapiens

<400> 20

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ggacgacaag gccatggcga tatcggatcc gaattcaagc ctttgggaatt aaataaacct 60
ggaacagggga aggtgaaagt tggagtgaaga tgtcttccat atctatacct ttgtgcacag 120
ttgaatggga actgtttggg tttagggcat cttagagttg attgatggaa aaagcagaca 180
ggaactgggt ggaggtcaag tggggaagtt ggtgaatgtg gaataactta cctttgtgct 240
ccacttaaac cagatgtgtt gcagcttccc tgacatgcaa ggatctactt taattccaca 300
ctctcattaa taaattgaat aaaaggggaat gttttggcac ctgatataat ctgccaggct 360
atgtgacagt aggaaggaat ggtttcccct aacaagccca atgcactggt ctgactttat 420

```


aaattatttta ataaatgaa ctattatc

448

<210> 21

<211> 411

<212> DNA

<213> Homo sapiens

<400> 21

ggcagtgaca ttcacatca tgggaaccac cttccctttt cttcaggatt ctctgtagtg 60
gaagagagca cccagtgttg ggctgaaaac atctgaaagt agggagaaga acctaaaata 120
atcagtatct cagaggggtc taagggtcca agaagtctca ctggacattt aagtgccaac 180
aaaggcatac tttcgggaatc gccaaagtcaa aactttctaa cttctgtctc tctcagagac 240
aagtgaact caagagtcta ctgcttttagt ggcaactaca gaaaactggg gttaccaga 300
aaaacaggag caattagaaa tggttccaat atttcaaagc tccgcaaaca ggatgtgctt 360
tcctttgccc atttagggtt tcttctcttt cctttctctt tattaaccac t 411

<210> 22

<211> 896

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 230, 320

<223> n = A,T,C or G

<400> 22

tgcgctgaaa acaacggcct cctttactgt taaaatgcag ccacagggtc ttagccgtgg 60
gcatctcaac caccagcctc tgtggggggc aggtgggcgt cctgtgggc ctctgggcc 120
acgtccagcc tctgtcctet gccttccgtt cttegacagt gttcccgcca tccctggta 180
cttggtactt ggcgtgggcc tctgtgtgtg ctccagcagc tctccaggn ggtcgggccg 240
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ggctgtcttc accctccggn gcacctctc cagctccagc tgcgtggcgg cctgcagcgt 360
ggccagctcg gccttggcct gcgcgctct cctctcarag gctgccagcc ggtcctcgaa 420
ctcctggcgg atcacctggg ccaggttgcg gcgctcgcta gaaagctgct cgttcacgcg 480
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gccctcgccc tcccgaagct ggcccttcag ctccgagcac cgtccttgaa gcttccgctc 600
cgactgtccc agctcggaga gctcggcctc gtacttgctc cgttaagcgt tgatgcggct 660
ctcggcagcc ttctcactct cctccttggc cagcgccatg tccgctcca gccggtgaat 720
gaccagctca atctccttgt cccggccttt ccgatttct tccctcagct cctgttcccg 780
gttcagcagc cagcctcct ccttctggt gcggccggcc tcccacgcct gcctctccag 840
ctccagctgc tgettcaggg tattcagctc catctggcgg gcctgcagcg tggcca 896

<210> 23

<211> 111

<212> DNA

<213> Homo sapiens

<400> 23

caacttatta cttgaaatta taatatagcc tgtccgtttg ctgtttccag gctgtgatat 60
attttcctag tggtttgact ttaaaaataa ataaggttta attttctccc c 111

<210> 24

<211> 531

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
<222> 472, 494
<223> n = A,T,C or G

<400> 24
tgcaagtcac gggagtttat ttatttaatt tttttccca gatggagact ctgtcgccca 60
ggctggagtg caatgggtg atcttggtc actgcaacct ccacctctg ggttcaagcg 120
attctcctgc cacagcctcc cgagtagctg ggattacagg tgcccgccac cacaccagc 180
taatttttat atttttagta aagacagggg ttccccatgt tggccaggct ggtcttgaac 240
ttctgacctc aggtgatcca cctgcctcgg cctcccaaa gtttgggatt acaggcgtga 300
gctacccgtg cctggccagc cactggagtt taaaggacag tcatgttggc tccagcctaa 360
ggcggcattt tccccatca gaaagcccg ggctcctgta cctcaaaata gggcacctgt 420
aaagtcagtc agtgaagtct ctgctctaac tggccaccgg gggccattgg cntctgacac 480
agccttgcca ggangcctgc atctgcaaaa gaaaagtcca cttcctttcc g 531

<210> 25
<211> 471
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 377
<223> n = A,T,C or G

<400> 25
cagagaatct kagaagatg tcgcgttttc ttttaatgaa tgagagaagc ccatttgtat 60
ccctgaatca ttgagaaaag gcggcggtgg cgacagcggc gacctaggga tcgatctgga 120
gggacttggg ggcgtgcag agacctctag ctgcagcgcg agggacctcc cgccgggatg 180
cctggggagc agatggacc tactggaagt cagttggatt cagatttctc tcagcaagat 240
actccttgcc tgataattga agattctcag cctgaaagcc aggttctaga ggatgattct 300
ggttctcact tcagtatgct atctcgacac cttcctaate tccagacgca caaagaaaat 360
cctgtgttgg atgttngtc caatccttga acaaacagct ggagaagaac gaggagaccg 420
gtaatagtgg gttcaatgaa catttgaaag aaaaccaggt tgcagaccct g 471

<210> 26
<211> 541
<212> DNA
<213> Homo sapiens

<400> 26
gactgtcctg aacaaggac ctctgaccag agagctgcag gagatgcaga gtggtggcag 60
gagtggaagc caaagaacac ccaccttctt cccttgagg agtagagcaa ccatcagaag 120
atactgtttt attgctctgg tcaaaacaagt cttcctgagt tgacaaaacc tcaggctctg 180
gtgacttctg aatctgcagt ccactttcca taagtcttgg tgcagacaac tgttcttttg 240
cttccatagc agcaacagat gcttgggggc taaaaggcat gtcctctgac cttgcaggtg 300
gtggattttg ctcttttaca acatgtacat ctttactggg ctgtgctgtc acagggatgt 360
ccttgctgga ctgttctgct atggggatat cttcgttggg ctgttcttca tgcttaattg 420
cagtattagc atccacatca gacagcctgg tataaccaga gttgggtggt actgattgta 480
gctgctcttt gtccacttca tatggcaca gtattttctt caacatcctg gctctgggaa 540
g 541

<210> 27
<211> 461
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature

<222> 367

<223> n = A,T,C or G

<400> 27

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gaaatgtata tttaatcatt ctcttgaacg atcagaactc traaatcagt tttctataac 60
arcatgtaat acagtcaccg tggctccaag gtccaggaag gcagtggta acacatgaag 120
agtgtgggaa gggggctgga aacaaagtat tcttttctt caaagcttca ttcctcaagg 180
cctcaattca agcagtcatt gtccttgctt tcaaaagtct gtgtgtgctt catggaaggt 240
atatgtttgt tgccttaatt tgaattgtgg ccaggaaggg tctggagatc taaattcaga 300
gtaagaaaaa ctgagctaga actcaggcat ttctcttaca gaacttggct tgcagggtag 360
aatgaangga aagaaactta gaagctcaac aagctgaaga taatcccatc aggcatttcc 420
cataggcctt gcaactctgt tcaactgagag atgttatcct g 461
```

<210> 28

<211> 341

<212> DNA

<213> Homo sapiens

<400> 28

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agtctggagt gagcaaacaa gagcaagaaa caarragaag ccaaaagcag aaggctccaa 60
tatgaacaag ataaatctat cttcaaagac atattagaag ttgggaaaaa aattcatgtg 120
aactagacaa gtgtgttaag agtgataagt aaaatgcacg tggagacaag tgcattccca 180
gatctcaggg acctccccct gcctgtcacc tggggagtga gaggacagga tagtgcattg 240
tctttgtctc tgaattttta gttatatgtg ctgtaatgtt gctctgagga agcccttgga 300
aagtcctatcc caacatatcc acatcttata ttccacaaat taagctgtag tatgtaccct 360
aagacgtctc taattgactg ccacttcgca actcaggggc ggctgcattt tagtaatggg 420
tcaaatgatt cactttttat gatgcttccc aagggtgcctt ggcttctctt cccaactgac 480
aatgccccaa gttgagaaaa atgatcataa ttttagcata aaccgagcaa tcggcgaccc 540
c 541
```

<210> 29

<211> 411

<212> DNA

<213> Homo sapiens

<400> 29

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tagctgtctt cctcactctt atggcaatga ccccatatct taatggatta agataatgaa 60
agtgtatttc ttacactctg tatctatcac cagaagctga ggtgatagcc cgcttgcatt 120
tgltatccat attctgggac tcaggcggga accttctgga atattgccag ggagcatggc 180
agagggggcac agtgcattct gggggaatgc acattggctc agcctgggta atgagtata 240
tcattacct ctgttcacaa ctcatgccc agcaccagtc acaaggcccc accaaatacc 300
agagcccaag aaatgtatgc ctgttgatat ggttttgctg tgtcccaacc caaatctcat 360
cttgaattgt aagctcccat aattcccatg tgttgtggga gggacctggt g 411
```

<210> 30

<211> 511

<212> DNA

<213> Homo sapiens

<400> 30

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atcatgagga tgttacaaaa gggatgttac taaaccattt gtattcgtct gttttcacac 60
tgctttgaag atactacctg agactgggta atttataaac aaaagagatt taattgactc 120
acagttctgc atggctgaag aggcctcagg aaacttacag tcatgggtga aggcaaggga 180
ggagcaagge atgtcttaca tgtcagtagg agagagagcg agagcaggag aacctgccac 240
ttataaacca ttcatatctc ataactccct atcatgagaa aaacatggag gaaaccaccc 300
tcatgatcca atcacctccc gccaggtccc tccctcgaca cgtggggatt ataattcagg 360
attagaggga cacagagaca aaccatatca tcattcatga gaaatccacc ctcatagtcc 420
```

aatcagctcc taccaggccc cacctccaac actggggatt gcaattcaac atgagatttg 480
gatggggaca cagattcaaa ccatatcata c 511

<210> 31
<211> 927
<212> DNA
<213> Homo sapiens

<400> 31
catggccttt ctccttagag gccagagggtg ctgccctggc tgggagtga gctccaggca 60
ctaccagctt lcctgatttt cccgtttggt ccatgtgaag agctaccacg agccccagcc 120
tcacagtgtc cactcaaggg cagcttggtc ctcttgctct gcagaggcag gctggtgtga 180
ccctgggaac ttgacccggg aacaacaggt ggcccagagt gagtgtggcc tggcccctca 240
acctagtgtc cgtcctcttc tctcctggag ccagtcttga gtttaaaggc attaagtgtt 300
agatacaagc tccttggtgc tggaaaaaca cccctctgct gataaagctc agggggcact 360
gaggaagcag agggcccttg ggggtgccct cctgaagaga gcgtcaggcc atcagctctg 420
tccctctggt gctcccacgt ctgttctca cctccatct ctgggagcag ctgcacctga 480
ctggccacgc gggggcagtg gaggcacagg ctccagggtg ccgggctacc tggcacctta 540
tggtttacaa agtagagttg gcccagtttc cttccacctg aggggagcac tctgactcct 600
aacagtcttc cttgccctgc catcatctgg ggtggctggc tgtcaagaaa ggccgggcat 660
gttttctaaa cacagccaca ggaggtctgt agggcatctt ccagggtggg aaacagtctt 720
agataagtaa ggtgacttgc ctaaggctc ccagcaccct tgatcttga gtctcacgc 780
agactgcatg tsaacaactg gaaccgaaaa catgcctcag tataaaa 827

<210> 32
<211> 291
<212> DNA
<213> Homo sapiens

<400> 32
ccagaacctc cttctctttg gagaatgggg aggcctcttg gagacacaga gggtttcacc 60
ttggatgacc tctagagaaa ttgcccaaga agcccacctt ctgggtccca cctgcagacc 120
ccacagcagt cagttggtca ggccctgctg tagaaggta cttgggtcca ttgcctgctt 180
ccaaccaatg ggccaggagag aaggccttta tttctcgccc acccattctc ctgtaccagc 240
acctccgttt tcagtcagyg ttgtccagca acggtaccgt ttacacagtc a 291

<210> 33
<211> 491
<212> DNA
<213> Homo sapiens

<400> 33
tgcatgtagt tttatttatg tgttttsgtc tggaaaacca agtgtcccag cagcatgact 60
gaacatcact cacttcccct acttgatcta caaggccaac gccgagagcc cagaccagga 120
ttccaaacac actgcacgag aatattgttg atccgctgtc aggttaagtgt ccgtcactga 180
cccaracgct gttacgtggc acatgactgt acagtgccac gtaacagcac tgtacttttc 240
tccccgaac agttacctgc catgtatcta catgattcag aacattttga acagttaatt 300
ctgacacttg aataatccca tcaaaaaccg taaaatcact ttgatgtttg taacgacaac 360
atagcatcac ttacgacag aatcatctgg aaaaacagaa caacgaatac atacatctta 420
aaaaatgctg ggggtggcca ggcacagctt cagcctgtga atcccagcac tttgggaggc 480
ttaagcgggt g 491

<210> 34
<211> 521
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> 453, 476, 487
<223> n = A,T,C or G

<400> 34
tggggcggaa agaagccaag gccaaaggagc tgggtcggca gctgcagctg gaggccgagg 60
agcagaggaa gcagaagaag cggcagagtg tgtcgggacct gcacagatac cttcacttgc 120
tggatggaaa tgaaaattac ccgtgtcttg tggatgcaga cggatgatgtg atttccttcc 180
caccaataac caacagttag aagacaaagg ttaagaaaac gacttctgat ttgtttttgg 240
aagtaacaag tgccaccagt ctgcagattt gcaaggatgt catggatgcc ctcattctga 300
aaatggcaag aaatgaaaaa gtacacttta gaaaataaag aggaaggatc actctcagat 360
actgaagccg atgcagtctc tggacaactt ccagatccca caacgaatcc cagtgtctgga 420
aaggacgggc ccttccttct ggtggtggaa cangtcccgg tggatgatct tggaanggaa 480
cctgaangtg gtgtaccccg tccaaggccg accttgacca c 521

<210> 35
<211> 161
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 18
<223> n = A,T,C or G

<400> 35
tcccgcgctc gcaggggncg tgccacntgc cygtccgccc gctcgtctgc tgcgccgccc 60
cgccgcgctg ccgaccgyca gcatgtgtcc gagagtgggc tgccccgcgc tgccgctgcc 120
gcccgcgccc ctgctgcgcg tgctgcccgt gctgctgctg c 161

<210> 36
<211> 341
<212> DNA
<213> Homo sapiens

<400> 36
ggcgggttag catggaactg agaagaacga agaagcttcc agactacgtg gggaagaatg 60
aaaaaaccaa aattatcgcc aagattcagc aaaggggaca gggagctcca gcccagagagc 120
ctattattag cagttaggag cagaagcagc tgatgtgtga ctatcacaga agacaagagg 180
agctcaagag attggaagaa aatgatgatg atgcctattt aaactcacca tgggcgggata 240
acactgcttt gaaaagacat tttcatggag tgaaagacat aaagtggaga ccaagatgaa 300
gttcaccagc tgatgacact tccaaagaga ttagctcacc t 341

<210> 37
<211> 521
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 516
<223> n = A,T,C or G

<400> 37
tctgaaggtt aaatgtttca tctaaatagg gataatgrra aacacctata gcatagagtt 60
gtttgagatt aaatgagata atacatgtaa aattatgtgc ctggcataca gcaagattgt 120
tgttggtgtt gatgatgatg atgatgatga taatattttt ctatccccag tgcacaactg 180
cttgaaccta ttagataatc aatacatgtt tcttgaaactg agatcaattt ccccatgttg 240

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tctgactgat gaagccctac atttctctct agaggagatg acatttgagc aagatcttaa 300
agaaaatcag atgccttcac ctgaccactg cttggtgatc ccatggcact ttgtacatct 360
ctccattagc tctcatctca ccagcccatc attattgtat gtgctgcctt ctgaagcttg 420
cagctggcta ccatcmggta gaataaaaat cctcctttca taaaatagt accctccttt 480
tttatttgca tttcccaaag ccaagcaccg tggganggta g 521
```

<210> 38
 <211> 461
 <212> DNA
 <213> Homo sapiens

```
<400> 38
tatgaagaag ggaaaagaag ataatttgtg aaagaaatgg gtccagttac tagtctttga 60
aaagggtcag tctgtagctc ttcttaatga gaataggcag crttcagttg ctgagggtca 120
gatttccctta gtggtgtatc taatcacagg aaacatctgt ggttccctcc agtctcttcc 180
tggtgggactt gggccactt ctcatctcat ttaattagag gaaatagaac tcaaagtaca 240
atttactgtt gtttaacaat gccacaaaga catggttggg agctatttct tgatttgtgt 300
aaaaagctgt tttgtgtgc tcataatggt tccaaaaatt ggggtgtggc caaagagaga 360
tactgttaca gaagccagca agaagacctc tgttcattca caccctcggt gatatcagga 420
attgactcca gtgtgtgcaa atccagtttg gcctatcttc t 461
```

<210> 39
 <211> 769
 <212> DNA
 <213> Homo sapiens

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<400> 39
tgagggaactg attggtttgc tctctgctat tcaattcccc aagcccaactt gttcctgcag 60
cgtccctctt ctcatctcct ttagttgtac cctctcttcc atctgagacc tttccttctt 120
gatgtgcctt tttctcttcc ttgcttttcc tgatgttctg ctacagcatgt tctgggtgct 180
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tcttttctt tttttgggg ggcttgcct ctgactgcag ttgaggggcc ccagggtcct 300
ggcctttgag acgagccagg aaggcctgct cctgggcctc taggcgagca agcttggcct 360
tcattgtgat cccaagacgg gcagccttgt gtgctgttcc cccctcacag gcttgagca 420
gcattctatc agtcagaatc tttggggact tggacccctg gttgtcttca tcaactgcagc 480
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tctgatacgc caagtgtggc ttgggatgat tataacgggt ggtctcttca gaaaggctcc 600
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gctcattcca ccagtgggtt gtgaactcct tggcagggtc atgtctacc ccatgagtgt 720
cttgcttcag ygtcacctg agagcctgag tgataccatt ctcttccg 769
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<210> 40
 <211> 292
 <212> DNA
 <213> Homo sapiens

```
<400> 40
gacaacatga aataaatcct agaggacaaa attaaactca atagagtgtg gtctagttaa 60
aaactcgaaa aatgagcaag tctggtggga gtggaggaag ggctatacta taaatccaag 120
tggtgctcct gatcttaaca agccatgctc attatacaca tctctgaact ggacatacca 180
cctttacgca ggaaacaggg cttggaactt ctaagggaaa ttaacatgca ccaccacat 240
ctaactacc tgcgggtag gtaccatccc tgcttcgctg aaatcagtg tc 292
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<210> 41
 <211> 406
 <212> DNA
 <213> Homo sapiens

<400> 41

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ttggaattaa ataacctgg aacaggaag gtgaaagttg gagtgaatg tcttccatat 60
ctataccttt gtgcacagtt gaatgggaac tggttggtt tagggcatct tagagttgat 120
tgatggaaaa agcagacagg aactgggtggg aggtcaagt gggaggttgg tgaatgtgga 180
ataacttacc ttgtgtctcc acttaacca gatgtgttc agctttcctg acatgcaagg 240
atctacttta attccacact ctcatataa aattgaataa aagggaatgt ttgtggcact 300
gatataatct gccaggctat gtgacagtag gaaggaatgg ttcccttaa caagcccaat 360
gcactggtct gactttataa attatttaatt aaaatgaact attatc 406
```

<210> 42

<211> 381

<212> DNA

<213> Homo sapiens

<400> 42

```
aaactggacc tgcaacagg acatgaattt actgcarggt ctgagcaagc tcagcccctc 60
tacctcaggg cccacagcc atgactacct cccccaggag cgggagggtg aagggggcct 120
gtctctgcaa gtggagccag agtggaggaa tgagctctga agacacagca cccagccttc 180
tcgcaccagc caagccttaa ctgcctgcct gacctgaac cagaaccag ctgaactgcc 240
cctccaaggg acaggaaggc tgggggaggg agtttacaac ccaagccatt ccaccccctc 300
ccctgctggg gagaatgaca catcaagctg ctaacaattg ggggaagggg aaggaagaaa 360
actctgaaaa caaatcttg t 381
```

<210> 43

<211> 451

<212> DNA

<213> Homo sapiens

<400> 43

```
catgcgtttc accactgttg gccaggcttg tctcgaactc ctggcctcaa gcaatccacc 60
cgcctcagcc tccaaaagtg ctgggattac agatgtgagc catggcacca tgccaaaagg 120
ctatattcct ggctctgtgt ttccgagact gcttttaac ccaactcttc tacatttaga 180
ttaaaaaata ttttattcat ggtcaatctg gaacataatt actgcatctt aagtttccac 240
tgatgtatat agaaggctaa aggcacaatt ttatcaaat ctagtagagt aaccaaacat 300
aaaatcatta attactttca acttaataac taattgacat tctcaaaag agctgttttc 360
aatcctgata gggtctttat tttttcaaaa tatatttgcc atgggagctt aatttgcaat 420
aaggcgcata atgagaatac cccaaactgg a 451
```

<210> 44

<211> 521

<212> DNA

<213> Homo sapiens

<400> 44

```
gttggacccc cagggactgg aaagacactt cttgcccgag ctgtggcggg agaagctgat 60
gttccttttt attatgcttc tggatccgaa ttgatgaga tggttggtgg tgtgggagcc 120
agccgtatca gaaatctttt tagggaagca aaggcgaatg ctccttgtgt tatatttatt 180
gatgaattag attctgttgg tgggaagaga attgaatctc caatgcatcc atattcaagg 240
cagaccataa atcaacttct tgctgaaatg gatggtttta aaccaatga aggagttatc 300
ataataggag ccacaaactt cccagaggca ttagataatg ccttaatacc gtcctggctc 360
ttttgacatg caagttacag ttccaaggcc agatgtaaaa ggtcgaacag aaattttgaa 420
atgggtatctc aataaaataa agtttgatca atcccgttga tccagaaatt atagcctcga 480
ggtactggtg gcttttccgg aagcagagtt gggagaatct t 521
```

<210> 45

<211> 585

<212> DNA

<213> Homo sapiens

<400> 45

```
gcctacaaca tccagaaaga gtctaccctg caccctggcg tscgtctcag aggtgggatg 60
cagatcttcg tgaagaccct gactggtaag accatcactc tcgaagtga gccagtgac 120
accatygaga acgtcaaagc aaagatccar gacaaggaag gortycctcc tgaccagcag 180
aggttgatct ttgccggaag gcagctggaa gatggdgcga ccctgtctga ctacaacatc 240
cagaagaggt cyaccctgca cctgggtgctc cgtctcagag gtgggatgca ratcttcgtg 300
aagaccctga ctggtaagac catcacccctc gaggtggagc ccagtgcacac catcgagaat 360
gtcaaggcaa agatccaaga taaggaaggc atccctcctg atcagcagag gttgatcttt 420
gctgggaaac agctgggaaga tggacgcacc ctgtctgact acaacatcca gaaagagtcc 480
actctgcact tggctctgcg cttgaggggg ggtgtctaag ttcccccttt taaggtttcm 540
acaaatttca ttgcactttc ctttcaataa agttgttgca ttccc 585
```

<210> 46

<211> 481

<212> DNA

<213> Homo sapiens

<400> 46

```
gaactgggccc ctgagcccaa gtcatgcctt gtgtccgcat ctgccgtgtc acctctgtkc 60
ctgcccctca cccctccctc ctggtcttct gagccagcac catctccaaa tagcctattc 120
cttctgcaa atcacacaca catcggggcc acacatacct gctgccctgg agatggggaa 180
gtaggagaga tgaatagagg cccatacatt gtacagaagg aggggcaggt gcagataaaa 240
gcagcagacc cagcggcagc tgaggtgcat ggagcacggt tggggccggc attgggctga 300
gcacctgatg ggcctcatct cgtgaatcct cgaggcagcg ccacagcaga ggagttaagt 360
ggcacctggg ccgagcagag caggagactg agggtcagag tggaggctaa gctgccctgg 420
aactcctcaa tcttgccctgc cccctagtat gaagccccc tccctgccct acaattcctg 480
a 481
```

<210> 47

<211> 461

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 128

<223> n = A, T, C or G

<400> 47

```
atggatctta ctttgccacc cagggtggag tgcagtgtg caatcttggc tcactgcagc 60
cttaacctcc caggetcaag ctatcctcct gccaaagcct tccacatagc tgggactaca 120
ggtacacngc caccacacc agctaaaatt tttgtatttt ttgtagagac gggatctcgc 180
cacgttgccc aggtgtgtcc catcctgacc tcaagcagat ctgcccacct cagcccccca 240
acgtgtctagg attacaggcg tgagccaccg caccagcct ttgttttgc tttaatggaa 300
tcaccagttc ccctccgtgt ctacagcagca gctgtgagaa atgctttgca tctgtgacct 360
ttatgaaggg gaacttccat gctgaatgag ggtaggatta catgctcctg tttcccgggg 420
gtcaagaaaag cctcagactc cagcatgata agcagggtga g 461
```

<210> 48

<211> 571

<212> DNA

<213> Homo sapiens

<400> 48

```
ataggggctt taaggaggga attcaggttc aatgaggtcg taaggccagg gctcttatcc 60
agtaagactg gggctccttag atgagaaaga gacacccgag gtccttctct ctgccgtgtg 120
aggatgcatc aagaaggcgg ccgtctgcaa gcgaaggaga ggccgcacca gaaaccgaca 180
```


ccttcattctt ggacttgcag cctctagaac tgagaaaata actgtctgtt ggtaagcca 240
cccagtttgt agtattctct tatggcttcc taagcagact aacaaacaaa caccacaaat 300
taactgatgg ottcgctgtc ttctgtaaaa attgctatga gagaactttt cactcactgt 360
tttgagttt ctcctcagtc ccctggttct ttcttctcac ataatccaa tttcaattta 420
tagttcatgg cccaggcaga gtcattcatt acggcatctc ctgagctaaa ccagcacctg 480
ctctgtctac ttcttgactg gctgtctcatt atcagccctc ttgcagagat ttcatttcct 540
cccgtgccag gtacttcacg caccaagctc a 571

<210> 49

<211> 511

<212> DNA

<213> Homo sapiens

<400> 49

ggataatgaa gttgttttat ttagcttggc caaaaaggca ttttctctata ttttcttata 60
caacaaatat ccccaaaaata aagcaagcat atatatcttg aatgtgtaat aatccagtga 120
taaacagag cagtacttta aaagaaaaaa aaatatgtat ttctgtcagg ttaaaatgag 180
aatcaaaaacc atttactctg ctaactcatt attttttgct ttcttttttg ttaagagagg 240
caatgcaata cactgaaaaa ggtttttatc ttatctggca ttggaattag acatattcaa 300
acccagagccc ccatttccaa actttaagac cacaacaag taatttactt ttctgaacat 360
tggttttttc tggaaaaatg gaattataaa atagactttg cagactctta tgagattaaa 420
taagataatg tatgaaattc tttcttcttt ttacttctt tttcttttt gagatggagt 480
ctacccccgt caccagagct ggagtacagt g 511

<210> 50

<211> 561

<212> DNA

<213> Homo sapiens

<400> 50

ccactgcact ccagcctggg tgacggagtg agactctgtc tcaaaaaaac aaacaaacaa 60
acaacaaaaa aactgaaaag gaaatagagt tcctctttcc tcataatga atatatatt 120
tcaacagatt gttgatcacc taccatatgc ttggtattgt tctaattgct ggggatacag 180
caagaggttc tgcagaactt catggagcat gaaagtaaat aaacaaagtt aatttcaagg 240
ccaggcatgg ttgctcacac ctttagtccc agcacttttg gaggtgagg cagggtgagc 300
acttggggccc aggagtcca ggctgcagtg agccaagatt gtgccactac tctccaggct 360
gggcaacaga gcaagaccct gtctcagggg gaacaaaaag ttaatttcag attttgttaa 420
gtgctgtaaa ggaagttaat aggttgatat tcaagagagc acctgaaggc caggcgtggg 480
ggctcacgcc tgtggtctaa cgctttggga agcccagcgg ggcggatcac aaggtcagga 540
gaattttggc caggcalggt g 561

<210> 51

<211> 451

<212> DNA

<213> Homo sapiens

<400> 51

agaatccatt tattgggttt taaactagtt acacaactga aatcagtttg gcactacttt 60
atacagggat tacgcctgtg tatgocgaca cttaaatact gtaccaggac cactgctgtg 120
cttaggtctg tattcagtca ttcagcatgt agatactaaa aatatactgt agtggtcctt 180
taagggaagac tgtacagggg gtgttgcaag atgacattca ccaattttgt aattatttca 240
accagaaga tacctttcac tctataaact tgctatagge aaacatgtgg tgttagcatt 300
gagagatgca cacaaaaatg ttacataaaa gttcagacat tctaatagata agtgaactga 360
aaaaaaaaa aaccccatat ctcaattttt gtaacaagat aaagaaaaata atttaaaaac 420
acaaaaaatg gcattcagtg ggtacaaagc c 451

<210> 52

<211> 682

<212> DNA

<213> Homo sapiens

<400> 52

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caaatattta atataaatct ttgaacaag ttcagakgaa ataaaaatca aagtttgcaa 60
aaacgtgaag attaacttaa ttgtcaaata ttccctcattg ccccaaatca gtattttttt 120
tattttctatg caaaagtatg ccttcaaact gcttaaatga tatatgatat gatacacaaa 180
ccagtttttca aatagtaaag ccagtcattt tgcaattgta agaaataggt aaaagattat 240
aagacacctt acacacacac acacacacac acacacacgt gtgcaccgcc aatgacaaa 300
aacaatttgg cctctcctaa aataagaaca tgaagacctt taattgctgc caggaggga 360
cactgtgtca cccctcccta caatccaggt agtttccttt aatccaatag caaatctggg 420
catatttgag aggagtgtt ctgacagcca csqgtgaaat cctgtgggga accattcatg 480
tccaccactt ggtgccctga aaaaatgccata ataatttttc gctccactt ctgctgctgt 540
ctcttcacata tectcacata gacccagac ccgctggccc ctggtggtgc atcgatttgc 600
tggttagagca agtcattaggt ctctctttt acgtcacaga agcgatacac caaattgcct 660
ggtcgggtcat tgtcataacc ag 682
```

<210> 53

<211> 311

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 208

<223> n = A,T,C or G

<400> 53

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tttgacttta gtagggtctt gaactattta ttttactttg ccmgtaatat ttaraccyta 60
tatatctttc attatgccat cttatcttct aatgbcaagg gaacagwtgc taamctggct 120
tctgcattwa tcacattaaa aatggctttc ttggaaaatc ttcttgatat gaataaagga 180
tcttttavag ccattattta aagcmgnntt ctctccaaca cgagtctgct sasgggggk 240
gagctgtgaa cctctggtga aggcctttccc atacacactg caatgacmtg gtttctgacc 300
agbgtgagtt a 311
```

<210> 54

<211> 561

<212> DNA

<213> Homo sapiens

<400> 54

```
agagaagccc cataaatgca atcagtgtgg gaaggccttc agtcagagct caagcctttt 60
cctccatcat cgggttcata ctggagagaa accctatgta tgtaatgaat gcgagagagc 120
ctttgggttt aactctcatc ttactgaaca cgtaaggatt cacacaggag aaaaacccta 180
tgtttgtaat gagtgcggca aagcctttcg tcggagttcc actettgttc agcatcgaag 240
agttcacact ggggagaagc cctaccagtg ogttgaatgt gggaaagctt tcagccagag 300
ctcccagctc accctacatc agccgagttc acactggaga gaagccctat gactgtggtg 360
actgtgggaa ggccttcagc cggaggtcaa cctcattca gcatcagaaa gttcacagcg 420
gagagactcg taagtgcaga aaacatggtc cagcctttgt tcatggctcc agcctcacag 480
cagatggaca gattccactt ggagagaagc acggcagaac ctttaaccat ggtgcaaatc 540
tcattctgctg ctggacagtt c 561
```

<210> 55

<211> 811

<212> DNA

<213> Homo sapiens

<400> 55

```

gagacagggc ctcactttgt caccacaggc ygaatgcagt ggtgcgactc tacgtagctc 60
actgcagccc tgacctcctg gactcaaaca attctcctgc ctcagccctg caagtagctg 120
ggactgtggg tgcacgccac catgcctggc taacttttgt agtttttgta aagatggggg 180
tttgccatgt tgcacatgct ggtcttgaac tcctgagctc aaacgatctg cccacctcgg 240
cctcccagaa tgttgggatt acaggggtaa accaccacgc ctggcccat tagggatttc 300
ttagcatcca cttgctcact gagattaate ataagagatg ataagcactg gaagaaaaaa 360
atttttaacta ggtttggat atttttttcc tttttcagct ttatacagag gattggatct 420
ttagttttcc ttttaactgat aataaaacat tgaaggaaa taagtttacc tgagattcac 480
agagataacc ggcacactc ccttgctcaa ttccagctt taccacatca attattttca 540
gaggtgcagg ataaaggcct tttagtctgct ttgcacactt ttcttccact tttttgtaa 600
cctgttgccg gacaaatgga attgacagcg tatgccatga ctattccatt tgtcaggcat 660
acgctgtcaa tttttccacc aatcccttgt ctctctttgg agagatcttc ttatcagcta 720
gtccttttgg aaaagtaatt gcaacttctt ctaggatttc tattgtccgt tccactgggt 780
gaacccctgg gaccaggact aaaacctcca g

```

<210> 56

<211> 591

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 45, 477, 490, 561

<223> n = A,T,C or G

<400> 56

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atctcatata tatatttctt cctgacttta tttgcttgct totgnacgc atttaaaata 60
tcacagagac caaaatagag cggctttctg gtggaacgca tggcagtcac aggacaaaat 120
acaaaactag ggggtctctg cttctcatac atcatacaat tttcaagtat tttttttatg 180
tacaagagac tactctalcl gaaaaaaaat taaaaataa atgagacaag atagtttatg 240
catcctagga agaaagaatg ggaagaaaga acggggcagt tgggtacaga ttctgtccc 300
ctgtttccag ggaccactac cttcctgcca ctgagttccc ccacagcctc acccatcatg 360
tcacagggca agtgccaggg taggtgggga ccagtggaga cagggaaccag caacatactt 420
tggcctggaa gataaggaga aagtctcaga aacacactgg tgggaagcaa tcccacnggc 480
cgtgccccan gagcttccca cctgctgctg gctccctggg tggctttggg aacagcttgg 540
gcaggccctt ttgggtgggg nccaactggg cctttggggc cgtgtggaag g

```

<210> 57

<211> 481

<212> DNA

<213> Homo sapiens

<400> 57

```

aaacattgag atggaatgat agggtttccc agaatcaggc ccatatttta actaaatgaa 60
aattatgatt tatagccttc tcaaatacct gccatacttg atatctcaac cagagctaata 120
tttacctctt tacaatttaa ataagcaagt aactggatcc acaatttata atacctgtca 180
attttttctg tattaaacct ctatcatagt ttaagcctat tagggtaactt aatccttaca 240
aataaacagg tttaaaatca cctcaatagg caactgccct tctggttttc ttctttgact 300
aaacaatctg aatgcttaag attttccact ttgggtgcta gcagtacaca gtgttacact 360
ctgtattcca gacttcttaa attatagaaa aaggaaatgta cactttttgt attctttctg 420
agcaggggccg ggaggcaaca tcatctacca tggtagggac ttgtatgcat ggactacttt 480
a

```

<210> 58

<211> 141

<212> DNA

<213> Homo sapiens

<400> 58
actctgtcgc ccaggctgga gcccabtggm gcgatctcga ctccctgcaa gctmcgcctc 60
acaggwtcat gccattctcc tgcctcagca tctggagtag ctgggactac aggcgccage 120
caccatgccc agctaatttt t 141

<210> 59
<211> 191
<212> DNA
<213> Homo sapiens

<400> 59
accttaaaga cataggagaa tttatactgg gagagaaagc ttacaaatgt aaggtttctg 60
acaagacttg ggagtgttc acacctggaa caacatactg gacttcacac tggabagaaa 120
cettacaagt gtaatgagtg tggcaaagcc tttggcaagc agtcaacact tattcaccat 180
caggcaattc a 191

<210> 60
<211> 480
<212> DNA
<213> Homo sapiens

<400> 60
agtcaggatc atgatggctc agtttccac agcgatgaat ggagggccaa atatgtgggc 60
tattacatct gaagaacgta ctaagcatga taaacagttt gataacctca aaccttcagg 120
aggttacata acagggtgatc aagcccgtag ttttttcta cagtcaggtc tgcgggcccc 180
ggtttttagct gaaatatggg ccttatcaga tctgaacaag gatgggaaga tggaccagca 240
agagttctct atagctatga aactcatcaa gttaaagttg cagggccaac agctgcctgt 300
agtccctcct cctatcatga aacaaccccc tatgttctct ccactaatct ctgctcgttt 360
tgggatggga agcatgccca atctgtccat tcatcagcca ttgcctccag ttgcacatat 420
agcaacaccc ttgtctctg ctacttcagg gaccagtatt cctccctaata gatgcctgct 480

<210> 61
<211> 381
<212> DNA
<213> Homo sapiens

<400> 61
ctttcgattt ccttcaattt gtacagtttg attttatgaa gttgttcaag ggctaactgc 60
tgtgtattat agctttctct gagttccttc agctgattgt taaatgaatc catltctgag 120
agcttagatg cagtttcttt ttcaagagca tctaattgtt ctttaagtct ttggcataat 180
tcttcctttt ctgatgactt tctatgaagt aaactgatcc ctgaatcagg tgtgttactg 240
agctgcatgt ttttaattct ttctgttaat agctgcttct caggggaccag atagataagc 300
ttatattgat attccttaag ctcttggtga agttgttcga ttcccataat ttccaggtca 360
cactgggttat cccaaacttc t 381

<210> 62
<211> 906
<212> DNA
<213> Homo sapiens

<400> 62
gtggaggatg aacggaggca agaaagggg ctacctcagg agcgagggac aaagggggcg 60
tgaggcacct aggccgcgac accccggcga caggaagccg tctgaaccg ggctaccggg 120
taggggaagg gcccgcgtag tccctgcagg gccccagagc tggagtcggc tccacagccc 180
cgggcccgtcg gcttctcact tccctggacct ccccgggcgc cgggcctgag gactggctcg 240
gcggagggag aagaggaaac agacttgagc agctccccgt tgtctcgcaa ctccactgcc 300
gaggaaactct catttcttcc ctgcctcctt cccccccac ctcatgtaga aagggtgctga 360

```

agcgtccgga gggaagaaga acctgggcta ccgtcctggc cttcccmccc ctttcccggg 420
gcgcttttgg gggcgtggag ttggggttgg ggggggtggg gggggttctt ttttggagtg 480
ctggggaaact tttttccctt cttcaggtca ggggaaaggg aatgcccaat tcagagagac 540
atgggggcaaa gaaggacggg agtggaggag cttctggaac tttgcagccg tcacgaggag 600
gcggcagctc taacagcaga gagcgtcacc gcttgggtatc gaagcacaag cggcataagt 660
ccaaacactc caaagacatg gggttgggtga cccccgaagc agcatccctg ggcacagtta 720
tcaaaccttt ggtggagtat gatgatata gctctgattc cgacaccttc tccgatgaca 780
tgcccttcaa actagaccga agggagaacg acgaacgtcg tggatcagat cggagcgacc 840
gcctgcacaa acatcgtcac caccagcaca ggcgttcccg ggacttacta aaagctaacc 900
agaccg                                     906

```

<210> 63
 <211> 491
 <212> DNA
 <213> Homo sapiens

```

<400> 63
gacatgtttg cctgcagggg accagagaca atgggattag ccagtgtcga ctgttcttta 60
tgettcacaga gaggatgggg acagctctca ggtcagaate caggctgaga aggccatgct 120
ggttgggggc ccccggaagc acgggtccga tcctccctgg catcagcgta gacccgctgc 180
tcaggcttgg ggtacaaaac tcagtctctg tactgttttg gccccatgag gtgagaggaa 240
aacctagaaa aagattgggtc gtgctaagga atcagctgcc cctcatcctt ccgcatacaa 300
tgctgggtgac aacatattcc ctctcccagg acacagactc ggtgactcca cactgggctg 360
agtggcctct ggaggctcgt ggcctaaggc agggctccgt aaggctgac ggctgaactg 420
ggtgggggtga gggtttctga ccttccgctt cccatcccat aacgctgtc aatgagctca 480
cactgtggtc a                                     491

```

<210> 64
 <211> 511
 <212> DNA
 <213> Homo sapiens

```

<400> 64
gatggcatgg tegtgtctaa tgtgcctgct gggatggagc acttccctct gtgagcccag 60
gggacccgcc tgtccctgga gcttggggca aggagggaag agtgatacca ggaagggtgg 120
gctgcagcca ggggccagag tcagttcagg gagtggctct cggccctcaa agctcctccg 180
gggactgtct aggagtgatg gtgccctgga gtttgcccca acttccctgg ccacctgga 240
agggtgcctg ctgctccagg cctctaggct gggctgatgg gtttctccag gacacaagta 300
tcattaaagc caccctctcc tcagcttgctc agggccgaca tgtgggacag gctgtgctca 360
caaccccttc gctgcctctg ccttccatca ggaggagcca gtggaacctt cggaaagctc 420
ccagcatctc agcagccctc aaaagtcgtc ctggggcaag ctctggttct cctgactgga 480
ggctcatctg gcttggcctg ctctctctcg c                                     511

```

<210> 65
 <211> 394
 <212> DNA
 <213> Homo sapiens

```

<400> 65
taaaaaagtg taacaaagt ttatttagac tttcttcatt cccccagatc caggatgtct 60
atgtaaacgg ttatcttaca aagaaagcac aatatttggg ataaactaag tcagtgaactt 120
gcttaactga aatagcgtcc atccaaaagt gggtttaagg taaaactacc tgacgatatt 180
ggcgggggac ctgcagtttg gactgcttgc cgggtttgtc cagggttccg ggtctgttct 240
tggcactcat ggggacaggc atcctgctcg tctgtggggc cccgctggag cccttacgtg 300
aagctgaagg tatcgacct agggggctct agggcagtg gaccttcatc cggaactaac 360
aagggtcggg gagaggcctc ttgggctatg tggg                                     394

```

<210> 66

<211> 359
<212> DNA
<213> Homo sapiens

<400> 66
caagcgttcc tttatggatg taaattcaaa cagtcattgt gagccatccc gggctgacag 60
tcacgtttaa gacactaggt cgggcgccac agtgcacccc aaggagaaga agaatttga 120
atctttccat gaagatgtac ggaaatctga tgttgaatat gaaaatggcc cccaaatgga 180
attccaaaag gttaccacag gggctgtaag acctagtac cctcctaagt gggaaagagg 240
aatggagaat agtattttctg atgcatcaag aacatcagaa tataaaactg agatcataat 300
gaaggaaaat tccatatcca atatgagttt actcagagac agtagaaact attcccagg 359

<210> 67
<211> 450
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 425
<223> n = A,T,C or G

<400> 67
taggaataac aaatgtttat tcagaaatgg ataagtaata cataatcacc ottcatctct 60
taatgccctt tctctccttt ctgcacagga gacacagatg ggtaacatag aggcattgga 120
agtggaggag gacacaggac tagcccacca ccttctcttc cgggtctccc aagatgactg 180
cttatagagt ggaggaggca aacagggtccc ctcaatgtac cagatgggtca cctatagcac 240
cagctccaga tggccacgtg gttgcagctg gactcaatga aactctgtga caaccagaag 300
atacctgctt tgggatgaga gggaggataa agccatgcag ggaggatatt taccatccct 360
accctaagca cagtgcgaag agtgagcccc cggctcccag tacctgaaaa accaaggcct 420
actgnctttt ggatgctctc ttgggccacg 450

<210> 68
<211> 511
<212> DNA
<213> Homo sapiens

<400> 68
aagcctcctg ccctggaaat ctggagcccc ttggagctga gctggacggg gcagggaggg 60
gctgagaggc aagaccgtct ccctcctgct gcagctgctt cccacagcag cactgctggg 120
cacagcagaa acgccagcag agaaaatggg agccgagagt ccttagccct ggagctgagg 180
ctgcctctgg gctgaccgcg ttgctgtacg tggccagaac tgggggtggc atctggcatc 240
cattttaggc caggggtggg gaaagggagg ccaacagagg aaaacctatt cctgctgtga 300
caacacagcc ctgtgccac gcagcctaag tgcagggagc gtgatgaagt caggcagcca 360
gtcggggagg acgaggtaac tcagcagcaa tgtcaccttg tagcctatgc gctcaatggc 420
ccggaggggc agcaaccccc cgcacacgtc agccaacagc agtgcctctg caggcaccac 480
gagagcgatg atggacttga gcgccgtgtt c 511

<210> 69
<211> 511
<212> DNA
<213> Homo sapiens

<400> 69
gtttggcaga agacatgttt aataacattt tcatatttaa aaaatacagc aacaattctc 60
tatctgtcca ccactcttgc ttgcccttcc tggggctgag gcagacaaag gaaaggtaat 120
gaggttaggg cccccaggcg ggctaagtgc tattggcctg ctctgtctca aagagagcca 180
tagccagctg ggcacggccc cctagccctt ccaggttgct gaggcggcag cggtggtaga 240

gtttttcact gagccgtggg ctgcagtcct gcagggagaa ctctgcacc agccctggct 300
ctacggcccg aaagaggtgg agccctgaga accggaggaa aacatccatc acctccagcc 360
cctccagggc ttctctctct tcctggcctg ccagttcacc tgccagccgg gctcgggccc 420
ccaggtagtc agcgttgtag aagcagccct ccgcagaagc ctgcccgtca aatctccccc 480
ctataggagc cccccgggag gggtcagcac c 511

<210> 70
<211> 511
<212> DNA
<213> Homo sapiens

<400> 70
caagttgaac gtcaggcttg gcagaggtgg agtgtagatg aaaacaaagg tgtgattatg 60
aagaggatgt gagtcctttg ggtgtaggag agaaaggctg ttgagcttct atttcaagat 120
acttttacct gtgcaaaaag cacattttcc acctccttct catggcattt gtgtaagggt 180
agtatgattc ctattccatc tgcatttttag aggtgaagaa taacgtacaa gggattcagt 240
gatttagcaag ggaccctca ctaagtgttg atggagttag gacagagctc agctgtttga 300
atctcagagc ccaggcagct ggagctgggt aggatcctgg agctggcact aatgtgaggt 360
gcattccctc caaccaggc tcagatccgg aacctgaccg tgctgacccc cgaaggggag 420
gcagggtga gctggccctg tgggctccct gctcctttca caccacactc tcgctttgag 480
gtgctgggct gggactactt cacagagcag c 511

<210> 71
<211> 511
<212> DNA
<213> Homo sapiens

<400> 71
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gcccctggag gagatctggc ctctctgtga ttctatcact gtgcacactc ctctcctgcc 180
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tggccagtgt gccggggctg cactggacgt gtttacggaa gagccgccac gggaccgggc 360
cttggtggac catgagaatg tcacagctg tccccacctg ggtgccagca ccaaggaggc 420
tcagagccgc tgtggggagg aaattgtctg tcagttcgtg gacatggtga aggggaaatc 480
tctcacgggg gttgtgaatg cccaggccct t 511

<210> 72
<211> 2017
<212> DNA
<213> Homo sapiens

<400> 72
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aacagtttga taacctcaaa ccttcaggag gttacataac agtgatcaa gcccgtaact 180
ttttcttaca gtcaggctcg ccggccccgg ttttagctga aatatgggcc ttatcagatc 240
tgaacaagga tgggaagatg gaccagcaag agttctctat agctatgaaa ctcatcaagt 300
taaagttagc gggccaacag ctgcctgtag tcctccctcc tatcatgaaa caacccccca 360
tgttctctcc actaatctct gctcgttttg ggatgggaag catgcccaat ctgtccattc 420
atcagccatt gcctccagtt gcacctatg caacacctt gtcttctgct acttcaggga 480
ccagtattcc tcctctaatt atgcctgctc ccttagtgcc ttctgttagt acatcctcat 540
taccgaatgg aactgcoagt ctcatcagc ctttatccat tccttattct tcttcaacat 600
tgccctcatg atcatcttac agcctgatga tgggaggatt tgggtgtgct agtatccaga 660
aggccagtc tctgattgat ttaggatcta gtagctcaac ttcctcaact gcttccctct 720
cagggaaact acctaagaca gggacctcag agtgggcagt tcctcagcct tcaagattaa 780
agtatcggca aaaatttaat agtctagaca aaggcatgag cggatacctc tcaggttttc 840

```

aagctagaaa tgccottctt cagtcaaatc tctctcaaac tcagctagct actatttga 900
ctctggctga catcgatggt gacggacagt tgaagctga agaatttatt ctggcgatgc 960
acctcactga catggccaaa gctggacagc cactaccact gacgttgccct cccgagcttg 1020
tccctccatc ttccagaggg ggaagcaag ttgattctgt taatggaact ctgccttcat 1080
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agcagcagca gagggaggct gaacgcaaag cccagaaaga gaaggaagag tgggagcggg 1260
aacagagaga actgcaagag caagaatgga agaagcagct ggagttggag aaacgcttg 1320
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ggcaggagct gctcagtcag aagaccaggg aacaagaaga cattgtcagg ctgagctcca 1500
gaaagaaaag tctccacctg gaactggaag cagtgaatgg aaaacatcag cagatctcag 1560
gcagactaca agatgtccaa atcagaaagc aaacacaaaa gactgagcta gaagttttgg 1620
ataaacagtg tgacctggaa attatggaaa tcaacaact tcaacaagag cttaaggaat 1680
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acatgcagct cagtaacaca cctgattcag ggtcagttt acttcataaa agtcatcag 1800
aaaaggaaga attatgcaa agacttaag aacaattaga tgctctgaa aaagaaactg 1860
catctaagct ctcaagaatg gattcattta acaatcagct gaaggaactc agagaaagct 1920
ataatacaca gcagttagcc cttgaacaac ttcataaat caaacgtgac aaattgaagg 1980
aatcgaaag aaaaagatta gagcaaaaaa aaaaaaa 2017

```

<210> 73
 <211> 414
 <212> DNA
 <213> Homo sapiens

```

<400> 73
atggcagtg cattccaccat catgggaacc accttccctt ttcttcagga ttctctgtag 60
tggaagagag caccagtggt tgggctgaaa acatctgaaa gtaggagaa gaacctaaaa 120
taatcagtat ctcaagagggc tctaaggtgc caagaagtct cactggacat ttaagtcca 180
acaaagcagc actttcggaa tcgccaaagc aaaactttct aacttctgtc tctctcagag 240
acaagtgaga ctcaagagtc tactgttcta gtggcaacta cagaaaactc gtgttaccga 300
gaaaaacagc agcaattaga aatggttcca atatttcaa gctccgcaaa caggatgtgc 360
tttctttg ccatctaggg tttcttctct ttcctttctc tttattaaac acta 414

```

<210> 74
 <211> 1567
 <212> DNA
 <213> Homo sapiens

```

<400> 74
atatctagaa gtctggagtg agcaaaacag agcaagaac aaaaagaagc caaaagcaga 60
aggctccaat atgaacaaga taaatctatc ttcaaagaca tattagaagt tgggaaaaata 120
attcatgtga actagacaag tgtgttaaga gtgataagta aaatgcacgt ggagacaagt 180
gcatcccccag atctcaggga cctccccctg cctgtcacct ggggagtgag aggacaggat 240
agtgcagttt ctttgtctct gaatttttag ttatatgtgc tgtaatgttg ctctgaggaa 300
gcccttgaa agtctatccc aacatatcca catcttatat tccacaaatt aagctgtagt 360
atgtacccta agacgtgtgt aattgactgc cacttcgcaa ctcaagggcg gctgcatttt 420
agtaatgggt caaatgattc actttttatg atgcttccaa aggtgccttg gcttctcttc 480
ccaactgaca aatgccaaag ttgagaaaaa tgatcataat tttagcataa acagagcagt 540
cgccgacacc gattttataa ataaactgag caccttcttt ttaaacaaac aaatgcgggt 600
ttattttca gatgatgttc atccgtgaat ggtccaggga aggaccttcc accttgacta 660
tatggcatta tgtcatcaca agctctgagc cttctccttt ccctcctgcg tggacagcta 720
agacctcagt ttcaatagc atctagagca gtgggactca gctggggtga tttcgcccc 780
catctccggg ggaatgtctg aagacaattt tgttacctca atgagggagt ggaggaggat 840
acagtgttac taccactagc tggataaagg ccagggatgc tgctcaacct cctancatgt 900
acaggacgtc tcccattac aactacccaa tcggaagtgt caactgtgtc aggaactaaga 960
aaccttggtt ttgagtagaa aagggcctgg azagagggga gccacaatat ctgtctgctt 1020

```



```

cctcacatta gtcattggca aataagcatt ctgtctcttt ggctgctgcc tcagcacaga 1080
gagccagAAC tctatcgggc accaggataa catctctcag tgaacagagt tgacaaggcc 1140
tatgggaaat gcctgatggg attatcttca gcttgttgag cttctaagtt tctttccctt 1200
cattctacco tgcaagccaa gttctgtaag agaaatgcct gagttctagc tcagggtttc 1260
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gaggccttga ggaatgaagc tttgaaggaa aagaatactt tgtttccagc ccccttccca 1440
cactcttcat gtgttaacca ctgccttcct ggaccttgga gccacggtga ctgtattaca 1500
tgttgttata gaaaactgat tttagagttc tgatcgttca agagaatgat taaatatata 1560
tttccta 1567

```

```

<210> 75
<211> 240
<212> DNA
<213> Homo sapiens

```

```

<400> 75
tcgagcggcc gcccgggcag gtccttcaga cttggactgt gtcacactgc caggcttcca 60
gggctccaac ttgcagacgg cctgtttgtg gacagtctct gtaatcgca aagcaaccat 120
ggaagacctg ggggaaaaca ccatggtttt atccacctg agatctttga acaacttcat 180
ctctcagcgt gcggaggagg gctctggact ggatatttct acctcggccg cgaccacgct 240

```

```

<210> 76
<211> 330
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 288
<223> n = A,T,C or G

```

```

<400> 76
tagcgyggtc gcggccgagg yctgcttytc tgtccagccc agggcctgtg gggtcagggc 60
ggtgggtgca gatggcatcc actccgggtg cttcccatc tttctctggc ctgagcaagg 120
tcagcctgca gccagagtac agagggccaa cactggtgtt cttgaacaag ggccttagca 180
ggccctgaag grccctctct gtagtggtga acttcctgga gccaggccac atgttctct 240
cataccgcag gytagygatg gtgaagttga ggggtgaaata gtattmangr agatggcttg 300
caracctgcc cgggcggccg ctcsaaatcc 330

```

```

<210> 77
<211> 361
<212> DNA
<213> Homo sapiens

```

```

<400> 77
agcgtggtcg cggccgagggt gtccttcagg gtctgcttat gcccttggtc aagaacacca 60
gtgtcagctc tctgtactct ggttgacagc tgaccttgc caggcctgag aaggatgggg 120
cagccaccag agtggatgct gtctgcaccc atcgtcctga ccccaaaagc cctggactgg 180
acagagagcg gctgtactgg aagctgagcc agctgaccca cggcatcact gagctgggcc 240
cctacacctt ggacagggac agtctctatg tcaatggttt caccatcgg agctctgtac 300
ccaccaccag caccgggggtg gtcagcgagg agccattcaa cctgcccggg cggccgctcg 360
a 361

```

```

<210> 78
<211> 356
<212> DNA

```

<213> Homo sapiens

<220>

<221> misc feature

<222> 7, 346, 350, 353

<223> n = A,T,C or G

<400> 78

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ttggggnttt mgagcggcgg cccgggcagg taccgggggtg gtcagcggagg agccattcac 60
actgaacttc accatcaaca acctgcggta tgaggagaac atgcagcacc ctggctccag 120
gaagttcaac accacggaga gggctcttca gggcctgctc aggtccctgt tcaagagcac 180
cagtgttggc cctctgtact ctggctgcag actgactttg ctgagacttg agaaacatgg 240
ggcagccact ggagtggacg ccactctgcac cctccgcctt gatcccaactg gtccctggact 300
ggacagagag cggctatact gggagctgag ccagtcctct ggcggngacn ccnctt 356
```

<210> 79

<211> 226

<212> DNA

<213> Homo sapiens

<400> 79

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agcgtggctg cggccgaggt ccagtcgcag catgctcttt ctccctgccc ctggcacagt 60
gaggaagatc tctgctgtca gtgagaaggc tgtcatccac tgagatggca gtcaaaagtg 120
catttaatac acctaacgta tcgaacatca tagcttgccc caggttatct catatgtgct 180
cagaacactt acaatagcct gcagacctgc cggggcgccc gctcga 226
```

<210> 80

<211> 444

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 23

<223> n = A,T,C or G

<400> 80

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gatggtgaag ttgaggggtg atggtaccag gagagggcca gcagccataa ttgtsgrgck 120
gsmgmssgag gmwggwgtyy cwgaggttcy rarrtccact gtggaggtcc caggagtgt 180
ggtggtgggc acagagstcy gatgggtgaa accattgaca tagagactgt tcctgtccag 240
ggtgtagggg cccagctctt yratgycatt ggycagttkg ctyagctccc agtacagccr 300
ctctckgyyg mwccagsgc ttttggggtc aagatgatgg atgcagatgg catccactcc 360
agtggctgct ccactcttct cggacctgag agaggtcagt ctgcagccag agtacagagg 420
gccaacactg gtgttctttg aata 444
```

<210> 81

<211> 310

<212> DNA

<213> Homo sapiens

<400> 81

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tcgagcggcc gcccgggcag gtcaggaagc acattggtct tagagccact gcctcctgga 60
ttccacctgt gctgcggaca tctccaggga gtgcagaagg gaagcaggtc aaactgtctca 120
gatcagtcag actggtgttt ctcaattctc acctgagcaa ggtcagcttg cagccagagt 180
acagagggcc aacctggtg ttcttgaaca agggcttgag cagacctgc agaacctct 240
tccgtggtgt tgaacttctt ggaaaccagg gtgttgcatg ttttctctca taatgcaagg 300
ttggtgatgg 310
```

<210> 82
<211> 571
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 202
<223> n = A,T,C or G

<400> 82
acggtttcaa tggacacttt tattgtttac ttaatggatc atcaattttg tctcactacc 60
tacaatgga atttcatctt gtttccatgc tgagtagtga aacagtgaca aagctaataca 120
taataaaccta catcaaaaga gaactaagct aacactgctc actttctttt taacaggcaa 180
aatataaata tatgcactct anaatgcaca atggtttagt cactaaaaaa ttcaaatggg 240
atcttgaaga atgtatgcaa atccagggtg cagtgaagat gagctgagat gctgtgcaac 300
tgtttaaggg ttctggcac tgcactctct ggccactagc tgaatcttga catggaaggt 360
tttagctaat gccaaagtga gatgcagaaa atgctaagtt gacttagggg ctgtgcacag 420
gaactaaaag gcaggaaagt actaaatatt gctgagagca tccaccccag gaaggacttt 480
accttccagg agctccaaac tggcaccacc cccagtgtc acatggctga ctttatcttc 540
cgtgttccat ttggcacagc aagtggcagt g 571

<210> 83
<211> 551
<212> DNA
<213> Homo sapiens

<400> 83
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aagggaaaag atgcttctgg gaacaagggt aaagccgagc cagccaaaat agaagctttc 120
cgagcttcac ttccaagct aggggatgtc tatgtcaatg atgcttttgg cactgctcac 180
agagcccaca gctccatggt aggaagtcaat ctgccacaga aggctggtgg gtttttgatg 240
aagaaggagc tgaactactt tgcaaaagcc ttggagagcc cagagcgacc cttcctggcc 300
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gtcaatgaga tgattattgg tgggtggaatg gcttttacct tccttaaggt gctcaacaac 420
atggagattg gcacttctct gtttgatgaa gagggagcca agattgtcaa agacctaatg 480
tccaaagctg agaagaatgg tgtgaagatt accttgctct ttgactttgt cactgctgac 540
aagtttgatg a 551

<210> 84
<211> 571
<212> DNA
<213> Homo sapiens

<400> 84
tttgttcctt acatttttct aaagagttac ttaaatcagt caactggtct ttgagactct 60
taagttctga ttccaactta gctaattcat tctgagaact gtggtatagg tggcgtgtct 120
cttctagctg ggacaaaagt tctttgtttt cccctgtag agtatcacag accttctgct 180
gaagctggac ctctgtcttg gccttgact cccaaatctg cttgtcatgt tcaagcctgg 240
aaatgttaat ctttaattct tccatatgga tggacatctg tctaagttga tccttttagaa 300
cactgcaatt atcttctttg agtctaattt cttcttcttt gctttgaatc gcatcactaa 360
acttctcttc ccatttctta gtttcatcta tcacctgtc acgatcatcc tggagggaag 420
acatgctctt agtaaaaggt gcaagctggg tcacagtact gtccaagttt tcctgaagtt 480
gctgaacttc cttgtcttcc ttgttcaaaag taacctgaat ctctccaatt gtctcttcca 540
agtggacttt ttctctgcgc aaagcatcca g 571

<210> 85

<211> 561
<212> DNA
<213> *Homo sapiens*

<400> 85

```
.tcattgcctg tgatggcatc tggaaatgtga tgagcagcca ggaagttgta gatttcattc 60
aatcaaagga ttcagcatgt ggtggaagct gtgaggcaag agaaacaaga actgtatggc 120
aagttaagaa gcacagaggg aaacaagaag gagacagaaa agcagttgca ggaagctgag 180
caagaaatgg aggaatgaa agaaaagatg agaaagtttg ctaaactctaa acagcagaaa 240
atcctagagc tggagaaga gaatgaccgg cttaggggcag aggtgcaccc tgcaggagat 300
acagctaaag agtgtatgga aacacttctt tcttccaatg ccagcatgaa ggaagaactt 360
gaaagggtca aaatggagta tgaaccctt tctaagaagt ttcagtcttt aatgtctgag 420
aaagactctc taagtgaaga ggttcaagat ttaaagcatc agatagaagg taatgtatct 480
aaacaagcta acctagaggg caccgagaaa catgataacc aaacgaatgt cactgaagag 540
ggaacacagt ctataccagg t                                     561
```

<210> 86
<211> 795
<212> DNA
<213> *Homo sapiens*

<400> 86

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aagccaataa tcaccattta ttactlaata tatgccaacc acigtacttg gcagttcaca 60
aattctcacc gttacaacaa ccccatgagg tattttattcc cattctatag atagggaaac 120
cacagctcaa gtaagttagg aaactgagcc aagtatacac agaatacga gggcacaac 180
tagaaggaaa gactgacact gctatctgct ggcctccagt gtcctggctc ttttcacacg 240
ggttcaatgt ctccagcgct gctgctgctg ctgcattacc atgccctcat tgtttttctt 300
cctctggtgt tcaactgcat ctttcaaaga atctaactca ttccagagac cacttatttc 360
tttctctctt tctgaaatta cttttaataa ttcttcatga gggggaaaag aagatgcctg 420
ttggtagttt tggtgtttta gctgctcaat ttgggactta aacaatttgt tttcatcttg 480
tacatcctgt aacagctgtg ttttgctaga aagatcactc tccctctctt ttatcatggc 540
ttctaaccctc ttcaattcat tttcttttc tttcaacaca atctcaagt cttcaaaactg 600
tgatgcagaa gaggcctctt tcaagttatg ttgtgctact tccatgaacat gtgcttttaa 660
agatttcattt tcttcttgaa gatcctgtaa ccacttccct gtattggcta ggtctttctc 720
tttctcttcc aaaacagcct tcatggtatt catctgttcc tcttttctt ttaataagtt 780
caggagcttc agaac                                     795
```

<210> 87
<211> 594
<212> DNA
<213> *Homo sapiens*

<400> 87

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caagcttttt tttttttttt aaaaagtgtt agcattaatg ttttattgtc acgcagatgg 60
caactgggtt tatgtcttca ttttttatat ttttgtaaat taaaaaaatt acaagtttta 120
aatagccaat ggctggttat attttcagaa aacatgatta gactaattca ttaatggtagg 180
cttcaagctt ttctttattg gctccagaaa attcaccac cttttgtccc ttcttaaaaa 240
actggaatgt tggcatgcat ttgacttcac actctgaagc aacatcctga cagtcatcca 300
catctacttc aaggaatatc acgttggaat acttttcaga gagggaaatga aagaaaggct 360
tgatcatttt gcaaggccca caccacgtgg ctgagaagtc aactactaca agtttatcac 420
ctgcagcgtc caaggcttcc tgaagagcag tcttgccttc gatctgcttc accatcttgg 480
ctgctggagt ctgacgagcg gctgtaagga ccgatggaaa tggatccaaa gcaccaaaaca 540
gagcttcaag actcgtctgt tggcttgaat tcggatccga tatcgccatg gcct 594
```

<210> 88
<211> 557
<212> DNA
<213> *Homo sapiens*

<400> 88
aagtgttagc attaatgttt tattgtcacg cagatggcaa ctgggtttat gtcttcatat 60
tttatatttt tgtaaatata aaaaattmca agttttaaat agccaatggc tggttatatt 120
ttcagaaaac atgattagac taattcatta atggtggcct caagcttttc cttattggct 180
ccagaaaatt caccacacct ttgtcccttc ttaaaaaact ggaatgttgg catgcatttg 240
acttcacact ctgaagcaac atcctgacag tcatccacat ctacttcaag gaatatcacg 300
ttggaatact ttccagagag ggaatgaaag aaaggcctga tcattttgca aggccccacac 360
cacgtggctg agaagtcaac tactacaagt ttatcacctg cagcgtccaa ggcttctctga 420
aaagcagctc tgcctcgcag ctgcttcaco atcctggctg ctggagctcg acgagcggtc 480
gtaaggaccg atggaatgg atccaaagca ccaaacagag cttcaagact cgctgcttgg 540
catgaattcg gatccga 557

<210> 89
<211> 561
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 544, 551
<223> n = A,T,C or G

<400> 89
tacaaacttt attgaaacgc acacgcgcac acacacaaac acccctgtgg atagggaaza 60
gcacctggcc acagggtcca ctgaaacggg gaggggatgg cagcttgtta tgtggctttt 120
gccacaaccc ccttctgaca gggaaggcct tagattgagg cccacacctc catggtgatg 180
gggagctcag aatggggtcc agggagaatt tggttagggg gaggtgctag ggaggcatga 240
gcagagggca ccctccgagt ggggtcccca gggctgcaga gtcttcagta ctgtccctca 300
cagcagctgt ctcaaggctg ggtccctcaa aggggcgtcc cagcgcgggg cctccctgcg 360
caaacacttg gtaccctctg ctgcgcagcg gaagccagca ggacagcagt ggcgcggatc 420
agcacaacag acgccctggc ggtagggaca gcaggccacg ccctgtcggg tgtctcggca 480
gcagggtctg ttatcatggc agaagtgtcc ttcccacact tcacgtcctt cacaccacag 540
tgaaggctac nggccaggaa g 561

<210> 90
<211> 561
<212> DNA
<213> Homo sapiens

<400> 90
cccgtgggtg ccatccacgg agttgttacc tgatcttttg aagcaggatc gcccgctctg 60
actgcagtgg aagccccctg ggcagcagtg atggccatcc ccgcatgcc aaggcctctg 120
gaaggggacg caactggaag tccctgagac ggtaaagatg caggagtgcc cggcagagca 180
gtggggcatc acctggcagg gcccaaccag atgcctgctc agtgttctgg gccatttctc 240
cagaagggga cggcagcagc ttagctgggc tccctccggg tccaggcagc aggccacagg 300
gcagaactga ccatctgggc accgcgttcc agccaccagc cctgctgtta aggccaccca 360
gtcaccagg gtccacatgg tctgcctgag tccgactccg cggtccttgg gccctgatgg 420
ttctacctgc tgtgagctgc ccagtgggaa gtatggctgc tgccaatgcc caacgccacc 480
tgctgctccg atcaactgca ctgctgcccc aagacactgt gtgtgacctg atccagagta 540
agtgcctctc caaggagaac g 561

<210> 91
<211> 541
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> 480, 491
<223> n = A,T,C or G

<400> 91
gaatcacctt tctggttttag ctagtacttt gtacagaaca atgaggtttc ccacagcgga 60
gtctccctgg gctctgtttg gctctcggtt aggcaggcct acaccttttc ctctcctcta 120
tggagagggg aatatgcatt aaggcgaaaa gtcaccttcc aaaagtgaaga aagggattcg 180
attgctgctt caggactgtg gaattatttg gaattgttta caaatgggtg ctacaaaaca 240
acaaaaaagg taattacaaa atgtgtacat cacaacatgc tttttaaaga cattatgcat 300
tgtgtcaca ttcccttaaa tgttgtttcc aaaggtgctc agcctctagc ccagctggat 360
tctccgggaa gaggcagaga cagtttggcg aaaaagacac aggggaaggag ggggtggtga 420
aaggagaaaag cagccttcca gttaaagatc agcctcagc taaaggtcag ctcccgcan 480
gctggcctca ngcggagtct gggtcagagg gaggagcagc agcagggtgg gactggggcg 540
t 541

<210> 92
<211> 551
<212> DNA
<213> Homo sapiens

<400> 92
aaccggagcg cgagcagtag ctgggtgggc accatggctg ggatcaccac catcgaggcg 60
gtgaagcgca agatccaggt tctgcagcag caggcagatg atgcagagga gcgagctgag 120
cgctccagc gagaagtga gggagaaaag cgggcccggg aacaggctga ggctgagggt 180
gcctccttga accgtaggat ccagctggtt gaagaagagc tggaccgtgc tcaggagcgc 240
ctggccactg ccctgcacaaa gctggaagaa gctgaaaaag ctgctgatga gagtgaaga 300
ggatgaagg ttattgaaaa ccgggcctta aaagatgaag aaaagatgga actccaggaa 360
atccaactca aagaagctaa gcacattgca gaagagcgag ataggaagta tgaagagggt 420
gctcgtaagt tgggtgatcat tgaaggagac ttggaacgca cagaggaacg agctgagctg 480
gcagagtcgc gttgccgaga gatggatgag cagattagac tgatggacca gaacctgaag 540
tgtctgagtg c 551

<210> 93
<211> 531
<212> DNA
<213> Homo sapiens

<400> 93
gagaacttgg cttttattgt gggccagga gggcacaag gtcaggagc ccaaggagg 60
gatctggttt tctgcatagc caggtcatag catgggtatc agtaggaac cgctgtagct 120
gcacaggcct cacttgctgc agttccgggg agaacacctg cactgcatgg cgttgatgac 180
ctcgtggtac acgacagagc cattggtgca gtgcaagggc acgcgcatgg gctccgtcct 240
cgagggcagc cagcaggagc attgctcctg cacatcctcg atgtcaatgg agtacacagc 300
tttctggca cactttccct ggcagtaatg aatgtccact tcctcttggg acttacaatc 360
tcccactttg atgtactgca ccttggctgt gatgtctttg caatcaggct cctcacatgt 420
gtcacagcag gtgctggaa ttttcacgat ttgctcctc tcagccagac acttgtgttc 480
atcaaatggt gggcagcccg tgaacctctt ctcccatgag tactctctc t 531

<210> 94
<211> 531
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 517
<223> n = A,T,C or G

<400> 94

```

gcctggacct tgcgggatca gtgccacaca gtgacttgct tggcaaatgg ccagacettg 60
ctgcagagtc atcgtgtcaa ttgtgaccat ggaccccgcc cttcatgtgc caacagccag 120
tctcctgttc ggggtggagga gacgtgtggc tgccgctgga cctgcccttg tgtgtgcacg 180
ggcagttcca ctccggcacat cgtcaccttc gatgggcaga atttcaagct tactggtagc 240
tgctcctatg tcattcttca aaacaaggag caggacctgg aagtgtcctt ccacaatggg 300
gcctgcagcc ccgggggcaaa acaagcctgc atgaagtcca ttgagattaa gcatgctggc 360
gtctctgctg agctgcacag taacatggag atggcagtgg atgggagact ggtccttgcc 420
ccgtacgttg gtgaaaacat ggaagtcagc atctacggcg ctatcatgta tgaagtcagg 480
tttaccatc ttggccacat cctcacatac accgccncaa aacaacgagt t 531

```

<210> 95

<211> 605

<212> DNA

<213> Homo sapiens

<400> 95

```

agatcaacct ctgctgggtca ggaggaatgc cttccttgct ttggatcttt gctttgacgt 60
tctcgatagt rwcaactkk r ytsramskma agkgyratgr wmttksywgw rasyktmwwm 120
rsgraraytt agacaycccm cctcwgagac gsagkaccar gtgcagaggt ggactctttc 180
tgatgttgt agtcagacag ggtgcgtcca tcttcagct gtttccagc aaagatcaac 240
ctctgctgat caggagggat gccttcctta tcttgatct ttgccttgac attctcgatg 300
gtgtcactgg gctccacctc gaggggtgat gtcttaccag tcagggtctt cacgaagaty 360
tgcatcccac ctctgagacg gacacaccag tgcagggttg actctttctg gatgtttag 420
tcagacaggg tgcgyccatc ttccagctgc tttccsagca aagatcaacc tctgctggc 480
aggagratg ccttccttgt cytggtctt tgcyttgacr ttctcratgg tgtcactcgg 540
ctccacttcg agagtgtatg tcttaccagt cagggtcttc acgaagatct gcattccacc 600
tctaa 605

```

<210> 96

<211> 531

<212> DNA

<213> Homo sapiens

<400> 96

```

aagtcacaaa cagacaaaaga ttattaccag ctgcaagcta tattagaagc tgaacgaaga 60
gacagaggtc atgattctga gatgattgga gaccttcaag ctggaattac atctttacaa 120
gaggaggtga agcatctcaa acataatctc gaaaaagtgg aaggagaaag aaaagaggct 180
caagacatgc ttaatcactc agaaaaggaa aagaataatt tagagataga ttttaactac 240
aaacttaaat cattacaaca acggttagaa caagaggtaa atgaacacaa agtaacacaa 300
gctcgtttta ctgacaaaaca tcaatctatt gaagaggcaa agtctgtggc aatgtgtgag 360
atggaaaaaa agctgaaaga agaaagagaa gctcgagaga aggctgaaaa tcgggttggt 420
cagattgaga aacagtgttc catgctagac gttgatctga agcaatctca gcagaaacta 480
gaacatttga ctggaaataa agaaaggatg gaggatgaag ttaagaatct a 531

```

<210> 97

<211> 1017

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 963, 995, 1001, 1008, 1010

<223> n = A,T,C or G

<400> 97

```

ccctccacc atgtccatca ggggtgaccca gaagtcctac aagggtgcca cctctggccc 60

```

```

ccgggccttc agcagccgct cctacacgag tgggcccgggt tcccgcacatca gctcctcgag 120
cttctcccga gtggggcagca gcaactttcg cgggtggcctg ggcgccggct atgggtggggc 180
cagcggcatg ggaggcatca ccgcagttac ggtcaaccag agcctgctga gccccctgt 240
cctggagggtg gacccaaca tccaggccgt gcgcacccag gagaaggagc agatcaagac 300
cctcaacaac aagtttgect ccttcataga caaggtagcg ttccctggagc agcagaacaa 360
gatgctggag acczagtgga gcctcctgca gcagcagaag acggctcgaa gcaacatgga 420
caacatgttc gagagctaca tcaacarcct tagggcgag ctggagactc tggggccagga 480
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caagtatgag gatgagatca ataagcgtac agagatggag aacgaatttg tcctcatcaa 600
gaaggatgtg gatgaagctt acatgaacaa ggtagagctg gagtctcgcc tgggaagggtc 660
gaccgacgag atcaacttcc tcaggcagct gtatgaagag gagatccggg agctgcagtc 720
ccagatctcg gacacatctg tgggtgctgtc catggacaac agccgctccc tggacatgga 780
cagcatcatt gctgaggtca aggcacagta cgaggatatt gccaacccga gccgggctga 840
ggctgagagc atgtaccagg tcaagtatga ggagctgcag agcctggctg ggaagcacgg 900
ggatgacctg cggcgacaaa agactgagat ctctgagatg aaccgggaac atcagccccg 960
ctncaggctg agattgaggg cctcaaaggc caganggctt nccctggangn ccgccat 1017

```

<210> 98

<211> 561

<212> DNA

<213> Homo sapiens

<400> 98

```

cccggagcca gccaacgagc ggaaaaatggc agacaatttt tgcgtccatg atgcgttata 60
tgggtctgga aacccaaacc ctcaaggatg gcctggcgca tgggggaacc agcctgctgg 120
ggcagggggc tcccaggggg ctctctatcc tggggcctac cccgggcagg cccccccagg 180
ggcttatcct ggacaggcac ctccaggcgc ctaccctgga gcacctggag ctatcccg 240
agcacctgca cctggagtct acccaggggc acccagcggc cctggggcct acccatcttc 300
tggacagcca agtgccaccg gagcctaccg tgccactggc cctatggcg cccctgctgg 360
gccactgatt gtgccttata acctgccttt gcctggggga gtggtgcttc gcatgctgat 420
aacaattctg ggacgggtga agcccaatgc aaacagaatt gctttagatt tccaaagagg 480
gaatgatgtt gccttcact ttaaccacg cttcaatgag aacaacagga gagtcatgg 540
ttgcaatata aagctggata a 561

```

<210> 99

<211> 636

<212> DNA

<213> Homo sapiens

<400> 99

```

gggaatgcaa caactttatt gaaaggaaag tgcaatgaaa tttgttgaaa ccttaaaagg 60
ggaaacttag acaccccccc tcragcgmag kaccaargtc araggtagac tctttctgga 120
tgtttagatc agacagggtg cgwccatctt ccagctgttt yccrgcaaag atcaacctct 180
gctgatcagg aggratgcct tccctatctt gcatctttgc cttgacattc tccatggtgt 240
cactgggctc cactcgagg gtgatggtct taccagtcag ggtcttcacg aagatytgca 300
tcccacctct gagacggagc accagggtgca ggttrgactc tttctggatg ttgtagtcag 360
acagggtgag yccatcttcc agctgcttcc csagcaaaga tcaacctctg ctggtcagga 420
ggratgcctt ccttgcteytg gatctttgcy ttgacrttct caatgggtgct actcggtccc 480
acttcgagag tgatggtctt accagtcagg gtcttcacga agatctgcat cccacctota 540
agacggagca ccagggtcag ggtggactct ttctggatgg ttgtagtcag acagggtgag 600
tccatcttcc agctgtttcc cagcaaagat caacct 636

```

<210> 100

<211> 597

<212> DNA

<213> Homo sapiens

<400> 100


```
agggtgatct ttgctgggaa acagctggaa gatggacgca cctgtgtga ctacaacat 60
ccagaaagag tccaccctgc acctgggtgct cgtctttaga ggtgggatgc agatcttctg 120
gaagaccctg actggtaaga ccatcactct cgaagtggag ccgagtgaac ccattgagaa 180
ygtcaargca aagatccarg acaagggaagg catycctcct gaccagcaga ggttgatctt 240
tgctsggaaa gcagctggaa gatggxgca cctgtgtga ctacaacatc cagaaagagt 300
cyaccctgca cctgggtgctc cgtctcagag gtgggatgca ratcttcgtg aagaccctga 360
ctggttaagac catcaccctc gaggtggagc ccagtgaac catcgagaat gtcaaggcaa 420
agatccaaga taagggaaggc atccctcctg atcagcagag gttgatottt gctgggaaac 480
agctggaaga tggacgcacc ctgtctgact acaacatcca gaaagagtcc acctytgcac 540
ytggtmctbc gtctyagagg kgggtgcaa atctwmgtkw agacactcac tkkyaagryy 600
atcamcmwtg akktcgakys castkwcact wtcraaamg tyrwwgcawa gatccmagac 660
aagggaaggca ttctcctga ccagcagagg ttgatct 697
```

<210> 101

<211> 451

<212> DNA

<213> Homo sapiens

<400> 101

```
atggagtctc actctgtcga ccaggctgga gcgctgtggt gcgatatcgg ctactgcag 60
tctccacttc ctgggttcaa ggcatactcc tgcctcagcc tcccagtag ctgggactac 120
aggcaggcgt caccataatt tttgtatctt tagtagagac atgggttctc catgttggct 180
gggctggctc cgaactcctg acctcaagtg atctgtcctg gcctcccaaa gtgttgggat 240
tacaggcgaa agccaacgct cccggccagg gaacaacttt agaataagg aaatatgcaa 300
aagaacatca catcaaggat caattaatta ccatctatta attactatat gtgggtaatt 360
atgactattt cccaagcatt ctacgttgac tgcttgagaa gatgtttgtc ctgcatggtg 420
gagagtggag aaggggccagg attcttaggt t 451
```

<210> 102

<211> 571

<212> DNA

<213> Homo sapiens

<400> 102

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agcgcggtct tccggcgaga gaaagctgaa ggtgatgtgg ccgcctcaa ccgacgcac 60
cagctcgttg aggaggagtt ggacagggtc caggaaacgac tggccacggc cctgcagaag 120
ctggaggagg cagaaaaagc tgcagatgag agtgagagag gaataagggt gatagaaaac 180
cgggccatga aggatgagga gaagatggag attcaggaga tgcagctcaa agaggccaag 240
cacattgcgg aagaggctga ccgcaaatac gaggaggtag ctctgaagct ggtcatcctg 300
gaggggtgagc tggagagggc agaggagcgt gcggaggtgt ctgaactaaa atgtggtgac 360
ctggaagaag aactcaagaa tcttactaac aatctgaaat cctggaggc tgcatctgaa 420
aagtattctg aaaaaggagga caaatatgaa gaagaaatta aacttctgtc tgacaaactg 480
aaagaggctg agaccctgac tgaatttgca gagagaacgg ttgcaaaact ggaaaagaca 540
attgatgacc tggaaagagaa acttgccacg c 571
```

<210> 103

<211> 451

<212> DNA

<213> Homo sapiens

<400> 103

```
gtgcacagggt cccatttatt gtagaaaata ataataatta cagtgatgaa tagctcttct 60
taaattacaa aacagaaacc acaaaagaagg aagaggaaaa accccaggac ttccaagggg 120
gaagctgtcc cctctcctc gccaccctcc caggctcatt agtgtctctg gaaggggcag 180
aggactcaga ggggatcagt ctccaggggc cctgggctga agcgggtgag gcagagagtc 240
ctgagggcac agagctgggc aacctgagcc gccctctctg cccctcccc caccactgcc 300
caaacctgtt tacagcactc tcgccctccc cctctaacc cgtccatcca ctctgcactt 360
cccaggcagg tgggtgggac aggcctcagc catactcctg ggcgcgggtt tcggtgagca 420
```

aggcacagtc ccagaggtga tatcaaggcc t

451

<210> 104

<211> 441

<212> DNA

<213> Homo sapiens

<400> 104

gcaaggaact ggtctgctca cacttgetcg cttgcgcac aggactggct ttatctcctg 60
actcacggty caaaggtgca ctctgcgaac gttaagtccg tccccagcgc ttggaatcct 120
acggccccca cagccggatc ccctcagcct tccaggtcct caactcccgt ggacgctgaa 180
caatggcctc catggggcta caggtaatgg gcacgcgcgt ggcgctcctg ggctggctgg 240
ccgtcatgct gtgctgcgcg ctgcccattgt ggcgcgtgac ggccttcac ggacgcaaca 300
ttgtcacctc gcagaccac tgggagggcc tatggatgaa ctgctgggtg cagagcaccg 360
gccagatgca gtgcaaggty taccactcgc tgcctggcact gccgcaggac ctgcaggcgg 420
cccgcgccct cgtcatcacc a 441

<210> 105

<211> 509

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 195

<223> n = A,T,C or G

<400> 105

tgcaaaaggg acacaggggt tcaaaaataa aaattttctt tccccctccc caaacctgta 60
ccccagctcc ccgaccacaa ccccttctct cccccggga aagcaagaag gaggcaggtg 120
ggcatctgca gctgggaaga gagaggccgg ggaggtgccg agctcggtyc tggctctttt 180
ccaaatataa atactngtgt cagaactgga aaatctctca gacccaccca ccaagcact 240
ctccgttttc tgccggtgtt tggagaggcg cggggggcag gggcgccagg caccggctgg 300
ctgcggtcta ctgcacccg tgggtgtgca ccccgcgagc ctctctgctg tcattgtaga 360
agagatgaca ctccgggtcc ccccggtatg tgggggctcc ctggatcagc ttcccggtgt 420
tgggggtcac acaccagcac tccccacgct gcccggtcag agacatcttg cactgtttga 480
ggttgtacag gccatgcttg tcacagttg 509

<210> 106

<211> 571

<212> DNA

<213> Homo sapiens

<400> 106

gggttggagg gaactggtct ttatttcaaa aagacacttg tcaatattca gtatcaaaac 60
agttgcacta ttgatttctc tttctcccaa tcggcccca agagaccaca taaaaggaga 120
gtacatttta agccaataag ctgcaggatg tacacctaac agacctcta gaaaccttac 180
cagaaaatgg ggactgggta gggaaggaaa cttaaaagat caacaaactg ccagcccaag 240
gactgcagag gctgtcacag ccagatggcg tggccagggt gccacaaacc caaagcaaag 300
tttcaaaata atataaaatt taaaaagttt tgtacataag ctattcaaga tttctccagc 360
actgactgat acaaagcaca attgagatgg cacttctaga gacagcagct tcaaaccag 420
aaaagggtga tgagatgagt ttcacatggc taaatcagtg gcaaaaacac agtcttcttt 480
ctttcttctt ttcaaggagg caggaaagca attaagtggc cacctcaaca taagggggac 540
atgatccatt ctgtaagcag ttgtgaaggg g 571

<210> 107

<211> 555

<212> DNA

<213> Homo sapiens

<400> 107

```

caggaaccg agcgcgagca gtagctgggt gggcaccatg gctgggatca ccaccatcga 60
ggcgggtgaag cgcaagatcc aggttctgca gcagcaggca gatgatgcag aggagcgagc 120
tgagcgctc cagcgagaag ttgagggaga aaggcgggcc cgggaacagg ctgaggctga 180
ggtggcctcc ttgaaccgta ggatccagct ggttgaagaa gagctggacc gtgctcagga 240
gcgcctggcc actgcctgc aaaagctgga agaagctgaa aaagctgctg atgagagtga 300
gagaggtatg aaggttattg aaaaccgggc cttaaaagat gaagaaaaga tggaaactcca 360
ggaaatccaa ctcaagaag ctaagcacat tgcagaagag gcagatagga agtatgaaga 420
ggtggctcgt aagttggtga tcattgaagg agacttgaa cgcacagagg aacgagctga 480
gctggcagag tcccgttgcc gagagatgga tgagcagatt agactgatgg accagaacct 540
gaagtgtctg agtgc 555

```

<210> 108

<211> 541

<212> DNA

<213> Homo sapiens

<400> 108

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atctacgtca tcaatcaggc tggagacacc atgttcaatc gagctaagct gctcaatatt 60
ggctttcaag aggccttgaa ggactatgat tacaactgct ttgtgttcag tgatgtggac 120
ctcattccga tggacgaccc taatgcctac aggtgttttt cgcagccacg gcacatttct 180
gttgcaatgg acaagttcgg gtttagcctg ccataatgttc agtatatttg aggtgtctct 240
gctctcagta aacaacagtt tcttgccatc aatggattcc ctaataatta ttgggggttg 300
ggaggagaag atgacgacat ttttaacaga ttagttcata aaggcatgtc tatatcacgt 360
ccaaatgctg tagtagggag gtgtcgaatg atccggcatt caagagacaa gaaaaatgag 420
cccaatctc agaggtttga ccggatcgca catacaaagg aaacgatgag ctctgatgg 480
ttgaactcac ttactacaa ggtgttgat gtcagagata cccgttatat acccaaatca 540
c 541

```

<210> 109

<211> 411

<212> DNA

<213> Homo sapiens

<400> 109

```

ctagacctct aattaaaagg cacaatcatg ctggagaatg aacagtctga ccccgagggc 60
cacagcgaat tttagggag gaggcaaaga ggtgagaagg gaaaggaaag aagggaaggaa 120
ggagaacaat aagaactgga gacgttgggt gggtcaggga gtgtgggtga ggctcggaga 180
gatggtaaac aaacctgact gctatgagtt ttcaacccca tagtctaggg ccatgagggc 240
gtcagttctt ggtggctgag ggtccttcca cccagccac ctgggggagt ggagtgggga 300
gttctgccag gtaagcagat gttgtctccc aagttcctga cccagatgtc tggcaggata 360
acgctgacct gttccctcaa caagggacct gaaagtaatt ttgctcttta c 411

```

<210> 110

<211> 451

<212> DNA

<213> Homo sapiens

<400> 110

```

ccgaattcaa gcgtcaacga tccytccctt accatcaaat caattggcca ccaatggtac 60
tgaacctacg agtacacga ctacggcggt actaatcttc aactcctaca tacttcccc 120
attattccta gaaccaggcg acctgcgact ccttgacgtt gacaatcgag tagtactccc 180
gattgaagcc cccattcgta taataattac atcacaagac gtcttgcaat catgagctgt 240
ccccacatta ggcttaaaaa cagatgcaat tcccggacgt ctaaggcaaa ccactttcac 300
cgctacacga ccgggggtat actacggtca atgctctgaa atctgtggag caaaccacag 360
tttcatgccc atcgtcctag aattaattcc cctaaaaatc tttgaaatag ggcccgtatt 420

```

taccctatag cccccctct accccctcta g

451

<210> 111

<211> 541

<212> DNA

<213> Homo sapiens

<400> 111

```
gctcttcaca cttttattgt taattctctt cacatggcag atacagagct gtcgtcttga 60
agaccaccac tgaccaggaa atgccacttt tacaaaatca tcccccttt tcatgattgg 120
aacagttttc ctgaccgtct gggagcgttg aagggtgacc agcacatttg cacatgcaaa 180
aaaggagtgga cccaaggcc tcaaccacac ttcccagagc tcaccatggg ctgcagggtga 240
cttgccagggt ttgggggttc tgagctttcc ttgctgctgc ggtggggagg ccctcaagaa 300
ctgagaggcc ggggtatgct tcatgagtgt taacatttac gggacaaaag cgcattatta 360
ggataaggaa cagccacagc acttcatgct tgtgaggggt agctgttaga gcgggtgaaa 420
ggattccagt ttatgaaaat ttaaagcaaa caacgggttt tagctgggtg ggaaacagga 480
aaactgtgat gtcggccaat gaccaccatt tttctgcca tgtgaaggtc cccatgaaac 540
c
```

541

<210> 112

<211> 521

<212> DNA

<213> Homo sapiens

<400> 112

```
caagcgcttg gcgtttggac ccagttcagt gaggttcttg ggtttlgtgc ctttggggat 60
tttggtttga ccaggggtc agccttagga aggtcttcag gaggaggccg agttcccctt 120
cagtaccacc cctctctccc cactttccct ctcccgcaa catctctggg aatcaacagc 180
atattgacac gttggagccg agcctgaaca tgcctctcgg ccccgacaca tggaaaacc 240
ccttccttgc ctaaggtgtc tgagtttctg gctcttgagg catttcaga cttgaaatc 300
tcateagtc attgctcttg agtctttgca gagaacctca gatcagggtc acctgggaga 360
aagactttgt cccacttac agatctatct cctcccttgg gaagggcagg gaatggggac 420
ggtgtatgga ggggaaggga tctctgctgc ccttcattgc cacacttggg gggaccatga 480
acatcttag tgtctgagct tctcaaatca ctgcaatagg a
```

521

<210> 113

<211> 568

<212> DNA

<213> Homo sapiens

<400> 113

```
agcgtcaaat cagaatggaa aagactcaaa accatcatca acaccaagat caaaaggaca 60
agratccttc aagaacacag aaaaaactcc taaaacacca aaaggaccta gttctgtaga 120
agacattaaa gcaaaaatgc aagcaagtat agaaaaagg ggttctcttc ccaaagtga 180
agccaaatc atcaattatg tgaagaattg cttccggatg actgaccaag aggtattca 240
agatctctgg cagtggagga agtctcttta agaaaatag ttaacaatt tgttaaaaa 300
ttttccgtct tatttcattt ctgtaacagt tgatatctgg ctgtcctttt tataatgcag 360
agtgagaact ttccctaccg tgtttgataa atgttgcca ggttctattg ccaagaatgt 420
gttgtccaaa atgcctgttt agtttttaaa gatggaactc cacccttgc ttggttttaa 480
gtatgtatgg aatgttatga taggacatag tagtagcggt ggtcagacat ggaaatgggt 540
ggsmgacaaa aatatacatg tgaataaa
```

568

<210> 114

<211> 483

<212> DNA

<213> Homo sapiens

<400> 114

```

tcgaattcc aagcgaatta tggacaaacg attcctttta gaggattact tttttcaatt 60
tcggttttag taatctaggc ttgcctgtta aagaatacaa cgatggattt taaatactgt 120
ttgtggaatg tgtttaaagg attgattcta gaacctttgt atatttgata gtattttctaa 180
ctttcatttc ttactgltt gcagtlaatg ttcatgttct gctatgcaat cgtttatatg 240
cacgtttctt taattttttt agatttttct ggatgtatag tttaaacaac aaaaagtcta 300
tttaaaactg tagcagtagt ttacagttct agcaaaggagg aaagtgtggg ggttaaactt 360
tgtattttct ttcttataga ggcttctaaa aaggattttt tatatgttct ttttaacaaa 420
tattgtgtac aacctttaaa acatcaatgt ttggatcaaa acaagaccca gcttattttc 480
tgc 483

```

```

<210> 115
<211> 521
<212> DNA
<213> Homo sapiens

```

```

<400> 115
tgtggtggcg cgggctgagg tggaggccca ggactctgac cctgcccctg ccttcagcaa 60
ggccccggcg agcgccggcc actacgaact gccgtgggtt gaaaaatata ggccagtaaa 120
gctgaatgaa attgtcggga atgaagacac cgtgagcagg cttagaggtct ttgcaaggga 180
aggaaatgtg cccaacatca tcattgcggg ccctccagga accggcaaga ccacaagcat 240
tctgtgcttg gcccgggccc tgctgggccc agcactcaaa gatgccatgt tggaaactcaa 300
tgcttcaaat gacaggggca ttgacgttgt gaggaataaa attaaaatgt ttgctcaaca 360
aaaagtcaact cttcccaaag gccgacataa gatcatcatt ctggatgaag cagacagcat 420
gaccgacgga gcccgagcaag ccttgaggag aacctatgaa atctactcta aaacctctcg 480
ttcgcccttg cttgtaatgc ttcgataag atcatcgagc c 521

```

```

<210> 116
<211> 501
<212> DNA
<213> Homo sapiens

```

```

<400> 116
ctttgcaaaag cttttatttc atgtctgagg catggaatcc acctgcacat ggcattcttag 60
ctgtgaagga gaaagcagtg cacgagaagg aatgagtggg cggaaccaac ggctccaca 120
agctgccttc cagcagcctg ccaaggccat ggcagagaga gactgcaaac aaacacaagc 180
aaacagagtc tcttcacagc tggagtctga aagctcatag tggcatgtgt gaactctgaca 240
aaattaaaag tgtgcatagt ccattacatg cataaaacac taataataat cctgtttaca 300
cgtgactgca gcaggcaggc ccagctccac cactgccctc ctgccacatc acatcaagtg 360
ccatggttta gagggttttt catatgtaat tcttttatte tgtaaaagggt aacaaaaatat 420
acagaacaaa actttccctt tttaaaacta atgttacaaa tctgtattat cacttgagata 480
taaatagtat ataagctgat c 501

```

```

<210> 117
<211> 451
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 320
<223> n = A,T,C or G

```

```

<400> 117
caagggatat atgttgaggg tacrgtgtga cactgaacag atcacaaagc acgagaacaa 60
ttagttctct cctcccccag cgtctccttc gtctccctgg ttttccgatg tccacagagt 120
gagattgtcc ctaagtaact gcatgatcag agtgctgkct ttataagact cttcattcag 180
cgtatccaat tcagcaattg cttcatcaaa tgccgttttt gccaggctac aggccttttc 240
aggagagttt agaatctcat agtaaaagac tgagaaattt agtgccagac caagacgaat 300

```

tggtgtgtga ggctgcattn ctttcttact aatttcaa at gctcctggt aagcctgctg 360
ggagttcgac acaagtgtt tgtttgttgc tccagatgcc acttcagaaa gatacctaaa 420
ataatctcct ttcattttca aagtagaaca c 451

<210> 118
<211> 501
<212> DNA
<213> Homo sapiens

<400> 118
tccggagccg gggtagtgcg cgcgcgcgcg gcgggtgcag ccactgcagg caccgctgcc 60
gccgcctgag tagtgggctt aggaaggaag aggtcatctc gctcggagct tcgctcggaa 120
gggtctttgt tccctgcagc cctcccacgg gaatgacaat ggataaaagt gagctggtag 180
agaaagccaa actcgtgag caggctgagc gatatgatga tatggctgca gccatgaagg 240
cagtccacaga acaggggcat gaactctcca acgaagagag aaatctgctc tctgttgctt 300
acaagaatgt ggttaaggccg cccgcgcgctc ttctggcgt gtcactctcca gcattgagca 360
gaaaacagag aggaatgaga agaagcagca gatgggcaaa gagtaccgtg agaagataga 420
ggcagaactg caggacatct gcaatgatgt tctggagctt gttggacaaa tatcttatte 480
caatgctaca caaccagaa a 501

<210> 119
<211> 391
<212> DNA
<213> Homo sapiens

<400> 119
aaaaagcagc argttcaaca caaaatagaa atctcaaatg taggatagaa caaaaccaag 60
tgtgtgaggg gggaagcaac agcaaaagga agaaatgaga tgttgcaaaa aagatggagg 120
agggttcccc tctcctctgg ggactgactc aaacactgat gtggcagtat acaccattcc 180
agagtcaggg gtgttcattc ttttttggga gtaagaaaag gtggggatta agaagacgtt 240
tctggaggct tagggaccaa ggctggcttc tttccccct cccaaccccc ttgatccctt 300
tctctgatca ggggaaagga gctcgaatga gggaggtaga gttggaaagg gaaaggattc 360
cacttgacag aatgggacag actccttccc a 391

<210> 120
<211> 421
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 409
<223> n = A,T,C or G

<400> 120
tggcaatagc acagccatcc aggagctctt cargcgcatc tcggagcagt tcaactgcat 60
gttccgcccg aaggccttcc tccactggta cacaggcgag ggcattggacg agatggagtt 120
caccgaggct gagagcaaca tgaacgacct cgtctctgag tatcaagcag taccaggatg 180
ccaccgcaga agaggaggag gatttcggtg aggaggccga agaggaggcc taaggcagag 240
cccccatcac ctcaggcttc tcagttccct tagccgtctt actcaactgc ccctttcttc 300
tccctcagaa tttgtgtttg ctgcctctat ctgtgttttt gttttttctt ctgggggggt 360
ctagaacagt gcctggcaca tagtaggcgc tcaataaata cttggttgnt gaatgtctcc 420
t 421

<210> 121
<211> 206
<212> DNA
<213> Homo sapiens

<400> 121

```
agctggcgct agggctcggt tgtgaaatac agcgtgtgca gcccttgccg tcagtgtaga 60
aaccacagcc tgtaaggctg gtcttcgtcc atctgctttt ttctgaaata cactaagagc 120
agccacaaaa ctgtaacctc aaggaaacca taaagcttgg agtgccctta tttttaacca 180
gtttccaata aaacggttta ctacct                                206
```

<210> 122

<211> 131

<212> DNA

<213> Homo sapiens

<400> 122

```
ggagatgaag atgaggaagc tgagtcagct acgggcargc gggcagctga agatgatgag 60
gatgacgatg tcgataccaa gaagcagaag accgacgagg atgactagac agcaaaaaag 120
gaaaagttaa a                                131
```

<210> 123

<211> 231

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 166, 202, 222, 225

<223> n = A,T,C or G

<400> 123

```
gatgaaaatt aaatacttaa attaatacaa aggcactacg ataccaccta aaacctactg 60
cctcagtggc agtakgctaa kgaagatcaa gctacagsac atyatctaata atgaatgtta 120
gcaattacat akcargaagc atgtttgctt tccagaagac tatggnacaa tggtcattwg 180
ggcccaagag gatatttggc cnggaaagga tcaagataga tnaangtaaa g          231
```

<210> 124

<211> 521

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 284, 412, 513

<223> n = A,T,C or G

<400> 124

```
gagtagcaac gcaaagcgct tggatttgag tctgtgggsg acttcgggtc cggctctctgc 60
agcagccgtg atcgcttagt ggagtgttta gggtagttgg ccaggatgcc gaatatcaaa 120
atcttcagca ggcagctccc accaggactt atctcasaaa attgctgacc gcctgggcct 180
ggagctaggc aaggltggta ctaagaaatt cagcaaccag gagacctgtg tggaaatttg 240
tgaaagtgtg ccgtggagag gatgtctaca ttgttcagag tggntgtggc gaaatcaatg 300
acaatttaat ggagcttttg atcatgatta atgcctgcaa gattgcttca gccagccggg 360
ttactgcagt catccctgc ttcccttatg ccccggcagg ataagaaaga tnagagccgg 420
gccgccaatc tcagccaagc ttggtgcaaa tatgtatct gttagcagtgc agatcatatt 480
atcaccatgg acctacatgc ttctcaaatt canggctttt t          521
```

<210> 125

<211> 341

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> 277
<223> n = A,T,C or G

<400> 125
atgcaaaagg ggacacaggg ggttcaaaaa taaaaatttc tcttccccct ccccaaacct 60
gtaccccagc tccccgacca caaccccoct cctcccccg ggaagcaag aaggagcagg 120
tgtggcatct gcagctggga agagagaggg cggggagggt ccgagctcgg tgctggtctc 180
tttccaaata taaatacgtg tgtcagaact ggaaaatcct ccagcaccca ccaccaagc 240
actctccgtt ttctgccggt gtttgagag gggcgnggg caggggcgc aggcaccggc 300
tggtgcggt ctactgcac cgetgggtgt gcaccccg a 341

<210> 126
<211> 521
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 353, 399, 455
<223> n = A,T,C or G

<400> 126
agggtggaga aggtcatgca ggtgcagatt gtccaggskc agccacaggg tcaagcccaa 60
caggcccaga gtggcactgg acagaccatg caggtgatgc agcagatcat cactaacaca 120
ggagagatcc agcagatccc ggtgcagctg aatgccggcc agctgcagta tatccgctta 180
gccagcctg tatcaggcac tcaagtgtg cagggacaga tccagacact tgccaccaat 240
gctcaacaga ttacacagac agaggtccag caaggacagc agcagttcaa gccagttcac 300
aagatggaca gcagctctac cagatccagc aagtcacat gcctgcgggc cangacctcg 360
ccagcccatg ttcatccagt caagccaacc agcccttcna cgggcaggcc cccaggtga 420
ccggcgactg aagggcctga gctggcaagg ccaangacac ccaacacaat ttttgccata 480
cagccccag gcaatgggca cagcctttct tcccagagga c 521

<210> 127
<211> 351
<212> DNA
<213> Homo sapiens

<400> 127
tgagatttat tgcatttcat gcagcttgaa gtccatgcaa aggrgactag cacagttttt 60
aatgcattta aaaaataaaa gggagggtgg cagcaaacac acaaagtcct agtttcctgg 120
gtccctggga gaaaagatg tggcaatgaa tccaccact ctccacaggg aataaatctg 180
tctcttaaat gcaagaatg tttccatggc ctctggatgc aaatacacag agctctgggg 240
tcagagcaag ggatggggag aggaccacga gtgaaaaagc agctacacac attcacctaa 300
ttccatctga gggcaagaac aacgtggcaa gtcttgggg tagcagctgt t 351

<210> 128
<211> 521
<212> DNA
<213> Homo sapiens

<400> 128
tccagacalg ctccctgtcct aggcggggag caygaaccag acctgctatg ggaagcagaa 60
agagtttaagg gaaggtttcc ttctattcct gttocttctc ttttgccttt gaacagtttt 120
taaatatact aatagctaag tcatttgcca gccaggctcc ggtgaacagt agagaacaag 180
gagcttgcta agaattaatt ttgctgtttt tcacccatt caaacagagc tgccctgttc 240


```

cctgatggag ttccattcct gccagggcac ggctgagtaa cacgaagcca ttcaagaaag 300
gcgggtgtga aatcactgcc accccatgga cagaccctc actcttcctt cttagccgca 360
gcgctactta ataaatataat ttatactttg aaattatgat aaccgatttt tcccatgcgg 420
catcctaagg gcacttgcca gctcttatcc ggacagtcaa gcactgttgt tggacaacag 480
ataaaggaaa agaaaaagaa gaaaacaacc gcaacttctg t 521

```

<210> 129
 <211> 521
 <212> DNA
 <213> Homo sapiens

```

<400> 129
tgagacggac cactggcctg gtccccctc atktgtgtgc gtaggacctg acatgaaacg 60
cagatctagt ggcagagagg aagatgatga ggaacttctg agacgtcggc agcttcaaga 120
agagcaatta atgaagctta actcaggcct gggacagtgt atcttgaaag aagagatgga 180
gaaagagagc cgggaaagggt catctctgtt agccagtgcg tacgattctc ccatcaactc 240
agcttcacat attccatcat ctaaaactgc atctctccct ggctatggaa gaaatgggct 300
tcaccggcct gttttacccg acttcgctca gtataacagc tatggggatg tcagcggggg 360
agtgcgagat taccagacac ttccagatgg ccacatgcct gcaatgagaa tggaccgagg 420
agtggtctatg cccaacatgt tggaaacaaa gatatttcca tatgaaatgc tcatggtgac 480
caacagaggg ccgaaaccaa atctcagaga ggtggacaga a 521

```

<210> 130
 <211> 270
 <212> DNA
 <213> Homo sapiens

```

<400> 130
tcactttatt tttcttctat aaaaacccta tgttgtagcc acagctggag cctgagtccg 60
ctgcacggag actctggtgt gggctcttgac gaggtggtca gtgaactcct gatagggaga 120
cttggtgaat acagtctcct tccagaggtc gggggtcagg tagctgtagg tcttagaaat 180
ggcatcaaag gtggccttgg cgaagtggcc cagggtggca gtgcagcccc gggctgaggt 240
gtagcagtca tcgataccag ccatcatgag 270

```

<210> 131
 <211> 341
 <212> DNA
 <213> Homo sapiens

```

<400> 131
ctggaatata gaccctgat cgacaaaact ttgaacgagg ctgactgtgc caccgtcccc 60
ccagccattc gctcctactg atgagacaag atgtggtgat gacagaatca gcttttgtaa 120
ttatgtataa tagctcatgc atgtgtccat gtcataactg tcttcatacg cttctgcact 180
ctggggaaga aggagtacat tgaagggaga ttggcaccta gtggctggga gcttgccagg 240
aaccagtggt ccagggagcg tggcacttac ctttgtccct tgcttcattc ttgtgagatg 300
ataaaactgg gcacagctct taaataaaat ataatgaac a 341

```

<210> 132
 <211> 844
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 37
 <223> n = A,T,C or G

<400> 132

```

tgaatgggga ggagctgacc caggaaatgg agcttgngga gaccaggcct gcaggggatg 60
gaaccttcca gaagtgggca tctgtggtgg tgcctcttgg gaaggagcag aagtacacat 120
gccatgtgga acatgagggg ctgcctgagc ccctcaccct gagatggggc aaggaggagc 180
ctccttcac caccaagact aacacagtaa tcattgctgt tccggttgtc cttggagctg 240
tggcatcctc tggagctgtg atggcttttg tgatgaagag gaggagaaac acaggtggaa 300
aaggagggga ctatgctctg gctccaggct cccagagctc tgatagtctc ctcccagatt 360
gtaaagtgtg aagacagctg cctggtgtgg acttggtgac agacaatgtc ttcacacatc 420
tcctgtgaca tccagagacc tcagttctct ttagtcaagt gtctgatgtt ccctgtgagt 480
ctgcgggctc aaagtgaaga actgtggagc ccagtcacc cctgcacacc aggaccctat 540
ccctgcactg ccctgtgttc ccttcacag ccaaccttgc tgctccagcc aaacattggt 600
ggacatctgc agcctgtcag ctccatgcta ccctgacctt caactcctca cttccacact 660
gagaataata atttgaatgt ggggtggctgg agagatggct cagcgctgac tgccttcca 720
aaggtcctga gttcaaatcc cagcaaccac atggtggctc acaaccatct gtaatgggat 780
ctaataccct cttctgcagt gtctgaagac asctacagtg tacttacata taataataaa 840
taag 844

```

<210> 133

<211> 601

<212> DNA

<213> Homo sapiens

<400> 133

```

ggccggggcgc gcgcgcccc gccacacgca cgccgggggt gccagtttat aaaggagag 60
agcaagcagc gagtcttgaa gctctgtttg gtgctttgga tccatttcca tccgtcctta 120
cagcgcctcg tcagactcca gcagccaaga tggatgaagc gatcgagagc aagactgctt 180
ttcaggaagc cttggacgct gcaggtgata aacttgtagt agttgacttc tcagccacgt 240
gggtgtgggc ttgcaaaatg atcaagcctt tctttcattc cctctctgaa aagtattcca 300
acgtgatatt ccttgaagta gatgtggatg actgtcagga tgttgcttca gagtgtgaag 360
tcaaatgat gccaacattc cagtttttta agaagggaca aaagggtgggt gaattttctg 420
gagccaataa ggaaaagcct gaagccacca ttaatgaatt agtctaata tgttttctga 480
aaatataacc agccattggc tatttaaaac ttgtaatttt ttaattttac aaaaatataa 540
aatatgaaga cataaacccm gttgccatct gcgtgacaat aaaacattaa tgctaacact 600
t 601

```

<210> 134

<211> 421

<212> DNA

<213> Homo sapiens

<400> 134

```

tcacataaga aatttaagca agttacrcta tcttaaaaaa cacaacgaat gcattttta 60
agagaaaacc ttccctccct ccacctccct cccccaccct cctcatgaat taagaatcta 120
agagaagaag taaccataaa accaagtttt gtggaatcca tcatccagag tgcctacatg 180
gtgattaggt taatattgcc ttcttacaata atttctattt taaaaaaat tataaccttg 240
attgcttatt acaaaaaaat tcagtacaaa agttcaatat attgaaaaat gcttttcccc 300
tccttcacag caccgtttta tatatagcag agaataatga agagattgct agtctagatg 360
gggcaatctt caaattacac caagacgcac agtggtttat ttaccctccc cttctcataa 420
g 421

```

<210> 135

<211> 511

<212> DNA

<213> Homo sapiens

<400> 135

```

ggaaggatt caagaattag aggacttgct tgctrragaa aaagacaact ctgcgcgat 60
gctgacagac aaagagagag agatggcgga aataagggat caaatgcagc aacagctgaa 120
tgactatgaa cagcttcttg atgtaaagtt agccctggac atggaatca gtgcttacag 180

```

```

gaaactctta gaaggcgaag aagagaggtt gaagctgtct ccaagccctt cttcccgtgt 240
gacagtatcc cgagcatcct caagtcgtag tgtaccgtac aactagagga aagcggaaga 300
gggttgatgt ggaagaatca gaggcgaagt agtagtgta gcatctctca ttccgcctca 360
accactggaa atgtttgcat cgaagaaatt gatgttgatg ggaaatttat cccgcttgaa 420
gaacacttct gaacaggatc aaccaatggg aaggcttggg agatgatcag aaaaattgga 480
gacacatcag tcagttataa atatacctca a                                     511

```

<210> 136
 <211> 341
 <212> DNA
 <213> Homo sapiens

```

<400> 136
catgggtttc accaggttgg ccaggtctgt cttgaactsc tgacctcagg tgatccaacc 60
gcctcggcct cccaaagtgc tgggattaca ggogtgagcc accacgccg gccccaag 120
ctgtttcttt tgtcttttagc gtaaaagtct cctgccatgc agtatctaca taactgacgt 180
gactgccagc aagctcagtc actccgtggt ctttttctct ttccagttct tctctctctc 240
ttcaagttct gcctcagtg aagctgcagg tccccagtta agtgatcagg tgagggttct 300
ttgaacctgg ttctatcagt cgaattaatc cttcatgatg g                                     341

```

<210> 137
 <211> 551
 <212> DNA
 <213> Homo sapiens

```

<400> 137
gatgtgttgg accctctgtg tcaaaaaaaa cctcacaagg aatccctgc tcattacaga 60
agaagatgca tttaaaatat gggtratttt caacttttta tctgaggaca agtatccatt 120
aattattgtg tcagaagaga ttgaatacct gcttaagaag cttacagaag ctatgggagg 180
aggttggcag caagaacaat ttgaacatta taaaatcaac tttgatgaca gtaaaaaatg 240
cctttctgca tgggaactta ttgagettat tggaaaaggga cagttagca aaggcatgga 300
ccggcagact gtgtctatgg caattaatga agtctttaat gaacttatat tagatgtgtt 360
aaagcagggg tacatgatga aaaagggcca cagacggaaa aactggactg aaagatgggt 420
tgtactaaaa cccaacataa tttcttacta tgtgagttag gatctgaagg ataagaaagg 480
agaactttct ttggatgaaa attgtctgtt agaagtcctt gcctgacaaa agatggaaag 540
aatgccttt t                                     551

```

<210> 138
 <211> 531
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 490
 <223> n = A,T,C or G

```

<400> 138
gactggttct ttatttcaaa aagacacttg tcaatattca gtrtcaaac agttgcacta 60
ttgattttct tttctcccaa tcggccccaa agagaccaca taaaaggaga gtacatttta 120
agccaataag ctgcaggatg tacacctaac agacctccta gaaaccttac cagaaaaatg 180
ggactgggta ggggaaggaaa cttaaaagat caacaaactg ccagccacag gactgcagag 240
gctgtcacag ccagatgggg tggccagggt gccacaaacc caaagcaaag tttcaaaata 300
atataaaatt taaaaagttt tgtacataag ctattcaaga tttctccagc actgactgat 360
acaaagcaca attgagatgg cacttctaga gacagcagct tcaaacccag aaaagggatg 420
tgagatgaag ttccacatgg ctaaatcagt ggcaaaaaca cagtcttctt tctttctttc 480
tttcaaggan gcaggaaagc aattaagtgg tcaccttaac ataaggggga c                                     531

```

<210> 139
<211> 521
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 517
<223> n = A,T,C or G

<400> 139
tgggtgggca ccatggctgg gatcaccacc atcgaggcgg tgaagcgcaa gatccaggtt 60
ctgcagcagc aggcagatga tgcagaggag cgagctgagc gcctccagcg agaagttgag 120
ggagaagagc gggcccgga acaggctgag gctgagggtg cctccttga cctgtaggac 180
cagctggttg aagaagagct ggaccgtgct caggagcgcc tggccactgc cctgcaaaaag 240
ctggaagaag ctgaaaaagc tgcctgatgag agtgagagag gtatgaaggt tattgaaaac 300
cgggccttaa aagatgaaga aaagatggaa ctccaggaaa tccaactcaa agaagctaag 360
cacattgcag aagaggcaga taggaagtat gaagaggtg ctcgtaagtt ggtgatcatt 420
gaaggagact tggaaaccga cagaaggaac gagcttgagc ttggcaaaaag tcccggtgcc 480
cagagatggg atgaaccaga ttagactgat ggaccanaac c 521

<210> 140
<211> 571
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 7
<223> n = A,T,C or G

<400> 140
aggggcngcg ggtgcgtggg ccactgggtg accgacttag cctggccaga ctctcagcac 60
ctggaagcgc cccgagagtg acagcgtgag gctgggaggg aggacttggc ttgagcttgt 120
taaaactctgc tctgagcctc cttgtgcgct gcatttagat ggctcccga aagaagggtg 180
gcgagaagaa aaagggcgt tctgccatca acgaagtggg aacccgagaa tacaccatca 240
acattcacia gcgcattcat ggagtggtgct tcaagaagcg tgcacctcg gcactcaaag 300
agattcgaa atttgccatg aaggagatgg gaactccaga tgtgcgcatt gacaccaggc 360
tcaaaaagc tgtctgggcc aaaggaataa ggaatgtgcc ataccgaatc cgggtgtcgg 420
ctgtccagaa aacgtaatga ggatgaagat tcaccaaata agctatatac tttggttacc 480
tatgtacctg ttaccacttt caaaaatcta cagacagtca atgtggatga gaactaatcg 540
ctgatcgtca gatcaataa agttataaaa t 571

<210> 141
<211> 531
<212> DNA
<213> Homo sapiens

<400> 141
tcgggagcca cacttgcccc tcttcctctc caaagsgcca gaacctcctt ctctttggag 60
aatggggagg cctcttgagg acacagaggg tttcaccttg gatgacctct agagaaattg 120
cccaagaagc ccacttctg gtcccaacct gcagacccca cagcagtcag ttggtcaggc 180
cctgctgtag aaggtcactt ggctccattg cctgcttcca accaatgggc agggagagaag 240
gcctttattt ctgcccacc cattctctct gtaccagcac ctccgttttc agtcagtgtt 300
gtccagcaac ggtaccgttt acacagtcac ctccagacaca ccatttcacc tcccttgcca 360
agctgttagc cttagagtga ttgcagtga cactgtttac acaccgtgaa tccattccca 420
tcagtccatt ccagttggca ccagcctgaa ccatttggtta cctggtgtta actggagtc 480
tgtttacaag gtggagtcgg ggcttgctga cttctcttca tttgagggca c 531

<210> 142
<211> 491
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 410
<223> n = A,T,C or G

<400> 142
acctagacag aaggtgggtg agggaggact ggtaggaggc tgaggcaatt ccttggtagt 60
ttgtcctgaa accctactgg agaagtcagc atgaggcacc tactgagaga agtgcccaga 120
aactgctgac tgcattctgtt aagagttaac agtaaaggag tagaagtgtg tttctgaatc 180
agagtgggag cgtctcaagg gtcccacagt ggaggtccct gagctacctc ccttccgtga 240
gtgggaagag tgaagcccat gaagaactga gatgaagcaa ggatgggggt cctgggctcc 300
aggcaagggc tgtgctctct gcagcagggg gccccacgag tcagaagaaa agaactaatc 360
atttitttga agaaaccttg cccggatact agcggaaaaa tggaggcggn ggtgggggca 420
caggaaagtg gaagtgattt gatggagagc agagaagcct atgcacagtg gccgagtcca 480
cttgtaaagt g 491

<210> 143
<211> 515
<212> DNA
<213> Homo sapiens

<400> 143
ttcaagcaat tgtaacaagt atatgtagat tagagtgagc aaaatcatat acaattttca 60
tttccagttg ctattttcca aattgttctg taatgtcggt aaaattectt aaaaattaac 120
aaagccaaaa attatattta tgacaagaaa gccatcccta cattaatctt acttttccac 180
tcaccggccc atctccttcc tctttttcct aactatgcca ttaaaactgt tctactgggc 240
cgggcgtgtg gctcatgcct gtaatcccag cattttggga ggccaaggca gccggatcat 300
gaggtcaaga gattgagacc atcctggcca acatggtgaa accccgcctc gactaagaat 360
acaaaaatta gctgggcatg gtggcgcatg cctgtagtct cagctactcg ggaggctgag 420
gcagaagaat cgcttgaacc cgggaggcag aggatgcagt gagccccgat cgcgccactg 480
cactctagcc tgggcgacag actgagactc tgctc 515

<210> 144
<211> 340
<212> DNA
<213> Homo sapiens

<400> 144
tgtgccagtc tacaggccta tcagcagcga ctccctcagc aacagatggg gtcccctggt 60
cagcccaacc ccagagccc ccagcagcat atgctcccaa atcaggccca gtcccacac 120
ctacaaggcc agcagatccc taattctctc tccaatcaag tgcgctctcc ccagcctgtc 180
ccttctccac ggccacagtc ccagccccc cactccagtc cttccccaag gatgcagcct 240
cagccttctc cacaccacgt ttcccacag acaagttccc cacatcctgg actggtagtt 300
gcccaggcca accccatgga acaaggcat tttgccagcc 340

<210> 145
<211> 630
<212> DNA
<213> Homo sapiens

<400> 145
tgtaaaaact tgtttttaat tttgtataaa ataaagggtg tccatgccca cgggggctgt 60

```

aggaaatcca agcagaccag ctgggggtggg gggatgtagc ctacctcggy ggactgtctg 120
tcctcaaaac gggctgagaa ggcccgtcag gggcccaggt cccacagaga ggcttgggat 180
actcccccac cccgaggggg agactgggca gtggggagcc cccatcgtc cccagagggtg 240
gccacaggct gaaggagggg cctgaggcac cgcagcctgc aacccccagg gctgcagtcc 300
actaaccttt tacagaataa aaggaaacatg gggatgggga aaaaagcacc aggtcaggca 360
gggcccaggg gcccagatc ccaggagggc caggactcag gatgccagca ccaccctagc 420
agctcccaca gctcctggca caggaggccg ccacggattg gcacaggccg ctgctggcca 480
tcacgccaca tttggagaac ttgtcccagc agaggtcagc tcggaggagc tcctcgtggg 540
cacacactgt acgaacacag atctccttgt taatgacgta cacacggcgg aggtcgcggg 600
gacagggcac gggaggtctc agccccactt

```

<210> 146
 <211> 521
 <212> DNA
 <213> Homo sapiens

```

<400> 146
atggctgtctg gatttaggtg gtaatagggg ctgtgggcca taaatctgaa gccttgagaa 60
ccttgggtct ggagagccat gaagagggaa ggaagagagg gcaagtcctg aacctaacca 120
atgacctgat ggattgctcg accaagacac agaagtgaag tctgtgtctg tgcactccc 180
acagactgga gtttttggtg ctgaatagag ccagttgcta aaaaattggg ggtttggtga 240
agaaatctga ttgttgtgtg tattcaatgt gtgattttaa aaataaacag caacaacaat 300
aaaaacctg actggctgtt tttccctgt attctttaca actatTTTT gaccctctga 360
aaatttatat acttcacctt aatggaagac tgctgtgttt gtggaaattt tgtaattttt 420
taattttttt tattctctct cctttttatt ttgcctgcag aatccgttga gagactaata 480
aggcttaata ttaatttgat ttgtttaata tgtatataaa t 521

```

<210> 147
 <211> 562
 <212> DNA
 <213> Homo sapiens

```

<400> 147
ggcatgcgag cgcactcgcc ggacgcaagg gcggcgggga gcacacggag cactgcaggc 60
gccgggttgg gacagcgtct tcgctgctgc tggatagtcg tgttttcggg gatcgaggat 120
actcaccaga aaccgaaaat gccgaaacca atcaatgtcc gagttaccac catggatgca 180
gagctggagt ttgcaatcca gccaaataca actggaaaac agctttttga tcaggtggta 240
aagactatcg gcctccggga agtgtggtac ttggcctcc actatgtgga taataaagga 300
tttccctacc ggctgaagct ggataagaag gtgtctgccc aggaggtcag gaaggagaat 360
cccctccagt tcaagtccg ggccaaagt ctaccctgaa gatgtggctg aggagctcat 420
ccaggacatc acccgaaaac tttcttctc tcaagtgaag gaaggaaatc ttagcgatga 480
gatctactgc cccccttgar actgccgtgc tcttgggggc ctacgcttgt gcatgccaaag 540
tttggggact accaccaaga ag

```

<210> 148
 <211> 820
 <212> DNA
 <213> Homo sapiens

```

<400> 148
gaaggagtcg ggatactcag cattgatgca ccccaatttc aaagcggcat tcttcggcag 60
gtctctggga caatctctag ggtcactacc tggaaactcg ttaggggtaca actgaatgct 120
gaaaggaag aacacctgca gaaccggaca gaaattcacc ccggcgatca gctgattgat 180
ctcggctgac cagaagtcat ggctaaagat gacgaggacg ttgtcaattc cctgggcttt 240
tcgaagttag tccagcagca gtctgaggta ttggggccgg ttatgcacct ggaccaccag 300
caccagctcc cggggggccc aggtgccagc cttatctaca ttctcagggt tctgatcaaa 360
gttcagctgg tacaccagg accggtaccg cagcgtcagg ttgtccgctc gggctggggg 420
accgccggga ccagggaagc cgccgacacg ttggagaccg tgcggatgcc cacagccaca 480

```

```

gaggggtggt cccacccgcg gccgcgggca ccccgcgcggt gttcggcgctc cagcaacggt 540
ggggcgaggg cctcgttctt cctttgtcgc ccattgctgc tccagaggac gaagccgcag 600
gcggccacca cgagcgctcag gattagcacc ttccgtttgt agatgcggaa cctcatggtc 660
tccagggcgc ggagcgcgag tacagctcga gcgtcggcgc cgcgctagg agccgcggct 720
cggtctcgtc tccgtcctct ccattcagca ccacgggtcc cggaaaaagc tcagccscgg 780
tcccaaccgc accctagctt cgttacctgc gcctcgcttg 820

```

<210> 149
 <211> 501
 <212> DNA
 <213> Homo sapiens

```

<400> 149
cagattttta tttgcagtcg tcaactggggc cgtttcttgc tgcttatttg tctgctagcc 60
tgctcttcca gctgcattggc caggcgcaag gccttgatga catctgcag ggctgagaaa 120
tgcttggtgt gctgggccag agcagattcc gctttgttca caaaggcttc caggctcatag 180
tctgggtgct cgggtcatctc agagagctca agccagtctg gtccttgctg tatgatctcc 240
ttgagctctt ccatagcctt ctctccagc tccctgatct gagtcattggc ttcgttaaag 300
ctggacatct gggaagacag ttctctctct tctttggata aattgcctgg aatcagcgcc 360
ccgttagagc aggtctccat ctcttctgtt tccatttgaa tcaactgctc tccactgggc 420
ccactgtggg ggctcagctc cttgaccctg ctgcatactt taagggtgtt taaaggatat 480
tcacaggagc ttatgcctgg t 501

```

<210> 150
 <211> 511
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 457, 479
 <223> n = A,T,C or G

```

<400> 150
ctctcttgg tacatgaacc caagttgaaa gtggacttaa caaagtatct ggagaaccaa 60
gcattctgct ttgactttgc atttgatgaa acagcttcca atgaagttgt ctacagggtc 120
acagcaaggc cactggtaca gacaatcttt gaaggtggaa aagcaacttg ttttgcata 180
ggccagacag gaagtggcaa gacacatact atggcgagg agctctctgg gaaagcccag 240
aatgcacca aaggatctta tgccatggcc ttccgggacg tcttcttctg aagaatcaac 300
cctgctaccg gaagtgggac ctggaagtct atgtgacatt cttcgagatc tacaatggga 360
agctgtttga cctgctcaac aagaaggcca agcttgccgc tgctggaaga cggcaagcaa 420
caggtgcaag tgggtggggc ttgcaggaa atctggntaa ctctgcttga tgatggcatt 480
caagatgatc gacatgggca gcgcctgcag a 511

```

<210> 151
 <211> 566
 <212> DNA
 <213> Homo sapiens

```

<400> 151
tcccgaattc aagcgacaaa ttggawagtg aaatggaaga tgcctatcat gaacatcagg 60
caaatctttt gcgccaagat ctgatgagac gacaggaaga attaagacgc atggaagaac 120
ttcacaatca agaaatgcag aaacgtaaaag aaatgcaatt gaggcaagag gaggaacgac 180
gtagaagaga ggaagagatg atgattcgct aacgtgagat ggaagaacaa atgagggccc 240
aaagagagga aagltacagc cgaatgggct acatggatcc acgggaaaga gacatgcgaa 300
tgggtggcgg aggagcaatg aacatgggag atccctatgg ttcaggaggc cagaaatttc 360
cacctctagg aggtgggtgt ggcatagggt atgaagctaa tcttggcggt ccaccagcaa 420
ccatgagtgg ttccatgatg ggaagtgaca tgcgtactga gcgctttggg cagggaggtg 480

```

cggggacctgt ggggtggacag ggtcctagag gaatggggcc tggaaactcca gcaggatatg 540
gtagagggag agaagagtac gaaggc 566

<210> 152
<211> 518
<212> DNA
<213> Homo sapiens

<400> 152
ttcgtgaaga ccctgactgg taagaccatc actctcgaag tggagcccg gtgacacccat 60
tgagaatgtc aaggcaaaaga tccaagacaa ggaaggcatc cctcctgacc agcakagggtt 120
gatctttgct gggaaacagc tggaaagatgg acgcaccctg tctgactaca acatccagaa 180
agagtccacc ctgcacctgg tgctccgtct cagaggtggg atgcaaatct tctggaagac 240
cctgactggt aagaccatca ccctcgaggt ggagcccagt gacaccatcg agaattgtcaa 300
ggcaaaagatc caagataagg aaggcatccc tcttgatcag cagaggttga tctttgctgg 360
gaaacagctg gaagatggac gcaccctgtc tgactacaac atccagaaag agtccactct 420
gcacttggtc ctgctgctga ggggggggtgt ctaagtttcc ccttttaagg tttcaacaaa 480
tttcattgca ctttcctttc aataaagttg ttgcattc 518

<210> 153
<211> 542
<212> DNA
<213> Homo sapiens

<400> 153
gcgcgggtgc gtgggccact gggtgaccga cttagcctgg ccagactctc agcacctgga 60
agcgccccga gagtgcagc gtgaggctgg gagggaggac ttggcttgag cttgttaaac 120
tctgctctga gcctccttgt cgcctgcatt tagatggctc ccgcaaaaga ggggtggcgag 180
aagaaaaagg gccgttctgc catcaacgaa gtggttaacc gagaatacac catcaacatt 240
cacaagcgca tccatggagt gggcttcaag aagcgtgcac ctggggcact caaagagatt 300
cggaattttg ccattgaagg gatgggaact ccagatgtgc gcattgacac caggctcaac 360
aaagctgtct gggccaaagg aataaggaat gtgccatacc gaatccgtgt gcggctgtcc 420
agaaaaacgta atgaggatga agattcacca aataagctat atactttggt tacctatgta 480
cctgttacca ctttcaaaaa tctacagaca gtcaatgtgg atgagaacta atcgtgatc 540
gt 542

<210> 154
<211> 411
<212> DNA
<213> Homo sapiens

<400> 154
aattctttat ttaaatcaac aaactcatct tctcaagcc ccagaccatg gtaggcagcc 60
ctccctctcc atccctcac cccaccctt agccacagtg aagggaatgg aaaatgagaa 120
gccacgaggg ccctgcccag ggaaggctgc cccagatgtg tggtagacac agtcagtga 180
gctgtggctg gggcagcagc tgccacaggg tctccctat aaattaagtt cctgcagcca 240
cagctgtggg agaagcatac ttgtagaagc aaggccagtc cagcatcaga aggcagaggg 300
agcatcagt actcccagcc atggaatgaa cggaggacac agagctcaga gacagaacag 360
gccaggggga agaaggagag acagaatagg ccagggcatg gcggtgaggg a 411

<210> 155
<211> 421
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 173

<223> n = A,T,C or G

<400> 155

```
tgatgaatct ggggtgggctg gcagtagccc gagatgatgg gctcttctct ggggatccca 60
actggttccc taagaaatcc aaggagaatc ctcggaactt ctcggataac cagctgcaag 120
agggaacaaa cgtgatcggg ttacagatgg gcaccaaccg cggggcgctc cangcaggca 180
tgactggcta cgggatgcca cgccagatcc tctgatccca ccccaggcct tgcctctgcc 240
ctcccacgaa tggttaatat atatgtatgt atatatttta gcagtgcacat tcccagagag 300
ccccagagct ctcaagctcc tttctgtcag ggtggggggg tcaagcctgt cctgtcacct 360
ctgaagtgcc tgctggcatc ctctcccca tgcttactaa tacattccct tcccacatgc 420
c 421
```

<210> 156

<211> 670

<212> DNA

<213> Homo sapiens

<400> 156

```
agcggagctc cctccccctg tggctacaac ccacacacgc caggctcagg catcgagcag 60
aactccagcg actgggtaac cactgacatt cagggtgaagg tgcgggacac ctacctggat 120
acacaggtgg tgggacagac aggtgtcatc cgcagtgtca cggggggcat gtgctctgtg 180
tacctgaagg acagtggaaa ggttgtcagc atttccagtg agcacctgga gcctatcacc 240
bccaccaaga acaacaagggt gaaagtgtgc ctgggcgagg atcgggaagc cacgggctgc 300
ctactgagca ttgatgttga ggaatggcatt gtccgtatgg acctgatga gcagctcaag 360
atcctcaacc tccgcttccct ggggaagctc ctggaagcct gaagcaggca gggccggtgg 420
acttcgtcgg atgaagatgt atectccttc ctccctggc ccttggtgtg gacacaagat 480
cctcctgcag ggctaggcgg attgttctgg atttcccttt gtttttccct ttaggtttcc 540
atcttttccc tccctgggtc tcattggaat ctgagtagag tctggggcag ggtccccacc 600
ttcctgtacc tccctccccc agcttgcctt tgtgtgtacc tctttcaata aaaagaagct 660
gtttggtcta 670
```

<210> 157

<211> 421

<212> DNA

<213> Homo sapiens

<400> 157

```
ggttcacagc actgctgctt gtgtgttgcc ggccaggaaat tccaggctca caaggctatc 60
ttagcagctc gttctccggg ttttagtgcc atgtttgaac atgaaatgga ggagagcaaa 120
aagaatcgag ttgaaatcaa tgatgtggag cctgaagttt ttaaggaaat gatgtgcttc 180
atttacacgg ggaaggctcc aaacctcgac aaaatggctg atgatttgct ggcagctgct 240
gacaagtatg ccctggagcg cttaaaggtc atgtgtgagg atgcccctctg cagtaacctg 300
tccgtggaga acgctgcaga aattctcatc ctggccgacc tccacagtgc agatcagttg 360
aaaactcagg cagtggattt catcaactat catgcttcgg atgtcttgga gacctcttgg 420
g 421
```

<210> 158

<211> 321

<212> DNA

<213> Homo sapiens

<400> 158

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tcgtagccat ttttctgctt ctttggagaa tgacgccaca ctgactgctc attgtcgttg 60
gttccatgcc aattgggtgaa atagaacctc atccggtagt ggagccggag ggacatcttg 120
tcatcaacyg lgatggttgc atttggagca taccagagct tgggtgtctc gccatacagg 180
gcaaagaggt tgtgacaaa aggagagata cggcatgcct gtgcagccct gatgcacagt 240
tcctctgctg tgtactctcc actgcccagc cggaggggct cctgtgccga cagatagaag 300
atcaactcca cccctgctt g 321
```

<210> 159
<211> 596
<212> DNA
<213> Homo sapiens

<400> 159
tggcacactg ctcttaagaa actatgawga tctgagattt ttttgtgtat gtttttgact 60
cttttgagtg gtaatcatat gtgtctttat agatgtacat acctccttgc acaaatggag 120
gggaattcat ttctcatcact gggagtgtcc ttagtgtata aaaaccatgc tggatatagg 180
cttcaagttg taaaaatgaa agtgacttta aaagaaaata ggggatggtc caggatctcc 240
actgataaga ctgtttttaa gtaacttaag gacctttggg tctacaagta tatgtgaaaa 300
aaatgagact tactgggtga ggaaattcat tgtttaaga tggctgtgtg tgtgtgtgtg 360
tgtgtgtgtg ttgtgtgtgt ttttgtttt taaggaggag aatttattat ttaccgttgc 420
ttgaaattac tgkgtaaata tatgtytgat aatgatttgc tytttgvcma ctaaaattag 480
gvctgtataa gtwctaratg cmtccctggg kgttgatytt ccmagatatt gatgatamcc 540
cttaaaattg taaccygcct ttttcccttt gctytcatt aaagtctatt cmaaag 596

<210> 160
<211> 515
<212> DNA
<213> Homo sapiens

<400> 160
gggggtaggc tctttattag acggttattg ctgtactaca gggtcagagt gcagtgtgaa 60
cagtgtcaga gggccgcgtt cagcccaaga atgtggattt tctctcccta ttgatcacag 120
tgggtgggtt tcttcagaaa agcccagag gcagggacca gtgagctcca aggttagaag 180
tggaactgga aggtttcagt cacatgtctc ttccacgctt ccaggctggg cagcaaggag 240
gagatgccca tgacgtgcca ggtctcccca tctgacacca gtgaagtctg gtaggacagc 300
agccgcacgc ctgcctctgc caggaggcca atcatggtag gcagcattgc agggtcagag 360
gtctgagtcg gaataggag caggggcagg tccctgcgga gaggcacttc tggcctgaag 420
acagctccat tgagccctg cagtacaggy gtagtgcctt ggaccaagcc cacagcctgg 480
taaggggagc ctgccagggc caggccagc aggca 515

<210> 161
<211> 936
<212> DNA
<213> Homo sapiens

<400> 161
taatttctta gtcgtttgga atccttaagc atgcaaaagc tttgaacaga agggttcaca 60
aaggaaaccag ggttgtctta tggcatccag ttaagccaga gctgggaatg cctctgggtc 120
atccacatca ggagcagaag cacttgactt gtccgtcctg ctgccacggt ttgggcgccc 180
accacgccca cgtccacctc gtctctccct gccgccagc cctgggcggc caaggtctcc 240
aaaattgac tccagctgag acgttatatc atttgcctgc ttccggaaat gatgggtccat 300
aaccgaatct tcagcatgag cctcttact ctttgattta tgaagaacaa atcccttctt 360
ccactgccca tcagcacctt catttggttt toggatatta aattctactt ttgccgggtc 420
cttattttga atagccttcc actcatccaa agtcatctct tttggacctt cctcttltac 480
ctcttcaact tcattctcct tattttcagt gtctgccact ggatgatgtt cttcaccttc 540
aggtgtttcc tcagtcacat ttgattgac caagtcagtt aattcgtctt tgacagttcc 600
ccagttgtga gatccgtac ctccacgttt gtccctcgtc ttcaggccag atctatcact 660
tccactatgc ctatcaaatt cagctttgcc acgagaatca aatccatctc ctccggccat 720
tccacgtcca cggccccctc gacctcttc aagaccacca cgacctgaa taggtcggtc 780
aataatcggt ctatcaactg aaaattcgcc tccctcacc ttttcttcaa gtggcctttc 840
gaatcttctg tcacgaggtg gtgcctcttc tggctctcta tcaattattt tcccttcacc 900
ctgaagttgt tgatcaggtc ttcttccaa cgtgtc 936

<210> 162

<211> 950
<212> DNA
<213> Homo sapiens

<400> 162
aagcggatgg acctgagtc gccgaatcct agccctctcc cttgggcctg ctgtgggtgt 60
cgacatcagt gacagacgga agcagcagac catcaaggct acgggaggcc cggggcgctt 120
gcgaagatga agtttggtcg cctctccttc cggcagcctt atgctggctt tgtcttaaat 180
ggaatcaaga ctgtggagac gcgctggcgt cctctgctga gcagccagcg gaactgtacc 240
atcgccgtcc acattgtctc cagggactgg gaaggcgatg cctgtcggga gctgctgtgt 300
gagagactcg gtagtactcc tgctcagatt caggccttgc tcaggaaagg ggaaaagttt 360
ggtcgaggag tgatagcggg actcgttgac attggggaaa ctttgcaatg ccccgagac 420
ttaactcccg atgaggttgt ggaactagaa aatcaagctg cactgaccaa cctgaagcag 480
aagtacctga ctgtgatttc aaacccaggg tggttactgg agcccatacc taggaaagga 540
ggcaaggatg tattccaggt agacatccca gagcacctga tccctttggg gcatgaagt 600
tgacaagtgt gggctcctga aaggaaatgt ccragagaaac cagctaaatc atggcacctt 660
caatttgcga tcgtgacgca gacctgtata aattaggtta aagatgaatt tccactgctt 720
tggagagtcc caccactaa gcactgtgca tgtaaacagg ttcctttgct cagatgaagg 780
aagttagggg tggggttttc cttgtgtgat gcctccttag gcacacaggc aatgtctcaa 840
gtactttgac cttagggtag aaggcaagc tgccagttaa tgtctcagca ttgtgtctaa 900
ttttggtcct gctagtttct ggattgtaca aataaatgtg ttgtagatga 950

<210> 163
<211> 475
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 301, 317, 331, 458, 464, 470
<223> n = A,T,C or G

<400> 163
tcgagcggcc gcccgggcag gtgtcggagt ccagcacggg aggcgtggtc ttgtagtgt 60
tctccgctg cccattgtct tccactcca cggcgatgtc gctgggtag aagcctttga 120
ccaggcaggc caggctgacc tggttcttgg tcatctctc cggggatggg gcagggtgt 180
acacctgtgg ttctcggggc tgccctttgg ctttggagat ggttttctcg atgggggctg 240
ggagggcttt gttggagacc ttgcaattgt actccttgcc attcaaccag tcctgggca 300
ngacgggtgag gacgctnacc acacggtacg ngctgggtga ctgctcctcc cgcggctttg 360
tcttggcatt atgcacctcc acgcggtcca cgtaccaatt gaacttgacc tcagggtctt 420
cgtggctcac gtccaccacc acgcatgtaa cctcaaanct cggncgcgan cagcg 475

<210> 164
<211> 476
<212> DNA
<213> Homo sapiens

<400> 164
agcgtgggtc cggccgaggc ctgaggttac atgcgtgggt gtggacgtga gccacgaaga 60
ccctgagggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa 120
gccgcgggag gagcagtaca acagcacgta ccgtgtgggt agcgtcctca ccgtcctgca 180
ccaggactgg ctgaatggca aggagtacaa gtgcaaggte tccaacaaag ccctcccgag 240
ccccatcgag aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac 300
cctgccccca tcccgggagg agatgaccaa gaaccaggte agcctgacct gcctggtcaa 360
aggcttctat cccagcgaca tcgcccgtgg agtgggagag caatgggcag ccggagaaca 420
actacaagac cagcctctcc gtgctggact ccgacacctg ccgggcggcc gctcga 476

<210> 165

<211> 256
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 10, 37, 249
<223> n = A,T,C or G

<400> 165
agcgtgggtt cggccgaggt cccaaccaag gctgcancct ggatgccatc aaagtcttct 60
gcaacatgga gactgggtgag acctgcgtgt accccactca gccagtggtg gccagaaga 120
actggtacat cagcaagaac cccaaggaca agaggcatgt ctggttcggc gagagcatga 180
ccgatggatt ccagttcgag tatggcggcc agggctccga ccctgccgat gtggacctgc 240
ccgggcggnc gctcga 256

<210> 166
<211> 332
<212> DNA
<213> Homo sapiens

<400> 166
agcgtgggtc cggccgaggt caagaacccc gcccgcacct gccgtgacct caagatgtgc 60
cactctgact ggaagagtgg agagtactgg attgacccca accaaggctg caacctggat 120
gccataaag tcttctgcaa catggagact ggtgagacct gcgtgtacct cactcagccc 180
agtgtggccc agaagaactg gtacatcagc aagaacccca aggacaagag gcatgtctgg 240
ttcggcgaga gcatgaccga tggattccag ttogagtatg gcggccaggg ctccgacct 300
gccgatgtgg acctgcccgg gcggccgctc ga 332

<210> 167
<211> 332
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 77, 109, 136, 184, 198
<223> n = A,T,C or G

<400> 167
tcgagcggtc gcccgggcag gtccacatcg gcagggtcgg agccctggcc gccatactcg 60
aactggaatc catcggnat gctctcgccg aaccagacat gcctcttgc cttggggttc 120
ttgctgatgt accagntctt ctgggccaca ctgggctgag tggggtaacac gcaggtctca 180
ccantctcca tgttgcanaa gactttgatg gcatccaggt tgcagccttg gttggggta 240
atccagtact ctccactctt ccagacagag tggcacatct tgaggtcacg gcaggtgcgg 300
gcgggggtct tgacctcggg cgcgaccacg ct 332

<210> 168
<211> 276
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 72, 84
<223> n = A,T,C or G

<400> 168

```

tcgagcggcc gcccgggcag gtcctcctca gagcggtagc tgttcttatt gccccggcag 50
cctccataga tnaagttatt gcangagttc ctctccacgt caaagtacca gcgtgggaag 120
gatgcacggc aaggcccagt gactgcgttg gcggtgcagt attcttcata gttgaacata 180
tcgctggagt ggacttcaga atcctgcctt ctgggagcac ttgggacaga ggaatccgct 240
gcattctcgc tgggtggacct cggccgcgac cacgct 276

```

<210> 169
 <211> 276
 <212> DNA
 <213> Homo sapiens

```

<400> 169
agcgtggtcg cggccgaggt ccaccagcag gaatgcagcg gattcctctg tcccaagtgc 60
tcccagaagg caggattctg aagaccacto cagcgatatg ttcaactatg aagaatactg 120
caccgccaac gcagtcactg ggccttgccg tgcctccttc ccacgctggt actttgacgt 180
ggagaggaac tcctgcaata acttcctcta tggaggctgc cggggcaata agaacagcta 240
ccgctctgag gaggacctgc ccgggcggcc gctcga 276

```

<210> 170
 <211> 332
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 294
 <223> n = A,T,C or G

```

<400> 170
tcgagcggcc gcccgggcag gtccacatcg gcagggtcgg agccctggcc gccatactcg 60
aactggaatc catcggtcat gctctcgccg aaccagacat gcctcttgtc cttggggttc 120
ttgctgatgt accagttctt ctgggccaca ctgggctgag tggggtacac gcaggtctca 180
ccagtcacca tgttgacagaa gactttgatg gcacccaggt tgcagccttg gttggggtca 240
atccagtact ctccactctt ccagccagaa tggcacatct tgaggtcacg gcangtgcgg 300
gcgggggtct tgacctcgcc cgcgaccacg ct 332

```

<210> 171
 <211> 333
 <212> DNA
 <213> Homo sapiens

```

<400> 171
agcgtggtcg cggccgaggt caagaacccc cggccgcacc tgccgtgacc tcaagatgtg 60
ccactctggc tggagagatg gagagtactg gattgacccc aaccaaggct gcaacctgga 120
tgccatcaaa gtcttctgca acatggagac tgggtgagacc tgcgtgtacc ccactcagcc 180
cagtgtggcc cagaagaact ggtacatcag caagaacccc aaggacaaga ggcatgtctg 240
gtcggcgagc agcatgaccg atggattcca gttcgagtat ggcgggcagg gctccgaccc 300
tgccgatgtg gacctgcccg ggccggccgct cga 333

```

<210> 172
 <211> 527
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 46, 125, 140, 148, 220, 229, 291, 388, 456
 <223> n = A,T,C or G

<400> 172

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agcgtggtcg cggccgaggt cctgtcagag tggcactggt agaagntcca ggaaccctga 60
actgtaaggg ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagtgt 120
cctgnaatgg ggcccatgan atggttgntc gagagagagc ttcttgctct acattcggcg 180
ggtatggtct tggcctatgc cttatggggg tggccgttgn gggcggtgng gtccgctaa 240
aaccatgttc ctcaaagatc atttggtgcc caacactggg ttgctgacca naagtgccag 300
gaagctgaat accatttcca gtgtcatacc caggggtggg gacgaaaggg gtcttttgaa 360
ctgtggaagg aacatccaag atctctgntc catgaagatt ggggtgtgga agggttacca 420
gttggggaag ctgctgtctc ttttccttcc aatcangggc tgcctcttct gaatattctt 480
cagggcaatg acataaattg tatattcgtt tcccggttcc aggccag 527
```

<210> 173

<211> 635

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 444, 453, 517, 540, 546, 551, 573, 593

<223> n = A,T,C or G

<400> 173

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tcgagcggcc gcccgggcag gtccaccaca cccaattcct tgctgggtatc atggcgagccg 60
ccacgtgccca ggattaccgg ctacatcatc aagtatgaga agcctgggtc tcctcccaga 120
gaagtgggtcc ctccggccccg ccctgggtgtc acagaggcta ctattactgg cctgggaaccg 180
ggaaccgaat atacaattta tgtcattgcc ctgaagaata atcagaagag cgagcccctg 240
attggaagga aaaagacaga cgagcttccc caactggtaa cccttccaca cccaatctt 300
catggaccag agatcttgga tgttccttcc acagttcaaa agacccctt cgtcaccac 360
cctgggtatg aacttggaat tggatttcag ctctctggca ctctctgtca gcaaccag 420
gttgggcaac aatgatctt tgangaacat gnttttaggc ggaccacacc ggccacaacg 480
ggcaccacca taaggcatag gccagaaca tccccgcga atgtaggaca agaagctctn 540
tctcanacaa ncatctcatg ggccccattc cangacactt ctgagtacat canttcatg 600
catcctggtg gcactgataa aaacccttac agtta 635
```

<210> 174

<211> 572

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 457, 511, 520, 552, 568

<223> n = A,T,C or G

<400> 174

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agcgtggtcg cgggcgaggt cctgtcagag tggcactggt agaagttcca ggaaccctga 60
actgtaaggg ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagtgt 120
cctggaatgg ggcccatgag atggttgctc gagagagagc ttcttgctct acattcggcg 180
ggtatggtct tggcctatgc cttatggggg tggccgttgt gggcggtgtg gtccgctaa 240
aaccatgttc ctcaaagatc atttggtgcc caacactggg ttgctgacca gaagtgccag 300
gaagctgaat accatttcca gtgtcatacc caggggtggg gacgaaaggg gtcttttgaa 360
ctgtggaagg aacatccaag atctctgtgc catgaagatt ggggtgtgga agggttacca 420
gttggggaag ctgctgtgtc ttttccttc caatcanggg ctgctcttc tgattattct 480
tcagggcaat gacataaatt gtatattcgg ntcccggtg cagccaataa taataaccct 540
ctgtgacacc anggcggggc cgaagganct ct 572
```

<210> 175

<211> 372
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 247
<223> n = A,T,C or G

<400> 175
agcgtggctc cggccgaggt cctcaccaga ggtaccacct acaacatcat agtggaggca 60
ctgaaaagacc agcagaggca taagggttcgg gaagagggtt ttaccgtggg caactctgtc 120
aacgaaggct tgaaccaacc tacggatgac tcgtgctttg acccctacac agtttcccat 180
tatgccgttg gagatgagtg ggaacgaatg tctgaatcag gctttaaact gttgtgccag 240
tgcttangct ttggaagtgg tcatttcaga tgtgattcat ctatgatggg ccattgacaat 300
ggtgtgaact acaagattgg agagaagtgg gaccgtcagg gagaaaatgg acctgcccgg 360
gcggccgctc ga 372

<210> 176
<211> 372
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 251
<223> n = A,T,C or G

<400> 176
tcgagcggcc gcccgggcag gtccatttcc tccctgacgg tcccacttct ctccaatctt 60
gtagttcaca ccattgtcat ggcaccatct agatgaatca catctgaaat gaccacttcc 120
aaagccaaag cactggcaca acagttttaa gcctgattca gacattcgtt cccactcacc 180
tccaacggca taatgggaaa ctgtgttaggg gtcaaagcac gagtcacccg taggttggtt 240
caagccttcg ntgacagagt tgcccacggg aacaacctct tcccgaacct tatgcctctg 300
ctggtcttcc agtgcctcca ctatgatgtt gtaggtggta cctctggtga ggacctcggc 360
cgcgaccacg ct 372

<210> 177
<211> 269
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 94, 225
<223> n = A,T,C or G

<400> 177
agcgtggccg cggccgaggt ccattggctg gaacggcatc aacttggaag ccagtgatcg 60
tctcagcctt ggtctccag ctaatgggtga tggnggtctc agtagcatct gtcacacgag 120
cccttcttgg tgggtgaca ttctccagag tggtgacaac accctgagct ggtctgcttg 180
tcaaagtgtc cttaagagca tagacaotca cttcatattt ggcgnccacc ataagtctctg 240
atacaaccac ggaatgacct gtcaggaaac 269

<210> 178
<211> 529
<212> DNA
<213> Homo sapiens

<400> 178
tcgagcggcc gcccgggcag gtcctcagac cgggttctga gtacacagtc agtgtggttg 60
ccttgacga tgatattgag agccagcccc tgattggaac ccagtccaca gctattcctg 120
caccaactga cctgaagttc actcaggta caccacaag cctgagcgc cagtggacac 180
caccaatgt tcagctcact ggatattgag tgcgggtgac cccaaggag aagaccggac 240
caatgaaaga aatcaacctt gctcctgaca gctcatccgt ggttgatca ggacttatgg 300
cggccaccaa atatgaagtg agtgtctatg ctcttaagga cactttgaca agcagaccag 360
ctcagggtgt tgtcaccact ctggagaatg tcagcccacc aagaagggt cgtgtgacag 420
atgctactga gaccaccatc accattagct ggagaacaa gactgagacg atcactggct 480
tccaagttga tgccgttcca gccaatggac ctgcgccgc accacgctt 529

<210> 179
<211> 454
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 64
<223> n = A,T,C or G

<400> 179
agcgtggtcg cggccgaggt ctggccgaac tgccagtga cagggaagat gtacatgtta 60
tagntcttct cgaagtcccg ggccagcagc tccacgggt ggtctcctgc ctccaggcgc 120
ttctcattct catggatctt ctccaccgc agcttctgct tctcagtcag aaggttgttg 180
tctctatccc tctcatcacg ggtgaccagg acgttcttga gccagtccc catgcgcagg 240
gggaattcgg tcagctcaga gtccaggcaa ggggggatgt atttgcaagg ccgatgtag 300
tccaagtgga gcttgtggcc ctcttgggt ccctccaagg tgcactttgt ggcaagaag 360
tggcagggaag agtcgaaggt ctgtgtgtca ttgctgcaca ctttctcaaa ctgcaccaatg 420
ggggtctggc agacctgccc gggcgccgc tcga 454

<210> 180
<211> 454
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 55, 299, 317, 332, 342, 348
<223> n = A,T,C or G

<400> 180
tcgagcggcc gcccgggcag gtctgccag ccccatctg cgagtttgag aaggngtgca 60
gcaatgacaa caagaccttc gactcttctt gccacttctt tgccacaaag tgcaccttg 120
agggcaccaa gaaggccac aagctccacc tgactacat cgggccttgc aaatacatcc 180
ccccttgctt ggactctgag ctgaccgaat tccccctgcg catgcgggac tggctcaaga 240
acgtcctggt caccctgtat gagagggatg aggacaacaa ctttctgact gagaagcana 300
agctcgggtt gaagaanac catgagaatg anaagcgctt gnaggcanga gaccacccc 360
tggagctgct ggccggggac ttcgagaaga actataacat gtacatcttc cctgtacact 420
ggcagttcgg ccagacctcg gccgcgacca cgct 454

<210> 181
<211> 102
<212> DNA
<213> Homo sapiens

<220>

<221> misc feature
<222> 8, 47, 60, 67
<223> n = A,T,C or G

<400> 181
agcgtggntg cggacgacgc ccacaaagcc attgtatgta gttttanttc agctgcaaan 60
aataccncca gcatccacct tactaaccag catatgcaga ca 102

<210> 182
<211> 337
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> 169, 195, 253, 314
<223> n = A,T,C or G

<400> 182
tcgagcgggc gcccgggcag gtctggggcg atagcaccgg gcatattttg gaatggatga 60
ggtctggcac cctgagcagc ccagcgagga ctgtgtctta gttgagcaat ttggctagga 120
ggatagtatg cagcacgggt ctgagtctgt gggatagctg ccatgaagna acctgaagga 180
ggcgctggct ggtanggggt gattacaggg ctgggaacag ctctacact tgccattctc 240
tgcataact ggntagttag gcgagcctgg cgctcttctt tgcgctgagc taaagctaca 300
tacaatggct ttngggacct cggcgcgac cacgctt 337

<210> 183
<211> 374
<212> DNA
<213> Homo sapiens

<400> 183
tcgagcgggc gcccgggcag gtccattttc tccctgacgg tcccacttct ctccaattctt 60
gtagttcaca ccattgtcat gacacccatct agatgaatca catctgaaat gaccacttcc 120
aaagcctaag cactggcaca acagtttaaa gcctgattca gacattcgtt cccactcactc 180
tccaacggca taatgggaaa ctgtgtaggg gtcaaaagcac gagtcatccg taggttggtt 240
caagccttcg ttgacagaag ttgccacgg taacaacctc ttcccgaaac ttatgcctct 300
gctgggtctt caagtgcctc cactatgatg ttgtagggtg cactctcgtt gaggacctcg 360
gccgcgacca cgct 374

<210> 184
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> 30, 174, 248, 285, 306, 332, 345, 368
<223> n = A,T,C or G

<400> 184
agcgtgggtt gcggccgagg tctcaccan aggtgocacc tacaacatca tagtggaggc 60
actgaaagac cagcagaggc ataaggttcg ggaagaggtt gttaccgtgg gcaactctgt 120
caacgaaggc ttgaaccaac ctacggatga ctctgtctt gaccctaca cagnttccca 180
ttatgccgtt ggagatygat gggaaacgaat gtctgaatca ggctttaaac tggttgcca 240
gtgcttange tttggaagtg gtcatttcag atgtgattca tctanatggt gtcattgcaa 300
tggtgngaac tacaagattg gagagaagtg gnaccgtcag ggganaaaat ggacctgccc 360
ggcgccgcgc ctcga 375

<210> 185
<211> 148
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> 28, 36, 86
<223> n = A,T,C or G

<400> 185
agcgtggtcg cggccgaggt ctggcttctc getcangtga ttatcctgaa ccatccagge 60
caaataagcg ccggtatgac ccctgnattg gattgccaca cggtcacat tgcattgcaag 120
tttgcctgagc tgaaggaaaa gattgatc 148

<210> 186
<211> 397
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> 78
<223> n = A,T,C or G

<400> 186
tcgagcggcc gcccgggcag gtccaattga aacaaacagt tctgagaccg ttcttcacc 60
actgattaaag agtggggngg cgggtattag ggataatatt catttagcct tctgagcttt 120
ctgggcagac ttggtgacct tgccagctcc agcagccttc tgggccactg ctttgatgac 180
acccaccgca actgtctgtc tcatatcacg aacagcaaag cgacccaaag gtggatagtc 240
tgagaagctc tcaacacaca tgggcttgcc aggaaccata tcaacaatgg gcagcatcac 300
cagacttcaa gaatttaagg gccatcttcc agctttttac cagaacggcg atcaatcttt 360
tccttcagct cagcaaaactt gcatgcaatg tgagccg 397

<210> 187
<211> 584
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> 145, 286, 363, 365, 425, 433, 452, 462, 471, 512, 514, 534,
536, 540, 565, 583
<223> n = A,T,C or G

<400> 187
tcgagcggcc gcccgggcag gtccagaggg ctgtgctgaa gtttgctgct gccactggag 60
ccactccaat tgctggccgc ttactctctg gaaccttcac taaccagatc caggcagcct 120
tccgggagcc acggcttctt gtgntactg accccagggc tgaccaccag cctctcacgg 180
aggcatctta tgttaacctt cctaccattg cgtgtgtgaa cacagattct cctctgcgct 240
atgtggacat tgccatccca tgcaacaaca agggagctca ctcagngggg tttgatgtgg 300
tggtatgctgg ctcggaagt tctgcgcatg cgtggcacca ttcccgta acaccatgg 360
gangncatgc ctgatctgga cttctacaga gatcctgaag agattgaaa agaagaacag 420
gctgnttgct ganaaagcaa gtgaccaag angaaatttc angggtgaaa nggactgctc 480
ccgctcctga attcactgct actcaacctg angntgcaga ctggctctga aggnagnacan 540
gggccctctg ggcctattta agcancttcg gtgcgaaca cgnt 584

<210> 188
<211> 579
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 7, 136, 486
<223> n = A,T,C or G

<400> 188
agcgtgngtc gcgccgaggg tgctgaatag gcacagaggg cacctgtaca ccttcagacc 60
agtctgcaac ctcaggctga gtagcagtga actcaggagc gggagcagtc cattcaccct 120
gaaattcctc cttggncaact gccttctcag cagcagcctg ctcttctttt tcaatctctt 180
caggatctct gtagaagtac agatcaggca tgacctccca tgggtgttca cgggaaatgg 240
tgccacgcat gcgcagaact tcccagagca gcatccacca catcaaacc actgagtgag 300
ctccctgtgt gttgcatggg atgggcaatg tccacatagc gcagaggaga atctgtgtta 360
cacagcgcaa tggtaggtag gttaacataa gatgcctccg cgagaagctg gtggtcagcc 420
ctggggtcaa gtaaccacaa gaagccgtgg ctcccggaa gctgcctgga tctggttagt 480
gaaggntcca ggagtgaagc ggccaacaat tggagtggct tcagtggcaa gcagcaaat 540
tcagcacaag cctctggac ctgcccggcg gccgctcga 579

<210> 189
<211> 374
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 41, 280, 314, 330, 350, 353
<223> n = A,T,C or G

<400> 189
tcgagcggcc gcccgggcag gtccattttc tccctgacgg ncccacttct ctccaatctt 60
gtagttcaca ccattgtcat ggcaccatct agatgaatca catctgaaat gaccacttcc 120
aaagcctaag cactggcaca acagttttaa gcctgattca gacattcgtt cccactcacc 180
tccaacggca taatgggaaa ctgtgtagcg gtcaaagcac gagtcatccg taggttggtt 240
caagccttcg ttgacagagt tgcccacggg aacaacctcn tcccgaacc ttatgctctc 300
gctgggcttt cagngcctcc actatgatgn tgtagggggg cacctctggn gangacctcg 360
gccgcgacca cgct 374

<210> 190
<211> 373
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 247, 304, 306, 332, 337
<223> n = A,T,C or G

<400> 190
agcgtgggtcg cgccgaggt cctcaccaga ggtgccacct acaacatcat agtggaggca 60
ctgaaagacc agcagaggca taaggctcgg gaagagggtt ttaccgtggg caactctgtc 120
aacgaaggct tgaaccaacc tacggatgac tcgtgctttg acccctacac agtttcccat 180
tatgccgttg gagatgagtg ggaacgaatg tctgaatcag gctttaaact gttgtgccag 240
tgcttangct ttggaagtgg gtcatttcag atgtgattca tctagatggg gccatgacaa 300
tggnngaac tacaagattg gagagaagtg gnaccgncag ggagaaaatg gacctgcccg 360

ggcggccgct cga

373

<210> 191

<211> 354

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 218, 299, 306, 326, 333, 337, 341

<223> n = A,T,C or G

<400> 191

```
agcgtggctc cggccgaggt ccacatcggc agggctcggag cccctggccgc catactcgaa 60
ctggaatcca tcggatcatgc tctcgcgcaa ccagacatgc ctctgtcctc tgggggttctt 120
gctgatgtac cagttcttct gggccacact gggctgagtg gggtagacgc aggtctcacc 180
agtctccatg ttgcagaaga ctttgatggc atccaggntg caaccttggg tgggggcaat 240
ccagtactct ccactcttcc agccagagtg gcacatcttg aggtcacggc aggtgcggnc 300
gggggntttt gcggtcgccc tctggncttc gngtgnctc natctgctgg ctca 354
```

<210> 192

<211> 587

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 276

<223> n = A,T,C or G

<400> 192

```
tcgagcggcc gcccgggcag gtctcgcggg cgcactgggt atgctgggtc tgttggtccc 60
cccggccctc ctggacctcc tggcccccct ggtcctccca gcgctgggtt cgaactcagc 120
ttcctgcccc agccacctca agagaaggct cacgatgggt gccgctacta ccgggctgat 180
gatgccaatg tgggttcgtga ccgtgacctc gaggtggaca ccacctcaa gagcctgagc 240
cagcagatcg agaacatccg gagcccagag ggcagncgca agaaccccgc ccgcacctgc 300
cgtgacctca agatgtgccca ctctgactgg aagagtggag agtactggat tgaccccaac 360
caagctgcaa cctggatgcc atcaaagtct tctgcaacat ggagactggg gagacctgcg 420
tgtacccac tcagcccagt gtggcccaaa agaactggta catcagcaag aaccccaagg 480
acaagaagca tgtctggttc ggcgagaaca tgaccgatgg attccagttc gagtatggcg 540
ggcagggctc cgacctgccc gatggggacc ttggccgcga acacgct 587
```

<210> 193

<211> 98

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 8, 9, 33, 58, 71, 90

<223> n = A,T,C or G

<400> 193

```
agcgtggng cggccgaggt ataaatatcc agnccatate ctccctccac acgctganag 60
atgaagctgt ncaaagatct cagggtggan aaaaccat 98
```

<210> 194

<211> 240

<212> DNA

<213> Homo sapiens

<400> 194

```
tcgagcggcc gcccgggcag gtccttcaga cttggactgt gtcacactgc caggcttcca 60
gggctccaac ttgcagacgg cctgttgtgg gacagtctct gtaatcgga aagcaaccat 120
ggaagacctg ggggaaaaca ccatggtttt atccaccctg agatctttga acaacttcat 180
ctctcagcgt gcggaggag gctctggact ggatatttct acctcggccg cgaccacgct 240
```

<210> 195

<211> 400

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 22, 37, 39, 105, 268, 276, 302, 323, 331, 335, 347, 351, 371, 378

<223> n = A,T,C or G

<400> 195

```
cgagcgggcg accgggcagg tncagactcc aatccanana accatcaagc cagatgtcag 60
aagctacacc atcacagggt tacaaccagg cactgactac aaganctacc tgcacacctt 120
gaatgacaat gctcgagct cccctgtggt catcgacgcc tccactgcca ttgatgcacc 180
atccaacctg cgtttctctg ccaccacacc caattctctg ctggtatcat ggcagccgcc 240
acgtgccagg attaccggtg catcatcnag tatganaagc ctgggcctcc tcccagagaa 300
gnggtccctc ggccccgcc tngtgcacca naggntacta ttactgngcc ngcaaccggc 360
aaccgatatc nattttgnca ttggccttca acaataatta 400
```

<210> 196

<211> 494

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 19, 83, 168, 252, 271, 292, 430

<223> n = A,T,C or G

<400> 196

```
agcgtggttc gcggccgang tcctgtcaga gtggcactgg tagaagttcc aggaaccctg 60
aactgtaagg gttcttcac agngccaaca ggatgacatg aatgatgta ctcagaagtg 120
tcctggaaatg gggcccatga gatggttgtc tgagagagag cttcttgncc tgtctttttc 180
cttccaatca ggggctcgt cttctgatta ttcttcaggg caatgacata aattgtatat 240
tcgggtcccg gntccaggcc agtaatagta ncctctgtga caccagggcg gngccgagg 300
accacttctc tgggaggaga cccaggcttc tcatacttga tgatgtaacc ggtaatcctg 360
gcacgtggcg gctgccatga taccagcaag gaattggggt gtggtggcca ggaaacgcag 420
gttggatggg gcataaatgg cagtggaggc cgtcgatgac cacaggggga gctccgacat 480
tgtcattcaa ggtg 494
```

<210> 197

<211> 118

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 8, 71, 96

<223> n = A,T,C or G

<400> 197

agcgtggncg cggccgaggt gcagcgcggt ctgtgccacc ttctgctctc tgcccaacga 60
taaggagggt ncctgcccc aggagaacat taactntccc cagctcggtc tctgccgg 118

<210> 198

<211> 403

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 41, 53, 98, 195, 350

<223> n = A,T,C or G

<400> 198

tgcagcggtc gcccgggcag gttttttttg ctgaaagtgg ntactttatt ggntgggaaa 60
gggagaagct gtggtcagcc caagagggaa tacagagncc cgaaaaaggg gagggcaggt 120
gggctggaac cagacgcagg gccaggcaga aactttctct cctcactgct cagcctggtg 180
gtggctggag ctcanaaatt gggagtgaac caggacacct tcccacagcc attgcggcgg 240
catttcactc ggccaggaca ctggctgtcc acctggcact ggtcccgaca gaagcccag 300
ctggggaaaag ttaatgttca cctgggggca ggaacctcc ttatcattgn gcagagagca 360
gaaggtggca cagcccgcgc tgcacctcgg ccgcgaccac gct 403

<210> 199

<211> 167

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 92, 107

<223> n = A,T,C or G

<400> 199

tgcagcggtc gcccgggcag gtccaccata agtcctgata caaccacgga tgagctgtca 60
ggagcaaggt tgatttcttt cattggtccg gntttctctc tgggggncac ccgcactcga 120
tatccagtga gctgaacatt ggggtggcgc cactgggcgc tcaggct 167

<210> 200

<211> 252

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 210, 226, 227, 230, 236

<223> n = A,T,C or G

<400> 200

tgcagcggtt cgcccgggca ggtccaccac acccaattcc ttgctgggtat catggcagcc 60
gccacgtgcc aggattaccg gctacatcat caagtatgag aagcctgggt ctctcccag 120
agaagcggtc cctcggtccc gccctgggtc cagagaggt actattactg gcctggaacc 180
gggaaccgaa tatacaattt atgtcattgn cctgaagaat aatcannaan agegancccc 240
tgattggaag ga 252

<210> 201
<211> 91
<212> DNA
<213> Homo sapiens

<400> 201
agcgtggtcg cgcccgaggt tgtacaagct tttttttttt tttttttttt tttttttttt 60
tttttttttt tttttttttt tttttttttt t 91

<210> 202
<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> 9, 354
<223> n = A,T,C or G

<400> 202
tcgagcggnc gcccgggcag gtctgccaac accaagattg gcccccgccg catccacaca 60
gtccgtgtgc ggggaggtaa caagaaatac cgtgccctga gggtggacgt ggggaatttc 120
tcctggggct cagagtgttg tactcgtaaa acaaggatca tcgatgttgt ctacaatgca 180
tctaataacg agctggttcg taccaagacc ctggtgaaga attgcatcgt gctcatcgac 240
agcacaccgt accgacagtg gtacgagtc cactatgcgc tgccccctgg ccgcaagaag 300
ggagccaagc tgactcctga ggaagaagag attttaaaca aaaaacgac taanaaaaaa 360
aaaacaat 368

<210> 203
<211> 340
<212> DNA
<213> Homo sapiens

<400> 203
agcgtggtcg cgcccgaggt gaaatggtat tcagcttctt ggcacttctg gtcagcaacc 60
cagtgttggg caacaaatga tctttgagga acatggtttt aggcggacca caccgccac 120
aacggccacc ccataaggc ataggccaag accatacccg ccgaatgtag gacaagaagc 180
tctctctcag acaaccatct catggggccc attccaggac acttctgagt acatcatttc 240
atgtcatcct gttggcactg atgaagaacc cttacagttc agggttcctg gaacttctac 300
cagtgcact ctgacaggac ctgcccgggc ggccgctcga 340

<210> 204
<211> 341
<212> DNA
<213> Homo sapiens

<400> 204
tcgagcggcc gcccgggcag gtctgtcag agtggcactg gtagaagttc caggaaacct 60
gaactgtaag ggttcttcat cagtgccaac aggatgacat gaaatgatgt actcagaagt 120
gtcctggaat ggggcccatt agatggttgt ctgagagaga gcttcttgct ctacattcgg 180
cgggtatggc cttggcctat gccttatggg ggtggccggt gtgggcccgt tgggtccgct 240
aaaaccatgt tcctcaaaga tcatttggtg cccaacactg ggttgctgac cagaagtgcc 300
aggaagctga ataccatttc acctcgccg cgaccacgct a 341

<210> 205
<211> 770
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature

<222> 529, 591, 623, 626, 629, 630, 656, 702, 709, 712, 717, 743, 746, 749, 759, 762, 766

<223> n = A,T,C or G

<400> 205

```
tcgagcggcc gcccgggcag gtctcccttc ttgcggccca ggggcagcgc atagtgggac 50
tcgtaccact gtcggtacgg tgtgctgtcg atgagcacga tgcaattctt caccagggtc 120
ttggtacgaa ccagctcgtt attagatgca ttgtagacaa catcgatgat ccttgtttta 180
cgagtacaac actctgagcc ccaggagaaa ttccccacgt ccaacctcag ggcacggtat 240
ttcttggtac ctccccgcac acggactgtg tggatgcggc gggggccaag ctgactcctg 300
aggaagaaga gattttaaac aaaaaacgat ctaaaaaaat tcagaagaaa tatgatgaaa 360
ggaaaaagaa tgccaaaatc agcagtcctc tggaggagca gttccagcag ggcaagcttc 420
ttgcgtgcac cgcttcaagg ccgggacagt gtgaccgagc agatggctat gtgctagagg 480
gcaagaagt ggagttctat cttaagaaaa tcagggccca gaatggtgng tcttcaacta 540
atccaaaggg gattttcaga ccagtgcgat cagcaaaaac attgatactg ntggccaaat 600
ttattggtgc agggcttgca cantlangann ggctgggtct tggggcttgg attggnacaa 660
gctttggcag ccttttcttt ggttttgcca aaaacctttt gntgaagang anacctnggg 720
cggacccctt aaccgattcc acnccngng gcgttctang gncccncttg 770
```

<210> 206

<211> 810

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 574, 621, 625, 636, 668, 673, 704, 728, 743, 767, 772, 786, 789, 807, 809, 810

<223> n = A,T,C or G

<400> 206

```
agcgtggctc cgcccgagggt ctgctgcttc agcgaagggt ttctggcata accaatgata 60
aggctgccaa agactgttcc aataccagca ccagaaccag ccactcctac tgttgacga 120
cctgcaccaa taaatttggc agcagtatca atgtctctgc tgattgcact ggtctgaaac 180
tccctttgga ttagctgaga cacaccatc tgggccctga ttttcctaag atagaactcc 240
aactctttgc cctctagcac atagccatct gctcggtcac actgtcccg ccttgaagcg 300
atgcacgcaa gaagcttgcc ctgctggaac tgctcctcca ggagactgct gatttttgga 360
ttcttttcc ttctcatcata tttcttctga attttttag atcgttttt gtttaaaatc 420
tcttcttcc caggagtcag cttggccccc gcgcaccca cacagtcctg gtgcggggag 480
gtaacaagaa ataccgtgcc ctgagggttg acgtggggaa tttctcctgg ggctcagagt 540
ggtgtactcg taaaacaagg atcatcgatg gtgnetacaa tgcatcta atacgagctg 600
gtcggaccca aagaacctgg ngaanaaatg gatcgnctca tcgacaggac accgtacccg 660
acaggggnac gantccact atgcgcttgc ccctgggccg caanaaagga aaactgcccg 720
ggcggccntc gaaagcccaa ttntggaaaa aatccatcac actgggnggc cngtcagaca 780
tgcatntana ggggccatt cccctnann 810
```

<210> 207

<211> 257

<212> DNA

<213> Homo sapiens

<400> 207

```
tcgagcggcc gcccgggcag gtccccaacc aaggctgcaa cctggatgcc atcaaagtct 60
tctgcaacat ggagactggg gagacctcg tgtacccac tcagcccagt gtggccaga 120
agaactggt catcagcaag aaccccaagg acaagaggca tgtctggttc ggcgagagca 180
```


tgaccgatgg attccagttc gagtatggcg gccagggtc cgaccctgcc gatgtggacc 240
tcggccgcga ccacgct 257

<210> 208
<211> 257
<212> DNA
<213> Homo sapiens

<400> 208
agcgtggtcg cggccgaggt ccacatcggc agggctcggag ccctggccgc catactcgaa 60
ctggaatcca tcggatcatgc tctcgccgaa ccagacatgc ctcttgctct tggggttctt 120
gctgatgtac cagttcttct gggccacact gggctgagtg gggtagacgc aggtctcacc 180
agtctccatg ttgcagaaga ctttgatggc atccagggtg cagccttggt tggggacctg 240
cccgggcggc cgctcga 257

<210> 209
<211> 747
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 453, 538, 540, 542, 546, 554, 556, 598, 659, 670, 679, 689,
693, 711, 723, 724, 731, 747
<223> n = A,T,C or G

<400> 209
tcgagcggcc gcccgggcag gtccaccaca cccaattcct tgctggtatc atggcagccg 60
ccacgtgcca ggattaccgg ctacatcatc aagtatgaga agcctgggtc tcctcccaga 120
gaagtgggtcc ctcgcccccg ccctggtgtc acagaggcta ctattactgg cctggaaccg 180
ggaaccggaat atacaattta tgtcattgcc ctgaagaata atcagaagag cgagccctg 240
attggaagga aaaagacaga cgagcttccc caactggtaa cccttccaca ccccaatctt 300
catggaccag agatcttggg tgttccttcc acagtccaac agacccttt cgtaaccac 360
cctgggtatg acactggaaa tggattcag ctctctggca cttctgtga gcaaccag 420
gttgggcaac aaatgatctt tgaggaacat ggnnttaggc ggaccacacc gccacaacg 480
gccaccccca taaggcatag gccaagacca taccgcccga atgtaggaca agaagctntn 540
tntcanacac catntnatgg gcccatttcc aggacacttc tgagtacatc atttatgna 600
tctgtggcac ttgatgaaa cccttacagt tcagggttct ggaacttta ccaggcctnt 660
tacaggactn ggccggacnc cttaagccna ttncaccctg gggcgttcta nggtcccact 720
cgnnactg ngaaaatggc tactgtn 747

<210> 210
<211> 872
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 165, 174, 181, 256, 260, 269, 271, 277, 286, 289, 294, 298,
300, 301, 303, 308, 311, 321, 325, 328, 329, 333, 338, 342,
346, 349, 351, 357, 359, 364, 366, 379, 385, 395, 396, 397,
407, 408, 410, 414, 415, 429, 431, 434, 435, 440, 443
<223> n = A,T,C or G

<221> misc_feature
<222> 444, 446, 447, 448, 449, 450, 451, 464, 470, 472, 475, 479,
483, 484, 485, 488, 494, 496, 497, 504, 508, 509, 511, 513,
517, 522, 524, 526, 532, 533, 542, 543, 553, 559, 566, 567,

571, 572, 578, 582, 588, 591, 594, 595, 596, 600, 606

<223> n = A,T,C or G

<221> misc_feature

<222> 612, 614, 617, 618, 629, 630, 631, 652, 654, 655, 661, 663,
664, 666, 671, 673, 678, 679, 681, 688, 690, 691, 698, 706,
707, 708, 714, 719, 721, 723, 726, 741, 751, 761, 762, 769,
770, 778, 779, 781, 782, 785, 791, 802, 807, 808, 812

<223> n = A,T,C or G

<221> misc_feature

<222> 815, 820, 827, 828, 830, 841, 844, 851, 857, 864, 866, 869,
872

<223> n = A,T,C or G

<400> 210

```
agcgtggtcg cgcccgaggt ccactagagg tctgtgtgcc attgcccagg cagagtctct 60
gcgttacaaa ctccataggag ggcttgcctgt gcggagggcc tgctatggtg tgctgcgggt 120
catcatggag agtggggcca aaggctgcga ggttgtggtg tctgngaaac tccnaggaca 180
ngagggctaa attccatgaa gtttgtggat ggccctgatga tccacaatcg gagaccctgt 240
taactactac cgtctnaccn cctgctgtnc ncccccttt ctgctnaana catngggntn 300
ntncttgnc ntccctgggt ngaanatma atngcctncc cnttctanc nctactngnt 360
ccananttg cctttaaaana atccnccctg ccttnnncac tgttcannntn tttnttcgta 420
aacccctatna nttnnattan atnntnnnnn nctcacccccc ctctcattn anccnatang 480
ctnnnaantc cttannncct cccncccnnt ncnctctac tnantncttc tnncccatna 540
cnnagctctt tcntttaana taatgnngcc nngctctnca tntctacnat ntgnnnaatn 600
cgcncncccc cnancgnntt tttgacctnn naacctcctt tctcttccc tcnnaaaatt 660
ncnnanttcc ncnttcnnc ntctcgntn ntcccatnct tccannnct tcantctanc 720
ncnctncaac ttatttctct ntcctcctt nttctttaca nccccctnn tctactcnrc 780
nnttncatta natttgaac tncacnncct anttnecten ctctacnntt ttattttncg 840
ntnctctac ntaatanntt aatnanttnt cn 872
```

<210> 211

<211> 517

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 462, 464, 506

<223> n = A,T,C or G

<400> 211

```
tgcagcggcc gcccgggcag gtctgccaaag gagaccctgt tatgctgtgg ggactggctg 60
gggcatggca ggcggctctg gcttcccacc cttctgttct gagatggggg tgggtggcag 120
tatctcatct ttgggttcca caatgctcac gtggtaaggc aggggcttct tagggccaat 180
cttaccagtt ggggtcccagg gcagcatgat cttcaccttg atgcccagca caccctgtct 240
gagcaacacg tggcgccaaa gcagtgtcaa cgtagtaagt taacagggtc tccgctgtgg 300
atcatcaggc catccacaaa cttcatggat ttagccctct gtccctggag tttcccagac 360
accacaacct cgcagccttt ggccccactc tccatgatga accgcagcac accatagcag 420
gccctccgca caagcaagcc ctccaaagaa ttgtgaacgc ananactctg ctggcaatcg 480
cacacaaacc tctagtggac ctcggncgcg accacgc 517
```

<210> 212

<211> 695

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> 432, 476, 522, 547, 621, 624, 647, 679
<223> n = A,T,C or G

<400> 212
tcgagcggcc gcccgggcag gtctgggtcca ggatagcctg cgagtcctcc tactgctact 60
ccagacttga catcatatga atcactactgg ggagaatagt tctgaggacc agtagggcat 120
gattcacaga ttccaggggg gccaggagaa ccagggggacc ctggttgtcc tggaaatacca 180
gggtcaccat ttctcccagg aataccagga gggcctggat ctcccttggg gccttgaggt 240
ccttgaccat taggagggcg agtaggagca gttggaggct gtgggcaaac tgcacaaat 300
tctccaaatg gaatttctgg gttggggcag tctaattctt gatccgtcac atattatgtc 360
atcgcagaga acggatcctg agtcacagac acatatttgg catggttctg gcttccagac 420
atctctatcc gncataggac tgaccaagat gggaacatcc tccttcaaca agcttncgt 480
tgtgccaaaa ataatagtgg gatgaagcag accgagaagt anccagctcc cctttttgca 540
caaaagctca tcatgtctaa atatcagaca tgagacttct ttgggcaaaa aaggagaaaa 600
agaaaaagca gttcaaagta nccnccatca agttgggtcc ttgcccnttc agcaccggg 660
ccccgttata aaacacctng ggccggaccc ccctt 695

<210> 213
<211> 804
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 552, 555, 592, 624, 629, 633, 658, 695, 697, 698, 700, 702,
745, 753, 755, 762, 773, 786, 788, 793, 795
<223> n = A,T,C or G

<400> 213
agcgtggtcg cggccgaggt gttttatgac gggcccggtg ctgaagggca ggaacaact 60
tgatggtgct actttgaact gcttttcttt tctccttttt gcacaaagag tctcatgtct 120
gatatttga catgatgagc tttgtgcaaa aggggagctg gctacttctc gctctgttc 180
atcccactat tattttggca caacaggaag ctgttgaagg aggatgttcc catcttggtc 240
agtcctatgc ggaatagat gtctggaagc cagaaccatg ccaaatatgt gtctgtgact 300
caggatccgt tctctgcat gacataatat gtgacgatca agaattagac tgcccacacc 360
cagaaattcc atttgagaa tgttgtgcag tttgccaca gctccaaact gctcctaact 420
gccctcctaa tggtaagga cctcaaggcc ccaagggaga tccaggccct cctggtattc 480
ctgggagaaa tggtagccct ggtattccag gacaaccagg gtcccctggt tctcctggcc 540
cccctggaat cngngaatc atgccctact ggtcctcaa ctattctccc anatgattca 600
tatgatgtca agtctgggat agcnagtang ganggactcg caggctattc tggaccanac 660
ctgccggggg ggcgttcgaa agcccgaatc tgcanaantn cnttcacact ggccggccgc 720
gagctgcttt aaaagggcca ttccncttt agngnggggg antacaatta ctnggcggcg 780
ttttanancg cngnctggg aaat 804

<210> 214
<211> 594
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 452, 509, 585
<223> n = A,T,C or G

<400> 214
agcgtggtcg cggccgaggt ccacatcggc agggtcggag ccctggccgc catactcgaa 60

```

ctggaatcca tcggtcatgc tctcgccgaa ccagacatgc ctcttgctct tggggttctt 120
gctgatgtac cagttcttct gggccacact gggctgagtg gggtagacgc aggtctcacc 180
agtctccatg ttgcagaaga ctttgatggc atccaggttg cagccttggt tgggggtcaat 240
ccagtactct ccactcttcc agtcagagtg gcacatcttg aggtcacggc aggtgcgggc 300
gggggttcttg cggctgccct ctgggctccg gatgttctcg atctgctggc tcaggctctt 360
gaggggtggtg tccacctcga ggtcacggtc acgaaccaca ttggcatcat cagcccggta 420
gtagcggcca ccatcgtag ccttctcttg angtggctgg ggcaggaaact gaagtcgaaa 480
ccagcgctgg gaggaccagg gggaccaana ggtccaggaa gggcccgggg gggaccaaca 540
ggaccagcat caccaagtgc gaccgcgag aacctgcccg gccgnccgct cgaa 594

```

<210> 215

<211> 590

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 8, 9

<223> n = A,T,C or G

<400> 215

```

tcgagcgnnc gcccgggcag gtctcgcggt cgcactggtg atgttggtcc tgttggtccc 60
cccgccctc ctggacctcc tgggtccctt ggtcctccca gcgctggtt cgacttcagc 120
ttcttgcccc agccacctca agagaaggct cacgatggtg gccgctacta ccgggctgat 180
gatgccaatg tgggtcgtga ccgtgacctc gaggtggaca ccacctcaa ggcctgagc 240
cagcagatcg agaacatccg gagcccgagag ggcagccgca agaaccctgc ccgcacctgc 300
cgtgacctca agatgtgcca ctctgactgg aagagtggag agtactggat tgaccccaac 360
caaggctgca acctggatgc catcaaagtc ttctgcaaca tggagactgg tgagacctgc 420
gtgtacccca ctcagcccag tgtggcccag aagaactggt acatcagcaa gaaccccaag 480
gacaagaggc atgtctggtt cggcgagagc atgaccgatg gattccagtt cgagtatggc 540
ggccagggct cccaccctgc cgatgtggac ctccggccgc gaccacctt 590

```

<210> 216

<211> 801

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 2, 22, 25, 26, 328, 373, 385, 440, 473, 534, 571, 572, 573, 582, 587, 589, 593, 600, 605, 617, 633, 642, 653, 672, 681, 685, 696, 699, 709, 715, 717, 726, 731, 739, 742, 745, 758, 769, 772, 778, 780, 788, 789, 791, 793, 796

<223> n = A,T,C or G

<400> 216

```

tngagcggcc gcccgggcag gntgnaacg ctggctctgc tggctcctct ggcaaggctg 60
gtgaagatgg tcaccttgga aaacccggac gacctggtga gagaggagtt gttggaccac 120
aggggtgctcg tggtttccct ggaactcctg gacttcttg cttcaaaggc attaggggac 180
acaatggtct gggatggattg aagggacagc ccggtgctcc tgggtgtaag ggtgaacctg 240
gtgcccttgg tgaaaatgga actccaggtc aaacaggagc ccgtggcctt cctggtgaga 300
gaggaccgtg ttggtgcccc tggcccanac ctggcccgcg accacgctaa gcccgattt 360
ccagcacact ggnngccggtt actantggat ccgagctcgg taccaagctt ggcgtaatca 420
tggcatagc tgtttcctgn gtgaaattgt tatccgctca caatttcaca cancatacga 480
agccggaaaag cataaagtg aaagccttgg ggtgctaagt agtgagctaa ctncattaa 540
attgcgttgc gctcactgcc cgcttttcca nnnnggaaac cntggcntng cngcttgcn 600
ttaantgaaa tccgcnaacc cccggggaaa agncggtttg cngtattggg gcnccttttc 660
cctttctcgc gnttacttga nttantgggc tttggnccgt tggggttgn gcgancnggt 720

```

tcaacntcac nccaaagng gnaanacggt tttcccanaa tccgggggnt ancccaangn 780
aaaacatnng ncnangggc t 801

<210> 217
<211> 349
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 10, 157, 170
<223> n = A,T,C or G

<400> 217
agcgtggttn gcgccgaggt tctgggcccag gggcaccaac acgtcctctc tcaccaggaa 60
gcccacgggc tcctgtttga cctggagttc ctttttcacc aggggcacca ggttcaccct 120
tcacaccagg agcaccgggc tgtcccttca atccatncag accattgtgn cccctaattgc 180
ctttgaagcc aggaagtcca ggagttccag ggaaccacc gagcaccctg tggccaaca 240
actcctctc caccagggtc tccgggtttt ccagggtgac catcttcacc agccttgcca 300
ggaggaccag caggaccagc gttaccaacc tgcccgggag gccgtcga 349

<210> 218
<211> 372
<212> DNA
<213> Homo sapiens

<400> 218
tcgagcggcc gcccgggcag gtccattttc tccctgacgg tcccacttct ctccaattctt 60
gtagttcaca ccattgtcat ggcaccatct agatgaatca catctgaaat gaccacttcc 120
aaagccctaag cactggcaca acagtttaaa gcctgattca gacattcgtt cccactcacc 180
tccaacggca taatgggaaa ctgtgtaggg gtcaaagcac gagtcacccg taggttggtt 240
caagccttcg ttgacagagt tgcccacggt aacaacctct tcccgaacct tatgcctctg 300
ctggtctttc agtgccctcca ctatgatgtt gtaggtggca cctctggtga ggacctgggc 360
cgcgaccacg ct 372

<210> 219
<211> 374
<212> DNA
<213> Homo sapiens

<400> 219
agcgtggtcg cggccgaggt cctcaccaga ggtgccacct acaacatcat agtgaggca 60
ctgaaagacc agcagaggca taagggtcgg gaagaggttg ttaocgtggg caactctgtc 120
aacgaaggct tgaaccaacc tacggatgac tcgtgctttg acccctacac agtttcccat 180
tatgccgttg gagatgagtg ggaacgaatg tctgaatcag gctttaaact gttgtgccag 240
tgcttaggct ttggaagtgg tcatttcaag atgtgattca tctagatggt gccatgacaa 300
tggtgtgaac tacaagattg gagagaagtg ggaccgtcag ggagaaaatg gacctgcccg 360
ggccggccgc tcga 374

<210> 220
<211> 828
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 8, 9, 557, 571, 587, 588, 601, 642, 643, 647, 654, 664, 681,
688, 698, 719, 720, 725, 734, 738, 743, 744, 757, 765, 773,

778, 780, 782, 783, 793, 798, 805, 809, 822, 827
 <223> n = A,T,C or G

<400> 220

```
tcgagcgnnc gcccgggcag gtccagtagt gccttcggga ctgggttcac ccccaggtct 60
gcggcagttg tcacagcgcc agccccgctg gcctccaaag catgtgcagg agcaaattgc 120
accgagatat tccttctgcc actgttctcc tacgtgggat gtcttcccat catcgtaaca 180
cgttgcctca tgagggtcac acttgaattc tccttttccg ttccaagac atgtgcagct 240
catttggctg gctctatagt ttggggaaaag tttgttgaaa ctgtgccact gacctttact 300
tcctccttct ctactggagc ttctgtacct tccacttctg ctgttggtaa aatggtggat 360
cttctatcaa ttctattgac agtaccact tctcccaaac atccagggaa atagtgtatt 420
cagagcgatt aggagaacca aattatgggg cagaataaag gggttttcc acaggttttc 480
ctttggagga agatttcagt ggtgacttta aaagaatact caacagtgtc ttcattccca 540
tagcaaaaga agaaacmgta aatgatggaa ngcttctgga gatgccnnca tttaagggaac 600
nccccagaact tcaccatcta caggacctac ttccagtttac annaagnca atantctgac 660
tcanaaagga cccaagtgc nccatggna gcacttttag cctttccct ggsgaaaann 720
ttacnttctt aaancctngg ccnngacccc cttaagncca aattntggaa aanttcctn 780
cnnctggggg gcngttcnac atgcntttna agggcccaat tncacct 828
```

<210> 221

<211> 476

<212> DNA

<213> Homo sapiens

<400> 221

```
tcgagcggcc gcccgggcag gtgtcggagt ccagcacggg aggcgtggtc ttgtagtgt 60
tctccggtg ccattgtct tccactcca cggcgatgtc gctgggatag aagcctttga 120
ccaggcaggt caggctgacc tggttcttgg tcactctctc ccgggatggg ggcaggggtg 180
acacctgtgg ttctcggggc tgcccttttg ctttgagat ggttttctcg atgggggctg 240
ggagggcttt gttggagacc ttgcaattgt actccttgcc attcagccag tcctgggtga 300
ggacggtgag gacgtgacc acacggtacg tgctgttgta ctgctcctcc cgcggctttg 360
tcttggcatt atgcacctcc acgcccgtcca cgtaccagtt gaacttgacc tcagggctct 420
cgtgggtcac gtccaccacc acgcatgtaa cctcagacct cggccgcgac cacgct 476
```

<210> 222

<211> 477

<212> DNA

<213> Homo sapiens

<400> 222

```
agcgtgggtg cggccgaggt ctgaggttac atgcgtgggt gtggacgtga gccacgaaga 60
ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa 120
gcccggggag gagcagtaca acagcacgta ccgtgtgggt agcgtcctca ccgtcctgca 180
ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc 240
cccctcgag aaaaccatct ccaaagccaa agggcaagcc ccgagaacca caggtgtaca 300
ccctgcccc atcccgggag gagatgacca agaaccaggt cagcctgacc tgcttggtca 360
aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag ccggagaaca 420
actacaagac cagcctccc gtgctggact ccgacacctg cccgggcggc cgctcga 477
```

<210> 223

<211> 361

<212> DNA

<213> Homo sapiens

<400> 223

```
tcgagcggcc gcccgggcag gttgaatggc tcctcgtgta ccaccccggt gctgggtggtg 60
ggtacagagc tccgatgggt gaaaccattg acatagagac tgtcctgtc cagggtgtag 120
gggcccagct cagtgtatgc gtgggtcagc tggctcagct tccagtacag ccgtctctg 180
```

```

tccagtccag ggcttttggg gtcaggacga tgggtgcaga cagcatccac tctggtggct 240
gccccatcct tctcaggcct gagcaaggtc agtctgcaac cagagtacag agagctgaca 300
ctggtgttct tgaacaaggg cataagcaga ccctgaagga cacctcggcc gcgaccacgc 360
t

```

<210> 224
 <211> 361
 <212> DNA
 <213> Homo sapiens

```

<400> 224
agcgtggctc cgcccgaggt gtccttcagg gtctgcttat gcccttggtc aagaacacca 60
gtgtcagctc tctgtactct gggtgcagac tgaccttgc caggcctgag aaggatgggg 120
cagccaccag agtgggatgct gtctgcaccc atcgtcctga ccccaaaagc cctggactgg 180
acagagagcg gctgtactgg aagctgagcc agctgaccca cggcatcact gagctgggcc 240
cctacaccct ggacaggggac agtctctatg tcaatggttt caccatcgg agctctgtac 300
ccaccaccag caccgggggtg gtcagcgagg agccattcaa cctgcccggg cggccgctcg 360
a

```

<210> 225
 <211> 766
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 574, 610, 631, 643, 657, 660, 666, 688, 712, 735, 747
 <223> n = A,T,C or G

```

<400> 225
agcgtggctc cgcccgaggt cctgtcagag tggcactggt agaagttcca ggaaccctga 60
actgtaaggg ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagtgt 120
cctggaatgg ggcccatgag atgggtgtct gagagagagc ttcttgcctt acattcggcg 180
ggtatggtct tggcctatgc cttatggggg tggccgttgt ggccggtgtg gtccgcctaa 240
aaccatgttc ctcaaagatc attgttgcc caacactggg ttgctgacca gaagtgccag 300
gaagctgaat accatttcca gtgtcatacc cagggtgggt gacgaaaggg gtcttttgaa 360
ctgtggaagg aacatccaag atctctgggt catgaagatt ggggtgtgga aggggtacca 420
gttggggaag ctctgtctgtc tttttccttc caatcagggg ctgcctcttc tgattattct 480
tcagggcaat gacataaatt gtatattcgg tcccggttcc aggccagtaa tagtagcctc 540
tgtgacacca gggcgggggc gagggaccct tctnttgaa gagaccagct tctcatactt 600
gatgatgagn ccggtaatcc tggcacgtgg nggttgcatg atnccaccaa ggaaatnggn 660
gggggnggac ctgcccggcg gccgttcnaa agcccaattc cacacacttg gnggccgtac 720
tatggatccc actcngtcca acttgngnga atatggcata actttt

```

<210> 226
 <211> 364
 <212> DNA
 <213> Homo sapiens

```

<400> 226
tcgagcggcc gcccgggcag gtccctgacc ttttcagcaa gtgggaaggt gtaatccgtc 60
tccacagaca aggccaggac tcgtttgtae ccgttgatga tagaatgggg tactgatgca 120
acagttgggt agccaatctg cagacagaca ctggcaacat tgcggacacc ctccagggaag 180
cgagaatgca gagtttcctc tgtgatatca agcatttcag ggttgtagat gctgccattg 240
tcgaacacct gctggatgac cagcccaag gagagggggg agatgttgag catgttcagc 300
agcgtggctt cgctggctcc cactttgtct ccagtcttga tcagacctcg gccgcgacca 360
cgct

```

<210> 227
<211> 275
<212> DNA
<213> Homo sapiens

<400> 227
agcgtgggtcg cggccgaggt ctgtcctaca gtcctcagga ctctactccc tcagcagcgt 60
ggtgaccgtg ccctccagca acttcggcac ccagacctac acctgcaacg tagatcacia 120
gcccagcaac accaaggtgg acaagagagt tgagcccaaa tcttgtgaca aaactcacac 180
atgccccaccg tgcccagcac ctgaactcct ggggggaccg tcagtcttcc tcttcccccg 240
catccccctt ccaaacctgc ccgggcggcc gtcg 275

<210> 228
<211> 275
<212> DNA
<213> Homo sapiens

<400> 228
cgagcggccg cccgggcagc tttggaaggc ggatgcgggc gaagaggaag actgacggtc 60
ccccaggag ttcaggtgct gggcacggcg ggcattgtgt agttttgtca caagatttgg 120
gctcaactct cttgtccacc ttggtgttgc tgggcttgtg atctacgttg caggtgtagg 180
tctgggtgcc gaagttgtcg gagggcacgg tcaccaacgt gctgaggagg tagagtcctg 240
aggactgtag gacagacctc ggccgcgacc acgct 275

<210> 229
<211> 40
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 1, 4, 5, 13, 15, 17, 29
<223> n = A,T,C or G

<400> 229
nggnnggtcc ggnengncag gaccactcnt cttcgaaata 40

<210> 230
<211> 208
<212> DNA
<213> Homo sapiens

<400> 230
agcgtgggtcg cggccgaggt cctcacttgc ctcttgcaaa gcaccgatag ctgcgctctg 60
gaagcgcaga tctgttttaa agtcctgagc aatttctcgc accagacgct ggaagggag 120
tttgccaatc agaagttcag tggacttctg ataactcta atttcacgga gcgccacagt 180
accaggacct gcccgggcgg ccgctcga 208

<210> 231
<211> 208
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 33
<223> n = A,T,C or G

<400> 231

```

tcgagcggcc gcccgggcag gtccctggtac tgnngcgctc cgtgaaatta gacgttatca 60
gaagtccact gaacttctga ttccgaaact tcccttcag cgtctggtgc gagaaattgc 120
tcaggacttt aaaacagatc tgcgcttcca gagcgagct atcggtgctt tgcaggaggc 180
aagtgaggac ctgcggccgc accacgct                                208

```

<210> 232

<211> 332

<212> DNA

<213> Homo sapiens

<400> 232

```

tcgagcggcc gcccgggcag gtccacatcg gcagggtcgg agccctggcc gccatactcg 60
aactggaatc catcggtcat gctctcgccg aaccagacat gcctcttgtc cttgggggttc 120
ttgctgatgt accagttctt ctggggcaca ctgggctgag tggggtagac gcagggtctca 180
ccagtctcca tgttgacagaa gactttgatg gcatccagg tgcagccttg gttgggggtca 240
atccagtact ctccactctt ccagtcagag tggcacatct tgaggtcacg gcagggtcgg 300
gcgggggttct tgacctcgcc cgcgaccacg ct                                332

```

<210> 233

<211> 415

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 6, 15, 19, 21

<223> n = A,T,C or G

<400> 233

```

gtgggnttga acccnttttna nctccgcttg gtaccgagct cggatccact agtaacggcc 60
gccagtgtgc tggaaattcgg cttagcgtgg tcgcgccga ggtcaagaac cccgcccga 120
cctgccgtga cctcaagatg tgccactctg actggaagag tggagagtac tggattgacc 180
ccaaccaagg ctgcaacctg gatgccatca asgtcttctg caacatggag actggtgaga 240
cctgcgtgta cccactcag cccagtgtgg ccagaagaa ctggtacatc agcaagaacc 300
ccaaggacaa gaggcatgtc tggttcggcg agagcatgac cgatggattc cagttcagat 360
atggcgcca gggctccgac cctgccgatg tggacctgcc cggcgcccg ctca 415

```

<210> 234

<211> 776

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 505, 550, 574, 601, 604, 608, 612, 649, 656, 657, 680, 711, 750, 776

<223> n = A,T,C or G

<400> 234

```

agegtggtcg cggccgaggt ctgggatgct cctgctgtca cagttagata ttacaggatc 60
acttacggag aaacaggagg aaatagccct gtccaggagt tcaactgtgc tgggagcaag 120
tctacagcta ccatcagcgg ccttaaacct ggagttgatt ataccatcac tgtgtatgct 180
gtcactggcc gtggagacag ccccgcaagc agcaagccaa ttccattaa ttaccgaaca 240
gaaattgaca aaccatccca gatgcaagt accgatgttc aggacaacag cattagtgtc 300
aagtggctgc cttcaagttc cctgttact ggttacagag taaccaccac tccccaaaat 360
ggaccaggac caacaaaaac taaaactgca ggtccagatc aaacagaaat gactattgaa 420
ggcttgacgc ccacagtgga gtatgtggtt aagtgtctat gctcagaatc caagcggaga 480

```

gaagtcagcc tctgggttcag actgnaagta accaaccattg atcgccataaa ggactggcat 540
 tcaactgatgn ggatgccgat tccatcaaaa ttgnttggga aaaccacacag gggcaagttt 600
 ncangtcnag gnggacctac tccagccctg aggatggaat ccttgactnt tccttncct 660
 gatggggaaa aaaaaccttn aaaacttgaa ggacctgccc gggcgccgt ncaaaaccca 720
 attccacccc cttgggggcg ttctatgggn cccactcgga ccaaacttgg ggtaan 776

<210> 235
 <211> 805
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 637, 684, 705, 724, 733, 756, 778, 793, 796, 804
 <223> n = A,T,C or G

<400> 235
 tccagcggcc gcccgggcag gtccttgacg ctctgcagtg tcttcttcac catcaggtgc 60
 agggaaatagc tcatggatlc catcctcagg gctcgagtag gtcacctgt acctggaaac 120
 ttgcccctgt gggctttccc aagcaatttt gatggaatcg gcatccacat cagtgaatgc 180
 cagtccttta gggcgatcaa tgttggttac tgcagtctga accagaggct gactctctcc 240
 gcttggtatc tgagcataga cactaaccac atactccact gtgggctgca agccttcaat 300
 agtcatttct gtttgatctg gacctgcagt tttagttttt gttggtcctg gtccattttt 360
 gggagtggtg gttactctgt aaccagtaac aggggaactt gaaggcagcc acttgacact 420
 aatgctgttg tccatgaacat cggtcacttg catctgggat ggtttgtcaa tttctgttcg 480
 gtaattaatg gaaattggct tctgcttgcc ggggcttgcc tccacggcca gtgacagcat 540
 acacagtgat ggtataatca actccagggt taagccgctg atggtagctg aaactttgct 600
 ccaggcacia gtgaactcct gacagggtta tttcctnctg ttctccgtaa gtgacctgt 660
 aatatctcac tgggacagca ggagcattc caaaacttcg ggcgngacce cctaagccga 720
 attntgcaat atncatcaca ctggcgggag ctcgancatt cattaagagg cccaatcncc 780
 cctatagga gtntantaca attng 805

<210> 236
 <211> 262
 <212> DNA
 <213> Homo sapiens

<400> 236
 tccagcggcc gcccgggcag gtcacttttg gtttttgggc atgttcgggtt ggtcaaagat 60
 aaaaactaag tttgagagat gaatgcaaag gaaaaaata ttttccaaag tccatgtgaa 120
 attgtctccc atttttttgg cttttgaggg ggttcagttt ggggttgcctg tctgtttccg 180
 ggttgggggg aaagtgggtt gsgtgggagg gagccagggt gggatggagg gattttacag 240
 gaagcagaca gggccaacgt cg 262

<210> 237
 <211> 372
 <212> DNA
 <213> Homo sapiens

<400> 237
 agcgtggtcg cggccgaggt cctcaaccaga ggtgccacct acaacatcat agtggaggca 60
 ctgaaagacc agcagaggca taaggttcgg gaagaggttg ttaccgtggg caactctgtc 120
 aacgaaggct tgaaccaacc tacggatgac tctgtctttg accctacac agtttcccat 180
 tatgccgttg gagatgagtg ggaacgaatg tctgaatcag gctttaaact gttgtgccag 240
 tgcttaggct ttggaagtgg tcatctcaga tgtgattcat ctatagtggt ccatgacaat 300
 ggtgtgaact acaagattgg agagaagtgg gaccgtcagg gagaaaatgg acctgcccg 360
 gcggccgctc ga 372

<210> 238
<211> 372
<212> DNA
<213> Homo.sapiens

<400> 238
tcgagcggcc gcccgggcag gtccattttc tccctgacgg tcccacttct ctccaattct 60
gtagttcaca ccattgtcat ggcaccatct agatgaatca catctgaaat gaccacttcc 120
aaagcctaag cactggcaca acagttaaaa gcttgattca gacattcgtt cccactcate 180
tccaacggca taatgggaaa ctgtgtaggg gtcaaagcac gagtcacccg taggttggtt 240
caagccttcg ttgacagagt tgcccacggg aacaacctct tcccgaaact tatgcctctg 300
ctggtctttc agtgccctca ctatgatgtt gtaggtggca cctctggtga ggacctcggc 360
cgcgaccacg ct 372

<210> 239
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 478, 557, 563, 566, 620, 660, 663, 672, 673, 684, 693, 695
<223> n = A,T,C or G

<400> 239
tcgagcggcc gcccgggcag gtccaccata agtcctgata caaccacgga tgagctgtca 60
ggagcaagggt tgatttcttt cattgggtccg gtcttctcct tgggggtcac ccgcactcga 120
tatccagtga gctgaacatt ggggtggtgc cactgggcgc tcaggcttgt ggggtgtgacc 180
tgagtgaact tcaggtcagt tgggtgcagga atagtgttga ctgcagctcg aaccagaggc 240
tgactctctc cgcttggatt ctgagcatag acactaacca catactccac tgtgggctgc 300
aagccttcaa tagtcatttc tgtttgatct ggacctgcag ttttagtttt tgttggtcct 360
ggtccatttt tgggagtggt ggttactctg taaccagtaa caggggaact tgaaggcagc 420
cacttgacac taatgctggt gtcttgaaca tcggtcactt gcactctgga tggtttgnc 480
atttctgttc ggtaattaat ggaatttggc ttgctgcttg cggggctgtc tccacggcca 540
gtgacagcat acacagngat ggnatnatca actccaagtt taaggccctg atggtaactt 600
taaacttgct cccagccagn gaacttccgg acagggtatt tcttctggtt ttccgaaagn 660
gancctggaa tntctcctt ggancagaag gancntccaa aacttgggcc ggaaccctt 720

<210> 240
<211> 691
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 564, 582, 640, 651, 666, 669, 690
<223> n = A,T,C or G

<400> 240
agcgtggtcg cggccgaggt cctgtcagag tggcactggt agaagttcca ggaaccctga 60
actgtaaggg ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagtgt 120
cctggaatgg ggcccatgag atggttgtct gagagagagc ttcttgtcct acattcggcg 180
ggtatggtct tggcctatgc ctatggggg tggccgttgt gggcgggtgt gtccgcctaa 240
aaccatgttc ctcaaagatc atttgttgc caacactggy ttgctgacca gaagtgccag 300
gaagctgaat accatttcca gtgtcatacc cagggtgggt gacgaaaggg gtcttttgaa 360
ctgtggaagg aacatccaag atctctgggt catgaagatt ggggtgtgga agggttacca 420
gttggggaag ctctctctgc tttttccttc caatcagggg ctctctcttc tgattattct 480

```

tcagggcaat gacataaatt gtatatccgg ttcccgggtc caggccagta atagtagcct 540
cttgtgacac caggcggggc ccanggacca cttctctggg angagaccca gcttctcata 600
cttcatgatg taaccgggta atcctgcacg tggcggctgn catgatacca ncaaggaatt 660
gggtgngngg gacctgcccc ggggcectcn a 691

```

<210> 241

<211> 808

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 680, 715, 721, 728, 735, 749, 757, 762, 772, 776, 779, 781, 792, 796, 800, 808

<223> n = A,T,C or G

<400> 241

```

agcgtgggtcg cggccgaggt ctgggatgct cctgctgtca cagttagata ttacaggatc 60
acttacggag aaacaggagy aaatagccct gtccaggagt tcactgtgcc tgggagcaag 120
tctacagcta ccatcagcgg ccttaaacct ggagttgatt ataccatcac tgtgtatgct 180
gtcactggcc gtggagacag ccccgaagc agcaagccaa tttccattaa ttaccgaaca 240
gaaattgaca aaccatccca gatgcaagt accgatgttc aggacaacag cattagtgtc 300
aagtggctgc cttcaagttc ccctgttact ggttacagag taaccaccac tcccaaaaat 360
ggaccaggag caacaaaaac taaaactgca ggtccagatc aaacagaaat gactattgaa 420
ggcttgacgc ccacagtggg gtatgtggtt agtgtctatg ctcagaatcc aagcggagag 480
agtcagcctc tggttcagac tgcagtaacc actattcctg caccaactga cctgaagtcc 540
actcaggtca caccacaag cctgagccgc cagtggacac caccaatgt tcactcactg 600
gatatcgagt gcyggtgacc cccaaggaga agaccgggac ccatgaaaga aatcaacctt 660
gtcctgaca gctcatccgn ggggtgtatca ggacttatgg gggactgccc cggcnggccg 720
ntcgaaancg aattntgaaa tttccttcnc actggngggc gnttcgagct tncctntana 780
nggcccaatt cncctntagn gggtcgtn 808

```

<210> 242

<211> 26

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 22

<223> n = A,T,C or G

<400> 242

agcgtgggtcg cggccgaggt cnagga

26

<210> 243

<211> 697

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 496, 541, 624, 662, 679, 688

<223> n = A,T,C or G

<400> 243

```

tcgagcggcc gcccgggcag gtccaccaca cccaattcct tgctggatc atggcagccg 60
ccacgtgcca ggattaccgg ctacatcatc aagtatgaga agcctgggtc tcctccaga 120

```

```
gaagtgggtcc ctgggccccg ccctgggtgtc acagaggcta ctattactgg cctggaaccg 180
ggaaccgaat atacaattta tgtcattgcc ctgaagaata atcagaagag cgagccccctg 240
attggaagga aaaagacaga cgagcttccc caactggtaa cccttccaca cccaatctt 300
catggaccag agatcttgga tgttccttcc acagttcaaa agacccttt cgtcaccac 360
cctgggtatg acaactggaaa tggatttcag ctctctggca cttctggtca gcaaccagt 420
gttggggcaac aatgatctt tgaggaaacat ggttttaggc ggaccacacc gccacaacg 480
ggcaccacca taaggnatag gccaaagacca taccctggcg aatgtaggac aagaagctct 540
ntctcaacaa ccatctcatg ggccccattc caggacactt ctgagtacat catttcatgt 600
catcctgggtg ggcacttgat gaanaaccct tacagttcag ggttctctgga acttctacca 660
gngccacttc tgacagganc ttgggcgnga ccacct 697
```

<210> 244
<211> 373
<212> DNA
<213> Homo sapiens

```
<400> 244
agcgtgggtcg cggccgaggt ccattttctc cctgacggtc ccacttctct ccaatcttgt 60
agttcacacc attgtcatyg caccatctay atgaatcaca tctgaaatga ccacttccaa 120
agcctaagca ctggcacaac agtttaaagc ctgattcaga cattcggtcc cactcatctc 180
caacggcata atgggaaact gtgtaggggt caaagcacga gtcacccgta gtttggttca 240
agccttcgtt gacagagttg cccacggtaa caacctcttc ccgaacctta tgcctctgct 300
ggtctttcag tgcctccact atgatgttgt aggtggcacc tctggtgagg acctgcccgg 360
gcggcccgtc cga 373
```

<210> 245
<211> 307
<212> DNA
<213> Homo sapiens

```
<400> 245
agcgtgggtcg cggccgaggt gtgccccaga ccaggaattc ggcttcgacg ttggccctgt 60
ctgcttctctg taaactccct ccattcccaac ctggctccct cccacccaac caactttccc 120
cccaaccggg aaacagacaa gcaacccaaa ctgaaccccc tcaaaagcca aaaaaatggg 180
agacaatttc acatggactt tggaaaatat ttttttctt tgcattcacc tctcaaaact 240
agtttttatc tttgaccaac cgaacatgac caaaaacaa aagtgcctg cccgggcccgc 300
cgctcga 307
```

<210> 246
<211> 372
<212> DNA
<213> Homo sapiens

```
<400> 246
tcgagcggcc gccggggcag gtctcaccga gagtgccac ctacaacatc atagtggagg 60
cactgaaaga ccagcagagg cataagggtc gggaagaggt tgttaccgtg ggcaactctg 120
tcaacgaagg cttgaaccaa cctacggatg actcgtgctt tgaccctac acagtttccc 180
attatgccgt tggagatgag tgggaacgaa tgtctgaatc aggcctttaa ctgttggtgc 240
agtgtttagg ctttggaagt ggtcatttca gatgtgattc atctagatgg tgccatgaca 300
atggtgtgaa ctacaagatt ggagagaagt gggaccgtca gggagaaaat ggacctcggc 360
cgcgaccacg ct 372
```

<210> 247
<211> 348
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> 284, 297, 299, 322, 325, 338, 342, 345
<223> n = A,T,C or G

<400> 247
tcgagcggcc gcccgggcag gtaccggggt ggtcagcgag gagccattca cactgaactt 60
caccatcaac aacctgcggt atgaggagaa catgcagcac cctgggtcca ggaagttcaa 120
caccacggag agggtccttc agggcctgct caggtccttg ttcaagagca ccagtgttgg 180
ccctctgtac tctggctgca gactgacttt gctcagacct gagaaacatg gggcagccac 240
tggagtggac gccatctgca ccctccgctc tgatccactc ggtinctggac tggacanana 300
gcggtctatac ttgggagctg anccnaacct ttggcgngga cncnctt 348

<210> 248
<211> 304
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 125
<223> n = A,T,C or G

<400> 248
gaggactggc tcagctccca gtatagccgc tctctgtcca gtccaggacc agtgggatca 60
aggcggaggg tgcagatggc gtccactcca gtggtgccc catgtttctc aagtctgagc 120
aaagncagtc tgcagccaga gtacagaggg ccaacactgg tgctcttgaa caggacctg 180
agcagggcct gaaggacct ctcctgggtg ttgaacttcc tggagccagg gtgctgcatg 240
ttctcctcat accgcagggt gttgatggtg aagttcagtg tgaatggctc ctcgctgacc 300
acc 304

<210> 249
<211> 400
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 308, 310, 312, 320, 331, 336, 383, 392, 396
<223> n = A,T,C or G

<400> 249
agcgtggctg cggccgaggt ccaccacacc caattccttg ctggtatcat ggcagccgcc 60
acgtgccagg attaccggt acatcatcaa gtatgagaag cctgggtctc ctcccagaga 120
agtggctcct cggcccgcc ctggtgtcac agaggctact attactggcc tggaaaccggg 180
aaccgaatat acaatttatg tcattgccct gaagaataat cagaagagcg agccctgat 240
tggaaagaaa aagacagacg agcttcccca actggtaacc cttccacacc ccaatcttca 300
tggaccanan ancttggatn gtcctttcac nggttnaaaa aacccttttc gccccccac 360
cttgggggatt aaccttggga aanggggatt tnacnttcc 400

<210> 250
<211> 400
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 338, 357, 361, 369, 388, 394
<223> n = A,T,C or G

<400> 250

```

tcgagcggcc gcccgggcag gtcctgtcag agtggcactg gtagaagttc caggaaccct 60
gaactgttaag ggttcttcat cagtgccaac aggatgacat gaaatgatgt actcagaagt 120
gtcctggaat ggggcccatg agatggttgt ctgagagaga gcttcttctg ctacattcgg 180
cgggtatggt cttggcctat gccttatggg ggtggccgtt gtgggcggtg tggccgcct 240
aaaaccatgt tcctcaaaga tcatttgttg cccaacactg ggttgctgac cagaagtgcc 300
aggaagctga ataccatttc cagtgtcata ccaggngng gtgaccaaag ggggtcnttt 360
ngacctggng aaaggaacca tccaaaanct ctgncccatg 400

```

<210> 251

<211> 514

<212> .DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 8, 107, 312, 338, 351, 352, 357, 363, 366, 373, 380, 405, 421, 444, 508

<223> n = A,T,C or G

<400> 251

```

agcgtggncg cggccgaggt ctgaggatgt aaactcttcc caggggaagg ctgaagtgt 60
gaccatggtg ctactgggtc cttctgagtc agatatgtga ctgatngaa ctgaagttag 120
tactgtatag ggtgaagtct ggtgtgccct aaatgctgca tctccagagc cttccatcat 180
taccgtttct tcttttgcta tgggatgaga cactgttgag tattctctaa agtcaccact 240
gaaatcttcc tccaaaggaa aacctgtgga aaagccctt atttctgcc cataatttgg 300
ttctcctaata cncctgaaa tcactatttc cctggaangt ttgggaaaaa nngggcnacc 360
tgncantgga aantggatan aaagatccca ccattttacc caacnagcag aaagtgggaa 420
nggtaccgaa aagctccaag taanaaaaaa gagggaaagta aaggtcaagt gggcaccagt 480
ttcaaacaaa actttcccca aactatanaa ccca 514

```

<210> 252

<211> 501

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 20, 21, 25, 44, 343, 347, 356, 362, 387, 391, 398, 409, 428, 430, 453, 494

<223> n = A,T,C or G

<400> 252

```

aagcgccgc cgggagcag ncagnagtgc cttcgggact gggntcacc ccaggtctgc 60
ggcagttgtc acagcgccag ccccgctggc ctccaaagca tgtgcaggag caaatggcac 120
cgagatatc cttctgccac tgttctccta cgtggtatgt cttcccatca tcgtaacacg 180
ttgcctcatg agggctcacac ttgaattctc cttttccgtt cccaagacat gtgcagctca 240
tttgctggc tctatagttt ggggaaagt ttgtgaaact gtgccactga ctttacttc 300
ctccttctct actggagctt tccgtacctt ccacttctgc tgnrtggnaaa aagggnggaa 360
cntcttatca atttcattgg acagtanccc ncttctncc caaacatnc aagggaaaat 420
attgattncn agagcggatt aaggaacaac ccnaattatg ggggccagaa ataaaggggg 480
ctttccaca ggtnttttcc t 501

```

<210> 253

<211> 226

<212> DNA

<213> Homo sapiens

<400> 253
tcgagcggcc gcccgggcag gtctgcaggc tattgtaagt gttctgagca catatgagat 60
aacctggggc aagctatgat gttcgatacg ttaggtgtat taaatgcact ttgactgcc 120
atctcagtggt atgacagcct tctcactgac agcagagatc ttctcactg tgccagtggg 180
caggagaaag agcatgtctgc gactggacct cggccgcgac cacgct 226

<210> 254
<211> 226
<212> DNA
<213> Homo sapiens

<400> 254
agcgtggtcg cggccgaggt ccagtcgcag catgctcttt ctctgccca ctggcacagt 60
gaggaagatc tctgtgtca gtgagaaggc tgtcatccac tgagatggca gtcaaaagtg 120
catttaatac acctaacgta tcgaacatca tagcttggcc caggttatct catatgtgct 180
cagaacactt acaatagcct gcagacctgc ccgggcggcc gctcga 226

<210> 255
<211> 427
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 327, 403
<223> n = A,T,C or G

<400> 255
cgagcggcgg cccgggcagg tccagactcc aatccagaga accaccaagc cagatgtcag 60
aagctacacc atcacagggt tacaaccagg cactgactac aagatctacc tgtacacctt 120
gaatgacaat gctcggagct cccctgtggt catcgacgcc tccactgccca ttgatgcacc 180
atccaacctg cgtttctctg ccaccacacc caattccttg ctggtatcat ggcagccgcc 240
acgtgccagg attaccggct acatcatcaa gtatgagaag cctgggtctc ctcccagaga 300
agtggtcctt cggcccccgc ctggtgnac agaaagctact attactggcc tggaaaccggg 360
aaccgaatat acaatttatg tcattgccct gaagaataat canaagagcg agcccctgat 420
tggaagg 427

<210> 256
<211> 535
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 347, 456, 475
<223> n = A,T,C or G

<400> 256
agcgtggtcg cggccgaggt cctgtcagag tggcactggt agaagttcca ggaaccctga 60
actgtaaggg ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagtgt 120
cctggaatgg ggcccatgag atggttgtct gagagagagc ttcttgtcct gtctttttcc 180
ttccaatcag gggctcgctc ttctgattat tcttcagggc aatgacataa attgtatatt 240
cggttcccgg ttccaggcca gtaatagtag cctctgtgac accagggcgg ggccgaggga 300
ccacttctct gggaggagac ccaggcttct calacttgat gatgtanccg gtaalcctgg 360
caccgtggcg gctgccatga taccagcaag gaattgggtg tgggtggcaa gaaacgcagg 420
ttggatgggt catcaatggc agtggaggcg tcgatnacca caggggagct ccgancattg 480
tcattcaagg tggacaggta gaattctgta atcagggtgcc tggtttgtaa acctg 535

<210> 257
<211> 544
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 495, 511
<223> n = A,T,C or G

<400> 257
tcgagcggcc gcccgggcag gtttcgtgac cgtgacctcg aggtggacac caccctcaag 60
agcctgagcc agcagatcga gaacatccgg agcccagagg gcagccgcaa gaaccccgcc 120
cgacacctgcc gtgacctcaa gatgtgccac tctgactgga agagtggaga gtactggatt 180
gaccccaacc aaggctgcaa cctggatgcc atcaaagtct tctgcaacat ggagactggg 240
gagacctgcg tgtacccacac tcagcccagt gtggcccaga agaactggta catcagcaag 300
aaccccaagg acaagaagca tgtctgggtc ggcgaaagca tgaccgatgg attccagtcc 360
gagtatggcg gccagggtcc cgacctgcc gatgtggacc tcggccgcga ccacgctaag 420
cccgaattcc agcacactgg cggccggttac tagtgggacg cgagcttcgg taccaagctt 480
ggcgtaataca tgggncatag ctgtttcctg ngtgaaaatg gtattccgct tcacaaattc 540
ccac 544

<210> 258
<211> 418
<212> DNA
<213> Homo sapiens

<400> 258
agcgtggtcg cggccgaggt ccacatcggc aggttcggag ccctggccgc catactcga 60
ctggaatcca tcggtcatgc tctcgcgaa ccagacatgc ctcttgtcct tggggttctt 120
gctgatgtac cagttcttct gggccacact gggctgagtg ggttacacgc aggtctcacc 180
agtctccatg ttgcagaaga ctttgatggc atccagggtg cagccttggt tgggggtcaat 240
ccagtactct ccactcttcc agtcagagtg gcacatcttg aggtcacggc aggtgcgggc 300
ggggttcttg cggctgccct ctgggctccg gatgttctcg atctgctggc tcaagctctt 360
gaaggggtgt gtccacctcg aggtcacggt cacgaaacct gccggggcgg ccgctcga 418

<210> 259
<211> 377
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 320, 326, 342, 352
<223> n = A,T,C or G

<400> 259
agcgtggtcg cggccgaggt caagaacccc gcccgcaact gccgtgacct caagatgtgc 60
cactctgact ggaagagtgg agagtactgg attgacccca accaaggctg caacctggat 120
gccatcaaag tcttctgcaa catggagact ggtgagacct gcgtgtaccc cactcagccc 180
agtgtggccc agaagaactg gtacatcagc aagaacccca aggacaagag gcatgtcttg 240
ttcggcgaga gcatgaccga tggattccag ttcgagtatg gcggccaggg ctccgacctt 300
gccgatgtgg acctgcccgn gccggncgcg tcgaaaagcc cnaatttcca gncacacttg 360
gccggccggt actactg 377

<210> 260
<211> 332

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<212> DNA

<213> Homo sapiens

<400> 260

```
tgcagcggcc gcccgggcag gtcacatcg gcagggtcgg agccctggcc gccatactcg 60
aactggaatc catcggtcat gctctcgccg aaccagacat gcctcttgtc cttgggggttc 120
ttgctgatgt accagtcttt ctggggcaca ctgggctgag tggggtacac gcagggtctca 180
ccagtctcca tgttcagaa gactttgatg gcatccagggt tgcagccttg gttgggggtca 240
atccagtact ctccactctt ccagtcagag tggcacatct tgaggtcacg gcagggtgcgg 300
gcgggggttct tgacctcgcc cgcgaccacg ct 332
```

<210> 261

<211> 94

<212> DNA

<213> Homo sapiens

<400> 261

```
cgagcggccg cccgggcagg tccccccct ttttttttt ttttttttt ttttttttt 60
ttttttttt ttttttttt ttttttttt tttt 94
```

<210> 262

<211> 650

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 412, 582, 612, 641, 646

<223> n = A,T,C or G

<400> 262

```
agcgtggctc cggccgaggt ctggcattcc ttcgacttct ctccagccga gtttcccaga 60
acatcacata tcactgcaaa aatagcattg catacatgga tcaggccagt ggaaatgtaa 120
agaaggccct gaagctgatg gggtc aaatg aaggtgaatt caaggctgaa ggaaatagca 180
aattcaccta cacagtctct gaggatggtt gcacgaaaca cactggggaa tggagcaaaa 240
cagtctttga atatcgaaca cgcaaggctg tgagactacc tattgtagat attgcaccct 300
atgacattgg tggctctgat caagaatttg gtgtggacgt tggccctggt tgccttttat 360
azaccaaaact ctatctgaaa tcccaacaaa aaaaatttaa ctccatattg gntcctcttg 420
ttctaattctt ggcaaccagt gcaagtgacc gacaaaattc cagttattta ttcccaaaat 480
gtttggaaac agtataattt gacaaaagaa aaaggatact tctctttttt tggctgggtcc 540
accaaaataca attcaaaagg ctttttggtt ttattttttt anccaattcc aatttcaaaa 600
tctctcaatg gngcttataa taaaataaac ttccaccctt nttttntgat 650
```

<210> 263

<211> 573

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 453, 458, 544

<223> n = A,T,C or G

<400> 263

```
agcgtggctc cggccgaggt ctgggaigct cctgctgtca cagtgaagata ttacaggatc 60
acttacggag aaacaggagg aaatagccct gtccaggagt tcactgtgcc tgggagcaag 120
tctacagcta ccatcagcgg ccttaaacct ggagttgatt ataccatcac tgtgtatgct 180
gtcactggcc gtggagacag ccccgaagc agcaagccaa ttccattaa ttaccgaaca 240
```

gaaattgaca aaccatccca gatgcaagtg accgatgttc aggacaacag cattagtgtc 300
aagtggctgc cttcaagttc ccctgttact ggttacagaa gtaaccacca ctcccaaaaa 360
tggaaccagga ccaacaaaaa ctaaaactgc aggtccagat caaacagaaa atggactatt 420
gaaggcttgc agccacacgt ggaagtatgt ggntagngt ctatgctcag aatcccaagc 480
cggagaaagt cagccttctg gtttagactg cagtaaccaa cattgatcgc cctaaaggac 540
tggncattca cttggatggt ggatgtccaa ttc 573

<210> 264

<211> 550

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 39, 174, 352, 526

<223> n = A,T,C or G

<400> 264

tcgagcggcc gcccgggcag gtccttgacg ctctgcagng tcttcttcac catcagggtgc 60
agggaaatagc tcatggattc cactctcagg gctcgagtag gtcacctgt acctggaaac 120
ttgccctgt gggctttccc aagcaatgtt gatggaatcg acatccacat cagngaagtc 180
cagtccttta gggcgatcaa tgttggttac tgcagtctga accagaggct gactctctcc 240
gcttggattc tgagcataga cactaaccac atactccact gtgggctgca agccttcaat 300
agtcatttct gtttgatctg gacctgcagt ttttaagttt tgggtggtcct gnccatttt 360
tgggaagtgg ggggttactc tgtaaccagt aacaggggaa cttgaaggca gccacttgac 420
actaatgctg ttgtcctgaa catcggtcac ttgcatctgg ggatggtttt gacaatttct 480
ggttcggcaa attaatggaa attggcttgc tgcttggcgg ggtgnctcc acgggccagt 540
gacagcatac 550

<210> 265

<211> 596

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 347, 352, 353, 534, 555, 587

<223> n = A,T,C or G

<400> 265

tcgagcggcc gcccgggcag gtccttgacg ctctgcagtg tcttcttcac catcagggtgc 60
agggaaatagc tcatggattc cactctcagg gctcgagtag gtcacctgt acctggaaac 120
ttgccctgt gggctttccc aagcaatgtt gatggaatcg acatccacat cagtgaatgc 180
cagtccttta gggcgatcaa tgttggttac tgcagtctga accagaggct gactctctcc 240
gcttggattc tgagcataga cactaaccac atactccact gtgggctgca agccttcaat 300
agtcatttct gtttgatctg gacctgcagt ttttaagttt tgttggncct gnnccatttt 360
tggggaaggg gtgggttactc ttgtaaccag taacagggga acttgaagca gccacttgac 420
actaatgctg gtggcctgaa catcggtcac ttgcatctgg gatggtttgg tcaatttctg 480
ttcggttaatt aatgggaaat tggcttactg gcttgcgggg gctgtctcca cggncagtga 540
caagcataca caggngatgg gtataatcaa ctccagggtt aaggccnctg atggta 596

<210> 266

<211> 506

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 393, 473

<223> n = A,T,C or G

<400> 266

```
agcgtggtcg cggccgaggt ctgggatgct cctgctgtca cagtgaagata ttacaggatc 60
acttacggag aacacaggag aaatagccct gtcaggaggt tcaactgtgcc tgggagcaag 120
tctacagcta ccatcagcgg ccttaaacct ggagttgatt ataccatcac tgtgtatgct 180
gtcactggcc gtggagacag ccccgcaagc agtaagccaa tttccattaa ttaccgaaca 240
gaaattgaca aaccatccca gatgcaagtg accgatgttc aggacaacag cattagtgtc 300
aagtggctgc cttcaagttc ccctgttact ggttacagag taaccaccac tcccaaaaat 360
gggaccagga ccaacaaaaa actaaaaactg canggtccag atcaaacaga aatgactatt 420
gaaggcttgc agcccacagt ggagtatgtg ggtagtgctc tatgtctcaga atnccaagcg 480
gagagagtca gcctctgtgt cagact                                     506
```

<210> 267

<211> 548

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 346, 358, 432, 510, 512

<223> n = A,T,C or G

<400> 267

```
tcgagcggcc gcccgggcag gtcagcgtc tcaggacgtc accaccatgg cctgggctct 60
gtctctcctc accctcctca ctcagggcac agggtcctgg gccagctctg ccctgactca 120
gcctccctcc gcgtccgggt ctectggaca gtcagtcacc atctcctgca ctggaaccag 180
cagtgaagtt ggtgcttatg aatttgtctc ctggtaccac caacaccag gcaaggcccc 240
caaaactcatg atttctgagg tcaactaagcg gccctcaggg gtccctgctc gcttctctgg 300
ctccaagctc ggcaacacgg cctccctgac cgtctctggg ctccangctg aggatgancg 360
tgattattac tggaagctca tatgcaggca acaacaattg ggtgttcggc ggaagggacc 420
aagctgaccg tncctaaggc aagcccaagg cttgcccccc tcgggtcactc tgttcccacc 480
ctcctctgaa gaagctttca agccaacaan gncacactgg gtgtgtctca taagtggact 540
ttctaccc                                     548
```

<210> 268

<211> 584

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 98, 380, 421, 454, 495, 506, 512, 561, 565, 579

<223> n = A,T,C or G

<400> 268

```
agcgtggtcg cggccgaggt ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc 60
tcaggtagct gctggcgcg tacttgttgt tgctttgntt ggagggtgtg gtggtctcca 120
ctcccgctt gacggggctg ctatctgcct tcaggccac tgtcaggct cccgggtaga 180
agtcaactat gagacacacc agtgtgcct tgttggcttg aagctcctca gaggagggtg 240
ggaacagagt gaccgagggg gcagccttgg gctgacctag gacggtcagc ttggtccctc 300
cgccgaacac ccaattgttg ttgcctgcat atgagctgca gtaataatca gcctcatcct 360
cagcctggag cccagagacn gtcaaggag gcccgtgttt gccaaagact ggaagccaga 420
naaycgatca gggaccctg agggccctt tacngacctc aaaaaatcat gaatttgggg 480
ggcctttgcc tgggngttgg ttggtnacca qnaaaacaaa atttcataaa gcaccaacgt 540
cactgctggt ttccagtgc ngsaanatgt gaactgaant gtcc                                     584
```

<210> 269
<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 265, 329
<223> n = A, T, C or G

<400> 269
agcgtggtcg cggccgaggt ccagcatcag gagccccgcc ttgccggctc tggtcacgc 60
ctttcttttt gtggcctgaa acgatgtcat caattcgcag tagcagaact gccgtctcca 120
ctgctgtctt ataagtctgc agcttcacag ccaatggctc ccatatgcc agttccttca 180
tgtccaccaa agtaccgctc tcaccattta cccccagggt ctacacagttc tcctgggtgt 240
gcttggcccc aagggaggta agtanacgga tgggtgctgt cccacagttc tggatcaggg 300
tacgagggaat gacctctagg gcctgggcna caagccctgt atggacctgc ccggggcggc 360
ccgctcga 368

<210> 270
<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 54, 163, 219, 229, 316
<223> n = A, T, C or G

<400> 270
tcgagcggcc gcccgggcag gtccatacag ggctgttgcc caggccctag aggn cattcc 60
ttgtaccctg atccagaact gtgggaccag caccatccgt ctacttacct cccttcgggc 120
caagcacacc caggagaact gtgagacctg gggtgtaaat gngagacgg gtactttggt 180
ggacatgaag gaactgggca tatgggagcc attggctgng aagctgcana cttataagac 240
agcagtggag acggcagttc tgctactgcy aattgatgac atcgtttcag gccacaaaaa 300
gaaaggcgat gaccanagcc ggcaaggcgg ggcttcctga tgctggacct cggccgcga 360
ccacgctt 368

<210> 271
<211> 424
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 279, 329, 362, 384, 400
<223> n = A, T, C or G

<400> 271
agcgtggtcg cggccgaggt ccactagagg tctgtgtgcc attgccagc cagagtctct 60
gcgttacaaa ctccataggag ggcttgctgt gcggagggcc tgctatggtg tgctgcggtt 120
catcatggag agtggggcca aaggctgcga ggttggtgtg tctgggaaac tccgaggaca 180
gagggctaaa tccatgaagt ttgtggatgg cctgatgatc cacagcggag accctgttaa 240
ctactacgtt gacactgctg tgcgccacgt gttgctcana cagggtgtgc tgggcatcaa 300
ggtgaagatc atgctgccct gggacccanc tggcaaaaat ggcccttaaa aaccctttgc 360
cntgaccacg tgaaccattt gtgngaaccc caagatgaan atacttgccc accaccccc 420
attc 424

<210> 272
<211> 541
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 422, 442, 510, 513, 515, 525
<223> n = A,T,C or G

<400> 272
tcgagcggcc gcccgggcag gtctgccaa gagaccctgt tatgctgtgg ggactggctg 60
gggcatggca ggcggtctct gcttcccacc cttctgttct gagatggggg tggggggcag 120
tatctcatct ttgggttcca caatgetcac gtggtcaggc aggggtctct tagggccaat 180
cttaccagtt ggggtccagg gcagcatgat cttcaccttg atgccagca caccctgtct 240
gagcaacacg tggcgcacag cagtgtcaac gtagtagtta acagggctct cgtgtggat 300
catcaggcca tccacaaact tcatggattt agccctctgt cctcggagtt tcccaaaaca 360
ccacaacctc gccagccttt gggtccctct tctcatgaa tgaaaccgca gcacaccatt 420
ancaaggccc ttccgcacag gnaagccctt cctaaggagt ttgtaaacg caaaaaactc 480
ttgcctgggg caaatgggca cacagacctn tantnggacc ttggnccgag aaccaccgct 540
t 541

<210> 273
<211> 579
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 223, 265, 277, 308, 329, 346, 360, 366, 429, 448, 517, 524,
531, 578
<223> n = A,T,C or G

<400> 273
agcgtggctg cgcccgaggt ctggccctcc tggcaaggct ggtgaagatg gtcaccctgg 60
aaaaccggga cgacctgggt agagaggagt tgttgacca cagggtgctc gtggtttccc 120
tggaactcct ggaactcctg gcttcaaagg cattagggga cacaatggtc tggatggatt 180
gaagggacag ccgggtgctc ctggtgtgaa ggtgaacct ggngcccctg gtgaaaatgg 240
aactccaggt caaacaggag cccgnggggt tcttgngag agaggacgtg ttggtgcccc 300
tggcccanac ctgcccgggc ggccgctcna aaagccgaaa tccagnacac tggcgcccg 360
tactantgga atccgaactt cggtaacaaa gcttgccgt aatcatggcc atagcttgtt 420
ccctggggng gaaattggta ttccgctncc aattccacac aacataccga acccggaag 480
cattaaagt taaaagccct gggggggcct aaatgangtg agcntaacte ncatttaatt 540
ggcgttgccg ttcactgccc cgcttttcca gtccgggna 579

<210> 274
<211> 330
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 171
<223> n = A,T,C or G

<400> 274
tcgagcggcc gcccgggcag gtctgggcca ggggcaccaa cagtcctct ctcaccagga 60
agccacggg ctcctgtttg acctggagt ccattttcac caggggcacc aggttcacc 120

```

ttcacaccag gagcaccggg ctgtcccttc aatccatcca gaccattgtg ncccctaata 180
cctttgaagc caggaagtcc aggagttcca gggaaaccac gagcaccctg tggccaaca 240
actcctctct caccaggctg tccgggtttt ccagggtgac catcttcacc agccttgcca 300
ggagggccag acctcggccg cgaccacgct 330

```

```

<210> 275
<211> 97
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 2, 35, 72
<223> n = A,T,C or G

```

```

<400> 275
ancgtggtcg cggccgaggt cctcaccaga ggtgncacct acaacatcat agtggaggca 60
ctgaaagacc ancagaggca taaggttcgg gaagagg 97

```

```

<210> 276
<211> 610
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 358, 360, 363, 382, 424, 433, 464, 468, 477, 491, 499, 511,
558, 584, 588, 590
<223> n = A,T,C or G

```

```

<400> 276
tcgagcggcc gcccgggcag gtccattttc tccctgaagg tcccaattct ctccaatctt 60
gtagttcaca ccattgtcat ggcacatct agatgaatca catctgaaat gaccacttcc 120
aaagcctaag cactggcaca acagtttaaa gcctgattca gacattcgtt cccactcacc 180
tccaacggca taatgggaaa ctgtgtaggg gtcaaagcac gagtcatccg taggttggtt 240
caagccttcg ttgacagagt tgtccacggg aacaacctct tcccgaacct tatgcctctg 300
ctggtctttc agtgccctca ctatgatggt gtaggtggca cctctgggtg ggacctcngn 360
ccngaacaac gcttaagccc gnattctgca gaataatccc atcacacttg gcggccgctt 420
cgancatgca tcntaaaagg ggccccaatt tcccccttat aagngaance gtatttncca 480
atttcactgg ncccgcgnt tttacaaacg ncggtgaact ggggaaaaac cctggcggtt 540
acecaacttt aatcgccntt ggcagcaca tcccccttt tcgnccanct tgggcgtaaa 600
taaccgaaaa 610

```

```

<210> 277
<211> 38
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 2, 5, 18, 21, 31
<223> n = A,T,C or G

```

```

<400> 277
ancgnggtcg cggccgangt nttttttctt nttttttt

```

38

```

<210> 278
<211> 443

```


<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 156, 212, 233, 245, 327, 331, 336, 361, 364, 381, 391, 397,
419, 437

<223> n = A,T,C or G

<400> 278

```
agcgtggtcg cggccgaggt ctgaggttac atgcgtggtg gtggacgtga gccacgaaga 60
ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa 120
gccgcgggag gagcagtaca acagcacgta ccgggnggtc agcgtcctca ccgtcctgca 180
ccagaattgg ttgaatggca aggagtacaa gngcaagggt tccaacaaag ccntcccage 240
ccccntcgaa aaaaccattt ccaaaagcaa agggcagccc cgagaaccac aggtgtacac 300
cctgccccca tcccgggagg aaaagancaa naaccnggtt cagccttaac ttgcttggtc 360
naangctttt tatcccaacg nacttcccc ntggaantgg gaaaaaccaa tgggccaanc 420
cgaaaaacaa ttacaanaac ccc 443
```

<210> 279

<211> 348

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 219, 256, 291, 297, 307, 314, 317

<223> n = A,T,C or G

<400> 279

```
tcgagcggcc gcccgggcag gtgtcggagt ccagcacggg aggcgtggtc ttgtagtgtg 60
tctccggctg cccattgctc tcccactcca cggcgatgtc gctgggatag aagcccttga 120
ccaggcaggt caggctgacc tggttcttgg tcattctctc ccgggatggg ggcagggtga 180
acacctgggg ttctcggggc ttgccctttg gttttgaana tggttttctc gatgggggct 240
ggaagggctt tgttgnaaac cttgcacttg actccttgcc attcaccag ncctggngca 300
ggacgngag gacnctnacc acacggaacc gggctggttg actgtccc 348
```

<210> 280

<211> 149

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 18, 34, 51, 118, 120, 140

<223> n = A,T,C or G

<400> 280

```
agcgtggtcg cggacgaggt cctgtcagag tggnaactggt agaagttcca ngaaccctga 60
actgtaaggg ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagngn 120
cctggaatgg ggcccatgan atggttgcc 149
```

<210> 281

<211> 404

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
<222> 383, 386, 388, 393
<223> n = A,T,C or G

<400> 281
tcgagcggcc gcccgggcag gtcaccaca cccaattcct tgctggtatc atggcagccg 60
ccacgtgccg ggattaccgg ctacatcatc aagtatgaga agcctgggtc tcctcccaga 120
gaagtgggtc ctcgggcccg ccctggtgtc acagaggcta ctattactgg cctggaaccg 180
ggaaccgaat atacaattta tgtcattgcc ctgaagaata atcagaagag cgagccctcg 240
attggaagga aaaagacaga cgagcttccc caactggtaa cccttcaca cccaatctt 300
catggaccag agatcttggg tgttccttcc acagttcaaa agacccttt cggcaccccc 360
cctgggtatg aacctgggaa aanggnantt aanctttcct ggca 404

<210> 282
<211> 507
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 320, 341, 424, 450, 459, 487, 490
<223> n = A,T,C or G

<400> 282
agcgtggtcg cgcccgaggt ctgggatgct cctgctgtca cagtgaagata ttacaggatc 60
acttacggag aaacaggagg aaatagccct gtccaggagt tcactgtgcc tgggagcaag 120
tctacagcta ccatcagcgg ccttaaacct ggagttgatt ataccatcac tgtgtatgct 180
gtcactggcc gtggagacag ccccgcaagc agcaagccaa ttccattaa ttaccgaaca 240
gaaattgaca aacctccca gatgcaagtg accgatgtc aggacaacag cattagtgtc 300
aagtgggtgc cttcaaggtn ccctggtact gggttacaga ntaaccacca ctcccaaaaa 360
tggaccagga accacaaaaa cttaaactgc aggggtccaga tcaaaacaga aatgactatt 420
gaangcttgc agccacaggt gggagtatgn gggtagtgnc tatgcttcag aatccaagcg 480
gaaaaangtc aagccttntg ggttcaa 507

<210> 283
<211> 325
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 216, 292, 303, 304
<223> n = A,T,C or G

<400> 283
tcgagcggcc gcccgggcag gtccttgcat ctctgcagtg tcttcttcac catcaggtgc 60
agggaaatgc tcatggattc catcctcagg gctcgagtag gtcacccctg acctggaac 120
ttgcccctgt gggctttccc aagcaatttt gatggaatcg acatccacat cagtgaatgc 180
cagtccttta gggcgatcaa tgttggttac tgcagnctga accagaggct gactctctcc 240
gcttggaatc tgagcataga cactaaccac atactccact gtgggctgca anccttcaat 300
aanncatctt tgtttgatct ggacc 325

<210> 284
<211> 331
<212> DNA
<213> Homo sapiens

<220>

<221> misc feature

<222> 54, 59, 63, 121, 312, 327

<223> n = A,T,C or G

<400> 284

```
tcgagcggcc gcccgggcag gtctggtggg gtctctggcag acgcacatgg gggngttgnt 60
ctnatccagc tgcccagccc ccattggcga gtttgagaag gtgtgcagca atgacaacaa 120
naccttcgac tcttcttgcc acttctttgc cacaaagtgc accctggagg gcaccaagaa 180
gggccacaag ctccacctgg actacatogg gccttgcaaa tacatcccc cttgectgga 240
ctctgagctg accgaattcc cccttgcgca tgcgggactg gctcaagaac cgtcctggca 300
cccttgtatg anagggatga agacacnacc c 331
```

<210> 285

<211> 509

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 316, 319, 327, 329, 339, 344, 357, 384, 398, 427, 443, 450, 478

<223> n = A,T,C or G

<400> 285

```
agcgtggtcg cgccgaggt ctgtcctaca gtctcagga ctctactccc tcagcagcgt 60
ggtgaccgtg ccctccagca acttcggcac ccagacctac acctgcaacg tagatcacia 120
gcccgagcaac accaaggtgg acaagagagt tgagcccaaa tcttgtgaca aaactcacac 180
atgccaccgg tgcccagcac ctgaactcct ggggggaccg tcagtcttcc tcttcccccg 240
catccccctt ccaaacctgc ccggcgcgcc gctcgaaaag cgaattccag cacttgccg 300
gccggtacta gtgganccna acttggnanc caacctgng gaantaatgg gcataaactg 360
tttctggggg gaaattggtg tccngtttac aattccnca caacatacga gccggaagca 420
taaaagncta aaagcctggg ggnggcctan tgaagtgaag ctaaactcac attaatngc 480
gttgccgctc actggcccgc ttttccagc 509
```

<210> 286

<211> 336

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 188, 251, 267

<223> n = A,T,C or G

<400> 286

```
tcgagcggcc gcccgggcag gtttggaagg gggatgcggg ggaagaggaa gactgacggt 60
ccccccagga gttcaggtgc tgggcacggt gggcatgtgt gagttttgtc acaagatttg 120
ggctcaactc tcttgtccac cttggtgttg ctgggcttgt gatctacgtt gcagggtgtg 180
gtctgggngc cgaagtgtct ggagggcacg gtcaccacgc tgctgaggga gtagagtctt 240
gaggactgta ngacagacct cggccgngac cagcctaagc cgaattctgc agatatccat 300
cacttgccg gccgctccga gcatgcattt tagagg 336
```

<210> 287

<211> 30

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
<222> 8, 18
<223> n = A,T,C or G

<400> 287
agcgtggncg cggacganga caacaacccc

30

<210> 288
<211> 316
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 22, 130
<223> n = A,T,C or G

<400> 288
tcgagcggcc gcccgggcag gncacatcg gcagggtcgg agccctggcc gccatactcg 60
aactggaatc catcggtcat gctcttgccg aaccagacat gcctcttgte cttgggggttc 120
ttgctgatgn accagttctt ctggggccaca ctgggctgag tgggggtacac gcagggtctca 180
ccagttctcca tgttcagaaa gactttgatg gcattccagggt tgcagccttg gttgggggtca 240
atccagtact ctccactctt ccagtcagag tggcacatct tgagggtcacg gcagggtgcgg 300
gcgggggttct tgacct 316

<210> 289
<211> 308
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 36, 165, 191, 195, 218, 235
<223> n = A,T,C or G

<400> 289
agcgtggtcg cggccgaggt ccagcctgga gataanggtg aagggtgtgc ccccggaactt 60
ccaggtatag ctggacctcg tggtagccct ggtgagagag gtgaaactgg ccctccagga 120
cctgctggtt tccctgggtg tcctggacag aatggtgaac ctggnggtaa aggagaaaga 180
ggggctccgg ntganaaaagg tgaaggaggc cctcctgnat tggcaggggc cccangactt 240
agaggtggag ctggccccc tggcccccga ggaggaaaag gtgctgctgg tcctcctggg 300
ccacctgg 308

<210> 290
<211> 324
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 184
<223> n = A,T,C or G

<400> 290
tcgagcggcc gcccgggcag gtctgggcca ggaggaccaa taggaccagt aggaccctt 60
gggccatctt tccctgggac accatcagca cctggaccgc ctggttcacc ctgtcacc 120
tttgaccag gacttccaag acctcctctt tctccaggca ttccttgca accaggagta 180
ccancagcac cagggtggccc aggaggacca gcagcaccct ttcctccttc gggaccaggg 240

ggaccagctc cacctctaag tcctggggcc cctgccaatc caggagggcc tccttcacct 300
 ttctcaccgc gagccctct ttct 324

<210> 291
 <211> 278
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 249, 267
 <223> n = A,T,C or G

<400> 291
 tcgagcggcc gcccgggcag gtccaccggg atattcgggg gtctggcagg aatgggaggc 60
 atccagaacg agaaggagac catgcaaagc ctgaacgacc gcctggcctc ttacctggac 120
 agagtgaaga gcctggagac cgacaaccgg aggctggaga gcaaaatccg ggagcacttg 180
 gagaagaagg gacccaggt cagagactgg agccattact tcaagatcat cgaggacctg 240
 agggctcana tcttcgcaa tactgcngac aatgcccc 278

<210> 292
 <211> 299
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 6, 19, 25, 51, 53, 61, 63, 70, 109, 136, 157, 241, 276
 <223> n = A,T,C or G

<400> 292
 atgcgnggtc gcggccgang accanctctg gtcatactt gactctaaag nontcaccag 60
 nanttacggn cattgccaat ctgcagaacg atgcgggcat tgccycant atttgcgaag 120
 atctgagccc tcaggncctc gatgatcttg aagtaanggc tccagtctct gacctggggt 180
 cccttctctt ccaagtgtct ccggattttg ctctccagcc tccggttctc ggtctccaag 240
 netttcact ctgtccagga aaagaggcca ggcggnccat cagggtcttt gcatggact 299

<210> 293
 <211> 101
 <212> DNA
 <213> Homo sapiens

<400> 293
 agcgtggtcg cggccgaggt tgtacaagct tttttttttt tttttttttt tttttttttt 60
 tttttttttt tttttttttt tttttttttt tttttttttt t 101

<210> 294
 <211> 285
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 64, 103, 110, 237, 282
 <223> n = A,T,C or G

<400> 294
 tcgagcggcc gcccgggcag gtctgccaac accaagattg gccccgcgcg catccacaca 60

```

gttngtgtgc ggggaggtaa caagaaatac cgtgccctga ggntggacgn ggggaatttc 120
tcctggggct cagagtgttg tactcgtaaa acaaggatca tcgatgttgt ctacaatgca 180
tctaataacg agctgggttcg taccaagacc ctggtgaaga attgcatcgt gctcatngac 240
agcacaccgt accgacagtg ggtaccgaag tcccactatg cncct 285

```

<210> 295
 <211> 216
 <212> DNA
 <213> Homo sapiens

```

<400> 295
tcgagcggcc gcccgggcag gtccaccaca cccaattcct tgctggatc atggcagccg 60
ccacgtgccca ggattaccgg ctacatcacc aagtatgaga agcctgggtc tcctcccaga 120
gaagtgggtcc ctggcccccg ccctgggtgc acagaggcta ctattactgg cctggaaccg 180
ggaaccgaat atacaattta tgcattgcc ctgaag 216

```

<210> 296
 <211> 414
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 7, 10, 33, 61, 62, 63, 88, 109, 122, 255, 298, 307, 340,
 355, 386, 393
 <223> n = A,T,C or G

```

<400> 296
agcgtgntcn eggcggagga tggggaagct cgnctgtctt ttcccttcca atcaggggct 60
nnntcttctg attattcttc agggcaanga cataaattgt atattcggnt cccggttcca 120
gnccagtaat agtagcctct gtgacaccag ggcggggccg agggaccact tctctgggag 180
gagacccagg cttctcatatc ttgatgatga agccggtaat cctggcacgt gggcggctgc 240
catgatacca ccaangaatt ggggtgtggtg gacctgcccg ggcgggccgc tcgaaaancc 300
gaattentgc aagaatatcc atcacacttg ggcggggccg tcgaaccatg catcntaaaa 360
gggcccgaat ttcccccta ttagnggaag ccncatttaa caattccac ttgg 414

```

<210> 297
 <211> 376
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 312, 326, 335, 361
 <223> n = A,T,C or G

```

<400> 297
tcgagcggcc gcccgggcag gtctcgcggt cgcactggtg atgctgggtc tgttgggtccc 60
cccggccctc ctggacctcc tgggtcccct ggtcctccca gcctggttt cgacttcagc 120
ttctgcccc agccacctca agagaaggct cacgatggtg gccgctacta ccgggtgat 180
gatgccaatg tggttcgtga ccgtgacctc gaggtggaca ccacctcaa gagccttgag 240
ccagcagaat cgaatacatt cggaacccaa gaagggaag cccgcaaaga aacccgccc 300
gcacctggcc gngaacctcc aagaangtgc ccacntcttg actgggaaaa aaagggaata 360
ntacttgga ttggac 376

```

<210> 298
 <211> 357
 <212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 345, 346

<223> n = A,T,C or G

<400> 298

```
agcgtggtcg cggccgaggt ccacatcggc agggtcggag ccctggccgc catactcgaa 60
ctggaatcca tcggtcatgc tctcgccgaa ccagacatgc ctcttgctct tggggttctt 120
gctgatgtac cagttcttct gggccacact gggctgagtg gggtaacacg aggtctcacc 180
agtctccatg ttgcagaaga ctttgatggc atccagggtg cagccttggt tggggtaaat 240
ccagtactct ccactcttcc agtcagaagt ggcacatctt gaggtcacgg cagggtgcgg 300
gcggggttct tgcgggctgc cttctgggc tcccggaatg ttctnngaac ttgctgg 357
```

<210> 299

<211> 307

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 281, 285, 306

<223> n = A,T,C or G

<400> 299

```
agcgtggtcg cggccgaggt ccactagagg tctgtgtgcc attgccagg cagagtctct 60
gcgttacaaa ctccatgagg ggcctgtctg gcggagggcc tgctatgggt tgctgcgggt 120
catcatggag agtggggcca aaggctgccg ggttggtgtg tctgggaaac tccgaggaca 180
gagggcctaa tccatgaagt ttgtggatgg cctgatgatc cacagcggag accctgttaa 240
ctactaagtt gacacttgct tgtgcgccac gtgttgctca nacanggggt ggctgggcat 300
caaggng 307
```

<210> 300

<211> 351

<212> DNA

<213> Homo sapiens

<400> 300

```
tcgagcggcc gcccgggcag gtctgccaaag gagaccctgt tatgctgtgg ggactggctg 60
gggcatggca ggcggctctg gcttcccacc cttctgttct gagatggggg tggtagggcag 120
tatctcatct ttgggttcca caatgtcac gtggtcaggc aggggcttct tagggccaat 180
cttaccagtt ggggtccagg gcagcatgat cttcaccttg atgccagca caccctgtct 240
gagcaacacg tggcgccacag caagtgtcaa cgtaagtaag ttaacagggt ctcgctgtg 300
gatcatcagg ccatccacaa acttcatgga tttaaccttc tgtcctcgga g 351
```

<210> 301

<211> 330

<212> DNA

<213> Homo sapiens

<400> 301

```
tcgagcggcc gcccgggcag gtgtttcaga ggttccaagg tccactgtgg aggtcccagg 60
agtgtggtg gtgggcacag aggtccgatg ggtgaaacca ttgacataga gactgttcct 120
gtccagggtg taggggcca gctctttgat gccattggcc agttggctca gctcccagta 180
cagccgtctc ctgttgagtc cagggtttt ggggtcaaga tgatggatgc agatggcatc 240
cactccagtg gctgctccat cttctcggc cctgagagag gtcagtctgc agccagagta 300
cagagggcca acactggtgt tctttgaata 330
```

<210> 302
<211> 317
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 129, 295
<223> n = A,T,C or G

<400> 302
agcgtggtcg cggccgaggt ctgtactggg agctaagcaa actgaccaat gacattgaag 60
agctgggccc ctacaccctg gacaggaaca gtctctatgt caatggtttc acccatcaga 120
gctctgtgnc caccaccagc actcctggga cctccacagt ggatttcaga acctcaggga 180
ctccatcctc cctctccagc cccacaatta tggctgctgg ccctctcctg gtaccattca 240
ccctcaactt caccatcacc aacctgcagt atggggagga catgggtcac cctgnctcca 300
ggaagttaaa caccaca 317

<210> 303
<211> 283
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 139, 146, 195
<223> n = A,T,C or G

<400> 303
tcgagcggcc gcccgacag gtctgggagg atagcaccgg gcatattttg gaatggatga 60
ggtctggcac cctgagcagt ccagcgagga ctgtgtctta gttgagcaat ttggctagga 120
ggatagtagt cagcacggnt ctgagnctgt gggatagctg ccatgaagta acctgaagga 180
ggtgctggct ggtangggtt gattacaggg ttgggaacag ctcgtacact tgccattctc 240
tgcataact ggtagtgag gtgagcctgg ccctcttctt ttg 283

<210> 304
<211> 72
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 59
<223> n = A,T,C or G

<400> 304
agcgtggtcg cggccgaggt gagccacagg tgaccggggc tgaagctggg gctgctggnc 60
ctgctggtcc tg 72

<210> 305
<211> 245
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 5, 11, 22, 98, 102

<223> n = A,T,C or G

<400> 305

```
cagcngctcc nacggggcct gngggaccaa caacaccgtt ttcaccetta ggccctttgg 60
ctctcttttc tccttttagca ccagggttgac cagcagcncc ancaggacca gcaaattccat 120
tggggccagc aggaccgacc tcaccacgtt caccagggtc tccccgagga ccagcaggac 180
cagcaggacc agcagcccca gcttcgcccc ggtcacctgt ggctcaccto ggcccgacc 240
acgct 245
```

<210> 306

<211> 246

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 144, 159

<223> n = A,T,C or G

<400> 306

```
tcgagcggtc gcccgggcag gtcaccggg atagccgggg gtctggcagg aatgggaggc 60
atccagaacg agaaggagac catgcaaagc ctgaacgacc gcctggcctc ttacctggac 120
agagtggagga gcctggagac cganaaccgg aggctggana gcaaatccg ggagcacttg 180
gagaagaagg gacccacggt caagagactg gagccattac ttcaagatca tcgagggacc 240
tggagg 246
```

<210> 307

<211> 333

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 5

<223> n = A,T,C or G

<400> 307

```
agcgnnggtcg cggccgaggt ccagctctgt ctcatcttg actctaaagt catcagcagc 60
aagacgggca ttgtcaatct gcagaacgat gcgggcattg tccgcagtat ttgcgaagat 120
ctgagccctc aggtcctcga tgatcttgaa gtaatggctc cagtctctga cctgggggtcc 180
cttcttctcc aagtgtctcc ggattttgct ctccagcctc cggttctcgg tctccaggct 240
cctcactctg tccaggtaag aaggccnagg cggtcgttca ggctttgcat ggtctccttc 300
tcgttctgga tgctcccat tcctgccaga ccc 333
```

<210> 308

<211> 310

<212> DNA

<213> Homo sapiens

<400> 308

```
tcgagcggcc gcccgggcag gtcaggaagc acattggtct tagagccact gcctcctgga 60
ttccacctgt gctgcggaca tctccaggga gtgcagaagg gaagcaggtc aaactgctca 120
gatcagtcag actggctgtt ctcatgtctc acctgagcaa ggtcagtcgt cagccagagt 180
acagagggcc aacctggtg ttcttgaaca agggcttgag cagaccctgc agaaccctct 240
tccgtggtgt tgaacttctt ggaaaccagg gtgttgcatg ttttctctca taatgcaagg 300
ttggtgatgg 310
```

<210> 309

<211> 429
<212> DNA
<213> Homo sapiens

<400> 309
agcgtgggtcg cgcccgaggt ccacatcggc agggtcggag ccctggccgc cataactcgaa 60
ctggaatcca tcggtcatgc tctcgccgaa ccagacatgc ctcttgctct tggggttctt 120
gctgatgtac cagttcttct gggccacact gggctgagtg gggtaacacg caggtctcac 180
cagtcctccat gttgcagaag actttgatgg catccaggtt gcagccttgg ttgggggtcaa 240
tccagtactc tccactcttc cagtcagaag tgggcacatc ttgaggtcac cggcaggtgc 300
cgggcccgggg gttcttgcgg ctgcccctct gggctccgga tgttctcgat ctgcttggct 360
caggtctctg aggggtgggtg tccacctcga ggtcacggtc accgaaacct gcccgggcgg 420
cccgtcga 429

<210> 310
<211> 430
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 342
<223> n = A,T,C or G

<400> 310
tcgagcgggtc gcccgggcag gtttcgtgac cgtgacctcg aggtggacac caccctcaag 60
agcctgagcc agcagatcga gaacatccg agcccagagg gcagccgcaa gaaccccgcc 120
cgacactgcc gtgacctcaa gatgtgccac tctgactgga agagtggaga gtactggatt 180
gaccccaacc aaggctgcaa cctggatgcc atcaaagtct tctgcaacat ggagactggg 240
gagacctcgg tgtacccccc tcagcccagt gtgggcccag aagaaactgg tacatcagca 300
aggaacccca aggacaagag gcattgtctt ggttcggcga gnagcatgac ccgatggatt 360
ccagtttcga gtattggcgg ccagggtctc ccgaccttg ccgatgtgga cctcgccgc 420
gaccaccgct 430

<210> 311
<211> 2996
<212> DNA
<213> Homo sapiens

<400> 311
cagccaccgg agtggatgcc atctgcaccc accgccccta cccacaggc cctgggctgg 60
acagagagca gctgtatttg gagctgagcc agctgaccca cagcatcact gagctggggc 120
cctacaccct ggacagggac agtctctatg tcaatggttt cacacagcgg agctctgtgc 180
ccaccactag cattcctggg acccccacag tggacctggg aacatctggg actccagttt 240
ctaaacctgg tccctcggct gccagccctc tccctgggtct attcactctc aacttcacca 300
tcaccaacct gcggtatgag gagaacatgc agcaccctgg ctccaggaag ttcaacacca 360
cggagagggt ccttcagggc ctgggtccctg ttcaagagca ccagtgttg ccctctgtac 420
tctggctgca gactgacttt gctcaggcct gaaaaggatg ggacagccac tggagtggat 480
gccatctgca cccaccaccc tgaccccaaa agccctaggc tggacagaga gcagctgtat 540
tgggagctga gccagctgac ccacaatatc actgagctgg gcccttatgc cctggacaac 600
gacagcctct ttgtcaatgg tttaactcat cggagctctg tgtccaccac cagcactcct 660
gggaccccca cagtgtatct gggagcatct aagactccag cctcgatatt tggcccttca 720
gctgccagcc atctcctgat actattcacc ctcaacttca ccatcactaa cctgcgggtat 780
gaggagaaca tgtggcctgg ctccaggaag ttcaacacta cagagagggt ccttcagggc 840
ctgctaaggc ccttgttcaa gaacaccagl gttggccctc tgtactctgg ctgcaggctg 900
acctgtctca ggccagagaa agatggggaa gccaccggag tggatgccat ctgcaccac 960
cgccctgacc ccacaggccc tgggctggac agagagcagc tgtatttga gctgagccag 1020
ctgaccacaa gcatactga gctgggcccc tacacactgg acagggacag tctctatgct 1080

```

aatggtttca cccatcgag ctctgtaccc accaccagca ccgggggtgt cagcgaggag 1140
ccattcacac tgaacttcac catcaacaac ctgcgctaca tggcggacat gggccaaccc 1200
ggctccctca agttcaacat cacagacaac gtcataaagc acctgctcag tcctttgttc 1260
cagaggagca gcctgggtgc acggtacaca ggctgcaggg tcatcgact aaggctctgtg 1320
aagaacgggtg ctgagacacg ggtggacctc ctctgcacct acctgcagcc cctcagcggc 1380
ccaggctctgc ctatcaagca ggtgttccat gagctgagcc agcagaccga tggcatcacc 1440
cggtggggcc cctactctct ggacaaagac agcctctacc ttaacggtta caatgaacct 1500
ggtccagatg agcctcctac aactcccaag ccagccacca cattcctgcc tcctctgtca 1560
gaagccacaa cagccatggg gtaccacctg aagacctca cactcaactt caccatctcc 1620
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gatctgcaat gactggaact tgcgggtgcc tgggggtgct tccccccagc cagggtccaa 2940
agaagcttgg ctggggcaga aataaacat attggtcgga cacaacaaaa aaaaaa 2996

```

<210> 312
 <211> 914
 <212> PRT
 <213> Homo sapiens

<400> 312
 Met Ser Met Val Ser His Ser Gly Ala Leu Cys Pro Pro Leu Ala Phe
 1 5 10 15
 Leu Gly Pro Pro Gln Trp Thr Trp Glu His Leu Gly Leu Gln Phe Leu
 20 25 30
 Asn Leu Val Pro Arg Leu Pro Ala Leu Ser Trp Cys Tyr Ser Leu Ser
 35 40 45
 Thr Ser Pro Ser Pro Thr Cys Gly Met Arg Arg Thr Cys Ser Thr Leu
 50 55 60
 Ala Pro Gly Ser Ser Thr Pro Arg Arg Gly Ser Phe Arg Ala Trp Ser
 65 70 75 80
 Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu
 85 90 95
 Thr Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly Val Asp Ala
 100 105 110
 Ile Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu
 115 120 125
 Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu
 130 135 140
 Gly Pro Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn Gly Phe Thr

145 150 155 160
 His Arg Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Pro Thr Val
 165 170 175
 Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile Phe Gly Pro Ser Ala
 180 185 190
 Ala Ser His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn
 195 200 205
 Leu Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys Phe Asn Thr
 210 215 220
 Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr
 225 230 235 240
 Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro
 245 250 255
 Glu Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg
 260 265 270
 Pro Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu
 275 280 285
 Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu
 290 295 300
 Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val
 305 310 315 320
 Pro Thr Thr Ser Thr Gly Val Val Ser Glu Pro Phe Thr Leu Asn
 325 330 335
 Phe Thr Ile Asn Asn Leu Arg Tyr Met Ala Asp Met Gly Gln Pro Gly
 340 345 350
 Ser Leu Lys Phe Asn Ile Thr Asp Asn Val Met Lys His Leu Leu Ser
 355 360 365
 Pro Leu Phe Gln Arg Ser Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg
 370 375 380
 Val Ile Ala Leu Arg Ser Val Lys Asn Gly Ala Glu Thr Arg Val Asp
 385 390 395 400
 Leu Leu Cys Thr Tyr Leu Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile
 405 410 415
 Lys Gln Val Phe His Glu Leu Ser Gln Gln Thr His Gly Ile Thr Arg
 420 425 430
 Leu Gly Pro Tyr Ser Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr
 435 440 445
 Asn Glu Pro Gly Pro Asp Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr
 450 455 460
 Thr Phe Leu Pro Pro Leu Ser Glu Ala Thr Thr Ala Met Gly Tyr His
 465 470 475 480
 Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn Leu Gln Tyr Ser
 485 490 495
 Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser Thr Glu Gly Val
 500 505 510
 Leu Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser Ser Met Gly Pro
 515 520 525
 Phe Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly
 530 535 540
 Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp Pro Val
 545 550 555 560
 Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu
 565 570 575
 Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser
 580 585 590
 Leu Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu
 595 600 605
 Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp

610	615	620
Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys		
625	630	635
Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe		640
645	650	655
Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu Val Thr Val Lys		
660	665	670
Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val Glu Gln Val Phe		
675	680	685
Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu Gly Ser Thr Tyr		
690	695	700
Gln Leu Val Asp Ile His Val Thr Glu Met Glu Ser Ser Val Tyr Gln		
705	710	715
Pro Thr Ser Ser Ser Thr Gln His Phe Tyr Leu Asn Phe Thr Ile		720
725	730	735
Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn		
740	745	750
Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe		
755	760	765
Arg Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr		
770	775	780
Phe Arg Ser Val Pro Asn Arg His His Thr Gly Val Asp Ser Leu Cys		
785	790	795
Asn Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val Ala Ile Tyr Glu		800
805	810	815
Glu Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr		
820	825	830
Leu Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Phe Pro Asn Arg Asn		
835	840	845
Glu Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp Ala Val Ile Leu		
850	855	860
Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly		
865	870	875
Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val		880
885	890	895
Gln Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp		
900	905	910
Leu Gln		

<210> 313
 <211> 656
 <212> DNA
 <213> Homo sapiens

<400> 313
 acagccagtc ggagctgcaa gtgttctggg tggatcgcy atatgcactc aaaatgctct 60
 ttgtaaagga aagccacaac atgtccaagg gacctgaggc gacttgaggc ctgagcaaaag 120
 tgcagtttgt ctacgactcc tcggagaaaa cccacttcaa agacgcagtc agtgctggga 180
 agcacacagc caactcgcac cacctctctg ccttggtcac ccccgctggg aagtcctatg 240
 agtgtcaagc tcaacaaacc atttcaactg cctctagtga tccgcagaag acggtcacca 300
 tgatcctgtc tgcggtccac atccaacctt ttgacattat ctcagatttt gtcttcagtg 360
 aagagcataa atgccagtg gatgagcggg agcaactgga agaaaccttg cccctgattt 420
 tggggctcat cttgggcctc gtcacatggt taacactcgc gatttaccac gtccaccaca 480
 aaatgactgc caaccaggtg cagatccctc gggacagatc ccagtataag cacatgggct 540
 agaggccgtt aggcaggcac cccctattcc tgcctcccca actggatcag gtagaacaac 600
 aaaagcactt ttccatcttg tacacgagat acaccaacat agctacaatc aaacag 656

<210> 314
<211> 519
<212> DNA
<213> Homo sapiens

<400> 314
tgtgcgtgga ccagtcagct tccgggtgtg actggagcag ggcttgtcgt cttcttcaga 60
gtcactttgc aggggttggg gaagctgctc ccacccatgt acagctccca gtctactgat 120
gtttaaggat ggtctcggtg gttaggccca ctagaataaa ctgagtccaa tacctctaca 180
cagttatgtt taactgggct ctctgacacc gggaggaagg tggcgggggt taggtgttgc 240
aaacttcaat ggttatgagg ggaatgtcac agagcaagct ttggtatcta gctagtctag 300
cattcattag ctaatggtgt cctttggtat ttattaaaat caccacagca tagggggact 360
ttatgtttag gttttgtcta agagttagct tatctgcttc ttgtgctaac agggctattg 420
ctaccaggga ctttgacat gggggccagc gtttgaaaac ctcatctagt ttttttgaga 480
gataggccac tggccttggg cctcgccgcg gaccacgct 519

<210> 315
<211> 441
<212> DNA
<213> Homo sapiens

<400> 315
cacagagcgt ttattgacac caccactcct gaaaattggg atttcttatt aggttcccct 60
aaaagttccc atgttgatta catgtaaata gtcacatata tacaatgaag gcagtttctt 120
cagaggcaac caggytttat agtgctaggt aaatgtcatc tcttttgtgc tactgactca 180
ttgtcaaacg tctctgcact gttttcagcc tctccacgtt gcctctgtcc tgcttcttag 240
ttccttcttt gtgacaaacc aaaagaataa gaggatttag aacaggactg cttttcccct 300
atgatttaaa aattccaatg actttcgccc ttgggagaaa ttccaagga aatctctctc 360
gctcgctctc tccgttttcc ttgtgagct tctggggag ggtagtggt gactttttga 420
tacgaaaaaa tgcattttgt g 441

<210> 316
<211> 247
<212> DNA
<213> Homo sapiens

<400> 316
tggcgcggt gctggatttc accttcttgc acctgccggt gagcgccctg ggtctaaagg 60
ggcgggatac tccattatgg cccctcgccc tgtagggtcg gaatagttag aaaaggcaac 120
ccagtctagc ttggttaagaa gagagacatg cccccaacct cggcgccctt tttctcacg 180
atctgctgtc cttacttcag cgactgcagg agcttcacct gcaagaaaac agcattgagc 240
tgctgac 247

<210> 317
<211> 409
<212> DNA
<213> Homo sapiens

<400> 317
tgacagggct cctggagttg ttaagtcacc aagtagctgc aggggatgga cactgcccc 60
cacgatgtgg gatgaacagc agccttggtt tgtagccag ggtgtccatg gatttgacc 120
gaatgctccc tggaggccct gtggcagga caggcactgg atggtccaga cctctggct 180
ggaggagtgg tggagccagg actgggctt cagccatgag ggctagaata acctgacctc 240
ttgatttcta acactgggtc attaatgaca cctttccagt ggaatgttga aaaaccaaca 300
ctgtcaggaa cctggccctg ggagggtca ggtgagctca caaggagag tcaagccaag 360
ccaagggtga ggkaacacac aacaccaggg gaaaccagcc cccaaacca 409

<210> 318
 <211> 320
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 6, 17, 24, 271
 <223> n = A,T,C or G

<400> 318
 caaggnagat ctttaagnggg gtentatgta agtgtgtctcc tgggtccagg gttcctggag 60
 cctcacgagg tcaggggaac cctttagtaa ctccaccagc agcatcatct cgtgaaggat 120
 gtcattgggc aggaagctgt cctggacgta ggcctctctc acatccatgg ggatgccata 180
 gtcaactgggc ctttgtctcg gaggaggcat caccagaaa ggcgagatct tggactcggg 240
 gcctgggttg ccagaatagt aaggggagca naggcaggcg aggcagggct ggaagccatt 300
 gctggagccc tgcagccgca 320

<210> 319
 <211> 212
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 172
 <223> n = A,T,C or G

<400> 319
 tgaagcaata gcgccccat tttacaggcg gagcatgaa gccagagagg tgggtggggg 60
 agggggctct tccctggctc aggcagatgg gaagatgagg aagccgctga agacgctgtc 120
 ggcctcagag ccctggtaaa tgtgacctt tttgggtct ttttcaacc anacctggtc 180
 acctgtctgc agacctcggc cgcgaccacg ct 212

<210> 320
 <211> 769
 <212> DNA
 <213> Homo sapiens

<400> 320
 tggaggtgta gcagttagag gagatyttag gcaagagtgt cacagcagag ccctaaascc 60
 tccaactcac cagttagaga tgagactgcc cagtactcag ccttcctctc ctggggccacc 120
 tggagggcgt ctttctccat cagcgcatat tgagcagggg tactcagatc cttcttggaa 180
 cctacaagga agagaagcac actggaaggg tcattctcct tcagggcacg gccagccac 240
 tgcctgccat gggaggtgga aagtaaggga tgagttagtc tgcagggccc ctccactga 300
 cattcatagg cccaattacc ccctctctgg tctacatgc attctcttc ttcctgacca 360
 cccctctgtt ctgaaccctc tcttcccgga gcctccatt atattgcagg atgtcactt 420
 acttggtagt ttccagagat gccacatcat tcagggtgaa gacaatgatg atggcttga 480
 agagtggcag aaacagcccc aggttgacag ggaagacact actgctcatt tcccactcc 540
 ttccagctcc atatgagaaa gccatgtgca ctctgagacc caccatcccc acttcaccca 600
 gcccttacc ttgagctect ctatagtagg ttgatgcaat gcatttgaac ctctcctgcc 660
 cagcgggtatc ccaactggaa ggaagggaaga gtgaagcaca ggtatgtatc ttggggggtg 720
 tgggtgtctg ggagaaggga tagctggaag ggtgtgga gcaactcaca 769

<210> 321
 <211> 690
 <212> DNA
 <213> Homo sapiens

<220>
<221> misc_feature
<222> 633, 666
<223> n = A,T,C or G

<400> 321
tgggctgtgg gcggcacctg tgctctgcag gccagacagc gatagaagcc tttgtctgtg 60
cctactcccc cggaggcaac tgggaggcca acgggaagac aatcatcccc tataagaagg 120
gtgcctgggtg ttgcgtctgc acagccagtg tctcaggctg cttcaaagcc tgggaccatg 180
cagggggggt ctgtgaggtc cccaggaatc cttgtcgcag gagctgccag aaccatggac 240
gtctcaacat cagcacctgc cactgccact gtccccctgg ctacacgggc agatactgcc 300
aagtgtagggt cagcctgcag tgtgtgcacg gccggttccg ggaggaggag tgctcgtgcg 360
tctgtgacat cggctacggg ggagcccagt gtgccaccaa ggtgcatttt cccttccaca 420
cctgtgacct gaggatcgac ggagactgct tcatgggtgc ttcagaggca gacacctatt 480
acagaagcca ggaatgaaatg tcagaggaaat ggcgggggtg tggcccagat caagagccag 540
aaagtgcagg acatcctcgc cttctatctg ggccgcctgg agaccaccaa cgaggtgact 600
gacagtgact ttgagaccag gaacttcttg atnnggctca cctacaagac cgccaaggac 660
tccttncgct gggccacagg ggagcaccag 690

<210> 322
<211> 104
<212> DNA
<213> Homo sapiens

<400> 322
gtcgcaagcc ggagcaccac catgtagcct ttcccgaagt accggacett ctctctctcc 60
acgtcacat caccgacatc atggagcagg accaccacct ggtc 104

<210> 323
<211> 118
<212> DNA
<213> Homo sapiens

<400> 323
gggccctggg cgcttccaaa tgaccagga ggtgggtctg cagcaatgcc ctaatgtcaa 60
actagtgaat gaagaacgaa cactggaagt agaaatagag cctgggggtga gagacgga 118

<210> 324
<211> 354
<212> DNA
<213> Homo sapiens

<400> 324
tgctctccgg gagcttgaag aagaaactgg ctacaaaggg gacattgccg aatgttctcc 60
agcgggtctg atggaccag gcttgtcaaa ctgtactata cacatcgtga cagtcaccat 120
taacggagat gatgccgaaa acgcaaggcc gaagccaaag ccaggggatg gagagtttgt 180
ggaagtcatt tctttacca agaattgacct gctgcagaga cttgatgctc tggtagctga 240
agaacatctc acagtggacg ccagggtcta ttctacgct ctagcgtga aacatgcaaa 300
tgcaagcca tttgaagtgc ccttcttgaa attttaagcc caaatatgac actg 354

<210> 325
<211> 642
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> 1

<223> n = A,T,C or G

<400> 325

```

ncatgcttga atgggctcct ggtgagagat tgccccctgg tggtgaaaca atcgtgtgtg 60
cccactgata ccaagaccaa tgaagagac acagttaagc agcaatccat ctcatctcca 120
ggcacttcaa taggtcgctg attggtcctt gcaccagcag tggtagtcgt acctatttca 180
gagaggtctg aaattcaggt tcttagtttg ccagggacag gccctacctt atattttttt 240
ccatcttcat catccacttc tgettacagt ttgctgctta caataactta atgatggatt 300
gagttatctg ggtgggtctct agccatctgg gcagtgtggt tctgtctaac caaagggcat 360
tggcctcaaa cctgcattt ggtttagggg ctaacagagc tcctcagata atcttcacac 420
acatgtaact gctggagatc ttattctatt atgaataaga aacgagaagt ttttccaaag 480
tgtagtcag gatctgaagg ctgtcattca gataaccag cttttccttt tggcttttag 540
cccattcaga ctttgccaga gtcaagccaa ggattgcttt tttgctacag ttttctgcca 600
aatggcctag ttcctgagta cctggaaacc agagagaaag ag 642

```

<210> 326

<211> 455

<212> DNA

<213> Homo sapiens

<400> 326

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tccgtgagga tgagcttcca gtccttcacc aggcactgca ggggcacagt cacgtcaatc 60
accttcacct tctcgtcttt cctgctcttg tcattgacaa acttcccgta ccaggcattg 120
acgatgatga ggcccattct ggactcttct gctcaatta tccttcggac agattcctgc 180
atcagccgga cagcggactc cgcctcttgc ttcttctgca gcacatcggt ggcggcgctt 240
tccctctgct tctccaattc cttctctttc tgagccctga ggtatggttt gatgatcaga 300
cgggtcatgg caaagtayac cactagaggc cccacgggtg catagaacat ggcgctgggc 360
agaagctggt ccgtcaagtg aatagggaag aagtatgtct gactggccct gttgagcttg 420
actttgagag aaacgccctg tggaactcca acgct 455

```

<210> 327

<211> 321

<212> DNA

<213> Homo sapiens

<400> 327

```

ttcactgtga actcgcagtc ctcgatgaac tcgcacagat gtgacagccc tgtctccttg 60
ctctctgagt tctcttcaat gatgctgatg atgcagtcca cgatagcgcg cttataactca 120
aagccaccct cttcccgag catggtgaac aggaagtcca taaggacggc gtgtttgcga 180
ggatatttct gacacagggc actgatggcc tggacaacca ccaccttgaa ttcattccgag 240
atttctgaca tgaaggagga gatctgcttc atgaggcggg cgatgctgct ctcgctgccc 300
gtcttaagga ggggtggtgat g 321

```

<210> 328

<211> 476

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 302, 311

<223> n = A,T,C or G

<400> 328

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tgaggagggg gccatggggg ctgtgaatgg gatgcagccc catggtgtcc ctgataaacc 60
cagtgtgcag tctgatgaag tctgggtggg tgtggtctac gggctggcag ctaccatgat 120
ccaagaggta atgcactcct ttcccatct ctccaccate tgtatcctgg ccmagaaaaa 180

```

```

cttcccttca aaccaaccaa aatttccttt caaaggcata acccaaatgc catccttgg 240
ccggtctaat aaagcctccc ccatttttcc cctggtatgc attcccaggc tccctggcct 300
tncagggctt nctgtctgtg ggtcatagtt tatctcctcc cacttgctgg gagctccttg 360
aaggcaaaga ctctactgcc tccatctatc cagtggaaagt ggctcttcag agggtgccaa 420
gttagtatgt atgactgtca tctctcccaa cagggcctga cttggsaggg cttcca 476

```

<210> 329

<211> 340

<212> DNA

<213> Homo sapiens

<400> 329

```

cgagggagat tgccagcacc ctgatggaga gtgagatgat ggagatcttg tcagtgctag 60
ctaaggggtga ccacagccct gtcacaaggg ctgctgcage ctgcctggac aaagcagtg 120
aatatgggct tatccaaccc aaccaagatg gagagtgagg ggggtgtccc tgggcccag 180
gctcatgcac acgctaccta ttgtggcagc gagagtaagg acggaagcag ctttgctgg 240
tggtggctgg catcccaaat actcttgccc atcctcgctt gctgccctag gatgcctct 300
gttctgagtc agcggccacg ttcagtcaca cagccctgct 340

```

<210> 330

<211> 277

<212> DNA

<213> Homo sapiens

<400> 330

```

tgtcaccatc acattgggtgc caaataccca gaagacatcg tagatgaaga gtccgcccag 60
caggatgcag ccagtgtgta cattgttgag gtgcaggagc tctactccat taaggagaa 120
ggccaggcca aaaagggtgt tgccaatcca gtgcttcctc agcaggtagc agacgccaac 180
gatgctgctc aggccaggc acaccaggtc cttggtgtca aattcataat tgatgatctc 240
ctccttgttt tcccagaacc ctgtgtgaag agcagac 277

```

<210> 331

<211> 136

<212> DNA

<213> Homo sapiens

<400> 331

```

ttgcttccca cctcctttct ctgtcctctc ctgaggttct gccttacaat ggggacactg 60
atacaacca cacacacaat gaggatgaaa acagataaca ggtaaaatga cctcacctgc 120
ccgggcggcc gctcga 136

```

<210> 332

<211> 184

<212> DNA

<213> Homo sapiens

<400> 332

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ttgtgagata aacgcagata ctgcaatgca ltaaaacgct tgaatactc atcaggyatg 60
ttgctgatct tattgtgtgc taagtagaga gttagaagag agacaggag accagaaggc 120
agtctggcta tctgattgaa gctcaagtca aggtattcga gtgatttaag accttataaa 180
gcag 184

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<210> 333

<211> 384

<212> DNA

<213> Homo sapiens

<400> 333

cgaaaaactt cgaggaattg ctcaaagtgc tgggggtgaa tgtgatgctg aggaagattg 60
ctgtggctgc agcgtccaag ccagcagtgg agatcaaaca ggaggagagac actttctaca 120
tcaaaacctc caccaccgtg cgcaccacag agattaactt caagggtggg gaggagtgtg 180
aggagcagac tgtggatggg aggccctgta agagcctggt gaaatgggag agtgagaata 240
aatgtgtctg tgagcagaag ctctgaagg gagagggcc caagacctcg tggaccagag 300
aactgaccaa cgatggggaa ctgatcctga ccatgacggc ggatgacgtt gtgtgcacca 360
gggtctacgt ccgagagtga gcgg 384

<210> 334
<211> 169
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 2, 165
<223> n = A,T,C or G

<400> 334
cnacaaacag agcagacacc ctggatccgg tcctgtact gccaggacg gctggaccgt 60
aaaattgaat ttccacttcc tgaccgccgc cagaagagat tgattttctc cactatcact 120
agcaagatga acctctctga ggaggttgac ttggaagact atgtngccc 169

<210> 335
<211> 185
<212> DNA
<213> Homo sapiens

<400> 335
ccaggtttgc agcccaggct gcacatcagg ggactgcctc gcaatacttc atgctgttgc 60
tgctgactga tgggtgtgtg acggatgtgg aagccacacg tgaggctgtg,gtgcgtgcct 120
cgaacctgcc catgtcagtg atcattgtgg gtgtgggtgg tgctgacttt gaggccatgg 180
agcag 185

<210> 336
<211> 358
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 26
<223> n = A,T,C or G

<400> 336
ctgccccctgc cttacggcgg ccaganacac acccaggatg gcattggccc caaacttggg 60
tttgttctca gtcccatcca actccagcat cagggtgtcc agtttctctt gctccaccac 120
agagagacct gagctgatga gggctggcgo gatggtggag ttgatgtggt ccactgcctt 180
caggacacct ttgcctaagt aacgctgttt gtctccatcc ctacgtcca gggectcata 240
gatgcccgta gagggtccac tgggcaactgc agcccgaaa agacctttgg cagtatagag 300
atccacctcc actgtggggg tcccgcggga gtccaggatc tcccgggccc agatcttc 358

<210> 337
<211> 271
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> 17
<223> n = A,T,C or G

<400> 337
cacaaagcca ccagccnggg aaatcagaat ttacttgatg caactgactt gtaatagcca 60
gaaatcctgc ccagcatggg attcagaacc tggctctgcaa ccaatccac cgtcaaagt 120
catcaggat aaaacaaatt caattgcctt ttccacatta atagcatcaa gcttcccaa 180
caaagccaaa gttgccaccg cacaaaaaga gaattctgtg tcaatttctc cctactttat 240
aaaagtagat ttttcacatc ccatgaagca g 271

<210> 338
<211> 326
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 15, 17, 18
<223> n = A,T,C or G

<400> 338
ctgtgctccc gactngnca tctcaggtag caccgactgc actgggcggg gccctctggg 60
gggaaaggct ccacggggca gggatacatc tcgaggccag tcatcctctg gaggcagccc 120
aatcaggta aagattttgc ccaactgggc ggcttcagag tttccacaga agagaggctt 180
tcgacgaaac atctctgcaa agatacagcc aacactccac atgtccacag gtgttgata 240
tgtggactgc agaagaactt cgggagctcg gtaccagagt gtaacaacca cgggtgtaag 300
tgccatctgg tagctgtaga ttctgg 326

<210> 339
<211> 260
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> 47, 54, 60, 69, 90, 91, 96, 113, 117, 119, 195
<223> n = A,T,C or G

<400> 339
ttcacctgag gactcatttc gtgccctttg ttgacttcaa gcaaagnct tcanggtctn 60
caaggacgnc acatttccac ttgcgaatgn nctcanggt catcttgaag aanaagnanc 120
ccaagtgtg gatccagac tcgggggtaa ccttgtgggt aagagctcat ccagtttatg 180
ctttaggagc tccanctact cgggggagct ggaagcctgc gtggatgagg ccctgctgga 240
cctcggccgc gaccacgcta 260

<210> 340
<211> 220
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> 15, 18
<223> n = A,T,C or G

<400> 340
ctggaagccc ggctngnct ggcagcggaa ggagccaggc aggttcacgc agcgggtgctg 60

gcagtagcgg tagcggcact cgtctatgto cacacactcg ggcccgatct tgcggtaacc 120
atcagggcag gtgcactgat aggagccagg caagttaggg cagtcctggc tggggcgaca 180
gtcgtgcagg gcctgggcac actcgtccac atccacacag 220

<210> 341
<211> 384
<212> DNA
<213> Homo sapiens

<400> 341
ctgctaccag gggagcggaga gctgactatc ccagcctcgg ctaatgtatt ctacgccatg 60
gatggagctt cacacgattt cctcctgcgg cagcggcgaa ggtcctctac tgetacaccg 120
ggcgtcacca gtggcccgtc tgcctcagga actcctccga gtgagggagg agggggctcc 180
tttcccagga tcaagggcac agggagggaag attgcacggg cactgttctg aggaggaagc 240
cccgttggtt tacagaagtc atgggtgtca taccagatgt gggtagccat cctgaatggt 300
ggcaattata tcacattgag acagaaattc agaaaggag ccagccacc tggggcagtg 360
aagtgccact ggttaccag acag 384

<210> 342
<211> 245
<212> DNA
<213> Homo sapiens

<400> 342
ctgggtaagc tcatcattgt tactggtggg caccatgtcc ttgaagcttc aggcaagcaa 60
tgtaaccaac aagaatgacc ccaagtcctt caacletcga gtcttcattg gaaacctcaa 120
cacagctctg gtgaagaaat cagatgtgga gaccatcttc tctaagtatg gccgtgtggc 180
cggctgttct gtgcacaagg gctatgcctt tgttcagtac tccaatgagc gccatgcccg 240
ggcag 245

<210> 343
<211> 611
<212> DNA
<213> Homo sapiens

<400> 343
ccaaaaaat caagatttaa tttttttatt tgcactgaaa aactaatcat aactgttaat 60
tctcagccat ctttgaagct tgaaagaaga gtcttttgta ttttgtaaac gttagcagac 120
tttctgcca gtgtcagaaa atcctattta tgaatcctgt cggattccct tggatatctga 180
aaaaaatacc aaatagtacc atacatgagt ttttctaaag tttgaaaaat aaaaagaaat 240
tgcacacac taattacaaa atacaagttc tggaaaaaat atttttcttc attttaaaac 300
tttttttaac taataatggc tttgaaagaa gaggttaat ttgggggtgg taactaaaaat 360
caaaagaaat gattgacttg aggtctctg tttgtaaga atacatcatt agcttaaaata 420
agcagcagaa ggttagtttt aattatgtag cttctgttaa tattaagtgt ttttgtctg 480
ttttacctca atttgaacag ataagtttgc ctgcatgctg gacatgcctc agaaccatga 540
atagcccgta ctagatcttg ggaacatgga tcttagagtc ctttgaata agttcttata 600
taaatacccc c 611

<210> 344
<211> 311
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 1, 275, 284, 296, 297, 300
<223> n = A, T, C or G

<400> 344

```
nctcgaaaaa gcccaagaca gcagaagcag acacctccag tgaactagca aagaaaagca 60
aagaagtatt cagaaaagag atgtcccagt tcatcgcca gtgcctgaac ccttaccgga 120
aacctgactg caaagtggga agaattacca caactgaaga ctttaaacat ctggctcgca 180
agctgactca cgtgttatg aataaggagc tgaagtactg taagaatcct gaggacctgg 240
agtgaatga gaatgtgaaa cacaaaacca aggantacat taanaagtac atgcannaan 300
tttggggctt g 311
```

<210> 345

<211> 201

<212> DNA

<213> Homo sapiens

<400> 345

```
cacacggta tcccactgc caacctggag gcccaggccc tgtggaagga gccgggcagc 60
aatgtacca tgagtgtgga tgctgagtgt gtgccatgg tcagggaacct tctcaggta 120
ttctactccc gaaggattga catcacctg tcgtcagta agtgcttcca caagctggcc 180
tctgcatatg gggccaggca g 201
```

<210> 346

<211> 370

<212> DNA

<213> Homo sapiens

<400> 346

```
ctgctccagg gcgtggtgtg ccttcgtggc ctctgcctcc tccgaggagc caggctgtgt 60
tctcttcaga atgttctgga gcagcagttt gaggcgggtg atgcgttga agggcagaat 120
cagaaaggac ttgagggaaa ggcgctggca gacggggtcg ctctccagct tctccaagac 180
ctcccggaaa ttgctgttgc tattcatcag gctctggaag gtgcgttcct gataggctg 240
gttggtgaca taaggcaggt agacccggcg gaagtctggg gcgtggttca ggactacgtc 300
acatacttg aagcagaaga tattgttctc aaagttctct tccaggctctg aaaggaacgt 360
ggcgctgacg 370
```

<210> 347

<211> 416

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 416

<223> n = A,T,C or G

<400> 347

```
ctgttgtgct gtgtatggac gtgggcttta ccatgagtaa ctccattcct ggtatagaat 60
ccccatttga acaagcaaag aagggtgataa ccatgtttgt acagcgacag gtgtttgctg 120
agaacaagga tgagattgct ttagtcotgt ttggtacaga tggcactgac aatccccctt 180
ctgggtggga tcagtatcag aacatcacag tgcacagaca tctgatgcta ccagattttg 240
atttgctgga ggacattgaa agcaaaatcc aaccaggttc tcaacaggct gacttcctgg 300
atgcactaat cgtgagcatg gatgtgatc aacatgaaac aataggaaag aagtttgag 360
aagaggcata ttgaaatatt cactgacctc aagcagcccg attcagcaaa agtcan 416
```

<210> 348

<211> 351

<212> DNA

<213> Homo sapiens

<400> 348

```

gtacaggaga ggatggcagg tgcagagcgg gactgagct ctgcaggta aagggctcgg 60
cagttggatg ctctcctgga ggctctgaaa ttgaaacggg caggaaatag tctggcagcc 120
tctacagcag aagaaacggc aggcagtgcc cagggacgag caggagacag atgccttcct 180
cttgtctcaa ctgcaaagag gcgttccttc ctctttcact aatcctcctc agcacagacc 240
ctttacgggt gtcaggctgg gggacagtaa ggtctttccc ttcccacaag gccatatctc 300
aggctgtctc agtgggggga aaccttggaac aatacccggg ctttcttggg c 351

```

<210> 349

<211> 207

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 1

<223> n = A,T,C or G

<400> 349

```

nccgggacat ctccaccctc aacagtggca agaagagcct ggagactgaa cacaaggcct 60
tgaccagtga gattgcactg ctgcagtcca ggctgaagac agagggtctc gatctgtgcg 120
acagagttag cgaatgcag aagctggatg cacagggtcaa ggagctgggt ctgaagtcgg 180
cggtggaggc tgagcgcctg gtggctg 207

```

<210> 350

<211> 323

<212> DNA

<213> Homo sapiens

<400> 350

```

ccatacaggg ctgttgccca ggccctagag gtcattcctc gtaccctgat ccagaactgt 60
ggggccagca ccatccgtct acttacctcc ctccgggcca agcacacca ggagaactgt 120
gagacctggg gtgtaaatgg tgagacgggt actttggtgg acatgaagga actgggcata 180
tgggagccat tggctgtgaa gctgcagact tataagacag cagtggagac ggcagttctg 240
ctactgcgaa ttgatgacat cgtttcaggc cacgaaaaga aaggcgatga ccagagccgg 300
caaggcgggg ctctgatgc tgg 323

```

<210> 351

<211> 353

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 12, 25, 39, 42

<223> n = A,T,C or G

<400> 351

```

cgccgcaccc cntggtcctc tccantccct ttctctttnt cngggaaact gtatgcgggt 60
tgtttttgtt ttgtagggtt tttttccttc tccacctctc cctgtctctt ttgtccatg 120
ttgtccgttt ctgtgggggt aggtttatgt ttttaacat ctgagggtcac gtctatttcc 180
tccggactcg cctgcttggg ggcgattctc caccggttaa tatggtgcgt cccttttttc 240
ttttgttgcg aatctgagcc ttcttctccc agcttctgcc ttttgaactt tgttcttcgg 300
ttctgaaacc atacttttac ctgagtttcc gtgaggctga ggctgtgtgc caa 353

```

<210> 352

<211> 467

<212> DNA

<213> Homo sapiens

<400> 352
ctgcccacac tgatcacttg cgagatgtcc ttaggggtaca agaacaggaa ttgaagtctg 60
aatlttgagca gaacctgtct gagaaactct ctgaacaaga attacaattt cgtcgtctca 120
gtcaagagca agttgacaac tttactctgg atataaatac tgcctatgcc agactcagag 180
gaatcgaaca ggtgtttcag agccatgcag ttgctgaaga ggaagccaga aaagcccacc 240
aaactctggct ttcagtggag gcattaaagt acagcatgaa gacctcatct gcagaaacac 300
ctactatccc gctgggtagt gcagttaggg ccatcaaagc caactgttct gataatgaat 360
tcacccaagc ttttaaccga gctatccctc cagagtcctt gaccctgggg gtgtacagtg 420
aagagaccct tagagccctt ttctatgctg ttcaaaaact ggcccga 467

<210> 353
<211> 350
<212> DNA
<213> Homo sapiens

<400> 353
ctgctgcagc cacagtagtt cctcccatgg tgggtggccc tcttggtcct gctggcccag 60
gaaatctgtc cccaccagga acagcccctg gaaaacggcc ccgtcctcta ccaccttggtg 120
gaaatgtctg acgggaactg cctcctggag gaccagcttt accttcccca gacatttgtc 180
ctgattgtgt agttttctct gactgcattt caaattgact caggaaactg ttattgcatg 240
gagtttacaac aggattctga ccatgaagtt ctcttttagg taacagatcc attaaacttt 300
ttgaagatgc ttcagatcca acaccaacaa gggcaaaccc ctttgactgg 350

<210> 354
<211> 351
<212> DNA
<213> Homo sapiens

<400> 354
atttagatga gatctgaggc atggagacat ggagacagta tacagactcc tagatttaag 60
ttttagggtt tttgttttcc taatcaccaa ttcttatata caatgtatat tttagaattcg 120
agcagatgat catcttcac ttaagtcatt ccttttgact gagtatggca ggattagagg 180
gaatggcagt atagatcaat gtctttttct gtaaagtata ggaaaaacca gagaggaaaa 240
aaagagctga caattggaag gtagtagaaa attgacgata atttcttctt aacaaataat 300
agttgtatat acaaggaggc tagtcaacca gattttattt gttgaggggc a 351

<210> 355
<211> 308
<212> DNA
<213> Homo sapiens

<400> 355
ttttggcgca agttttacag attttattaa agtcgaagct attggtcttg gaagatgaaa 60
atgcaaatgt tgatgagggt gaattgaagc cagataacct aataaaaatta tatcttggtt 120
ataaaaaata gaaettaagg gtttaacatca atgtgccaat gaaaaccgaa cagaagcagg 180
aacaagaaac cacacacaaa aacatcgagg aagaccgcaa actactgatt caggcggcca 240
tcgtgagaat catgaagatg aggaagggtc tgaaacacca gcagttactt ggcgagggtc 300
tcactcag 308

<210> 356
<211> 207
<212> DNA
<213> Homo sapiens

<400> 356
ctgtcccaag tgctcccaga aggcaggatt ctgaagacca ctccagcgat atgttcaact 60
atgaagaata ctgcaccgcc aacgcagtca ctgggccttg ccgtgcaccc ttcccaagct 120

ggtactttga cgtggaagagg aactcctgca ataacttcat ctatggaggc tgccggggca 180
ataagaacag ctaccgctct gaggagg 207

<210> 357
<211> 188
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> 25, 29
<223> n = A,T,C or G

<400> 357
tcgaccacgc cctcgtagcg catgngctnc aggacgatgc tcagagtgat gaacaccccg 60
gtgcggccca cgccagcact gcagtgcacc gtgataggcc catcctgtcc aaactgtctc 120
ttggtcttat gcacctgccc gatgaagtca atgaatccct cgcctgtctt gggcacgccc 180
tgcctctgg 188

<210> 358
<211> 291
<212> DNA
<213> Homo sapiens

<400> 358
ctgggagcat cggcaagcta ctgccttaaa atccgatctc cccgagtgc caatttctgt 60
cccttttaag gggtcacaac actaaagatt tcacatgaaa gggttgtgat tgatttgagc 120
aggcagggcg tacgtgacag gggctgcatg caccgggtgg cagagagaaa cagaacaggg 180
caggggaattt cacaatgttc ttctatacaa tggctggaat ctatgaataa catcagtttc 240
taagtattgg gttgattttt aactactggg tttaggccag gcagggccag.g 291

<210> 359
<211> 117
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> 79, 98, 100
<223> n = A,T,C or G

<400> 359
gccaccacac tcagcctgg gcaatacagc aagactgtct caaaaaaaaa aaaaaaaaaa 60
ccccaaaaaa ctcaaaaang taatgaatga taccgaangn gccttttcta gaaaaag 117

<210> 360
<211> 394
<212> DNA
<213> Homo sapiens

<400> 360
ctgttcctct ggggtgggtcc agttctagag tgggagaaaag ggagtcaggc gcattgggaa 60
tcgtgggtcc agtctggttg cagaatctgc acatttgcca agaaatttc cctgtttgga 120
aagtttgccc cagctttccc gggcacacca ccttttgctc caagtgtctg ccggtcgacc 180
aatctgcctg ccacacattg accaagccag acccggttca cccagctcga ggatcccagg 240
ttgaagagtg gcccttgag gccctggaaa gaccaatcac tggacttctt cccttgagag 300
tcagaggtca cccgtgatc tgctgcacc ttatcattga tctgcagtga tttctgcaaa 360
tcaagagaaa ctctgcaggg cactccctg tttc 394

<210> 361
 <211> 394
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 28, 31
 <223> n = A,T,C or G

<400> 361
 ctgggcggat agcaccgggc atattnntt natggatgag gtctggcacc ctgagcagtc 60
 cagcgaggac ttggtcttag ttgagcaatt tggctaggag gatagtatgc agcacggttc 120
 tgagtcctg ggatagctgc catgaagtaa cctgaaggag gtgctggctg gtaggggttg 180
 attacagggg tgggaacagc tcgtacactt gccattctct gcatatactg gttagtggag 240
 tgagcctggc gctcttcttt gcgctgagct aaagctacat acaatggctt tgtggacctc 300
 ggccgcgacc acgctaagcc gaattccagc aactggcgg ccgttactag tggatccgag 360
 clcgygtacca agcttggcgl aatcatggtc atag 394

<210> 362
 <211> 268
 <212> DNA
 <213> Homo sapiens

<400> 362
 ctgcgcgtgg accagtcagc ttccgggtgt gactggagca gggcttgtcg tttcttctcag 60
 agtcactttg caggggttgg tgaagctgct cccatccatg tacagctccc agtctactga 120
 tgtttaagga tggctctcgtt ggttaggccc actagaataa actgagtcca atacctctac 180
 acagttatgt ttaactgggc tctctgacac cgggaggaag gtggcggggt ttaggtgttg 240
 caaacttcaa tggttatgct gggatgtt 268

<210> 363
 <211> 323
 <212> DNA
 <213> Homo sapiens

<400> 363
 ccttgacctt ttcagcaagt gggaagggtt aatccgtctc cacagacaag gccaggactc 60
 gtttgtacct gttgatgata gaattgggta ctgatgcaac agttgggtag ccaatctgca 120
 gacagacact ggcaacattg cggacaccct ccaggaagcg agaatgcaga gtttctctctg 180
 tgatatcaag cacttcaggg ttgttagatgc tgccattgtc gaacacctgc tggatgacca 240
 gcccaaagga gaagggggag atgttgagca tgttcagcag cgtggcttct ctggtctcca 300
 cttgtctctc agtcttgatc aga 323

<210> 364
 <211> 393
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 29
 <223> n = A,T,C or G

<400> 364
 ccaagctctc catcgcccc gtgcgcagng gctactgggg gaacaagatc ggcaagcccc 60
 acactgtccc ttgcaagggt acaggccgct ggggtctgt gctggtacgc ctcatcactg 120

```
caccagggg cactggcgc gtctccgcac ctgtgcctaa gaagctgctc atgatggctg 180
gcatcgatga ctgtacaccc tcagcccggg gctgcactgc caccctgggc aacttcgcca 240
aggccacctt tgatgccatt tctaagacct acagctacct gacccccgac ctctggaagg 300
agactgtatt caccaagtct ccctatcagg agttcactga ccacctcgtc aagaccaca 360
ccagagtctc cgtgcagcgg actcaggtc cag 393
```

<210> 365

<211> 371

<212> DNA

<213> Homo sapiens

<400> 365

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cctctcaga gcggtagctg ttcttattgc cccggcagcc tccatagatg aagtatttgc 60
aggagttcct ctccacgtca aagtaccagc gtgggaagga tgcacggcaa ggcccagtga 120
ctgcgtttggc ggigcagtat tcttcatagt tgaacatata cctggagtgg tcttcagaat 180
cotgccttct gggagcactt gggacagagg aatccgctgc attcctgctg gtggacctcg 240
gccgcgacca cgctaagccg aattccagca cactggcggc cgttactagt ggatccgagc 300
tcggtacca cgttggcgta atcatgggtca tagctgttct ctgtgtgaaa ttgttatccg 360
ctcacaattc c 371
```

<210> 366

<211> 393

<212> DNA

<213> Homo sapiens

<400> 366

```
atttcttgcc agatgggagc tctttggtga agactccttt cgggaaaagt tttttggctt 60
cttcttcagg gatggttgya aggaccatca cactatcccc atccttccaa tcaactgggg 120
tggaaccctt tttttctgct gtcagctgga gagagatgac taccctgaga atctcatcaa 180
agttcctgcc agtggtagct gggtagagga tagacagctt cagcttctta tcaggaccaa 240
aaacaaacac cacacgagct gccacaggca tgcccttttc atccttctct gctggatcca 300
gcatgcccaa caggatggca agctcccgat tcctatcctc gatgatggga aaaggtaact 360
tttctgtggg ctcttcacaa ttgtaagcat tga 393
```

<210> 367

<211> 327

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 34, 54, 55

<223> n = A, T, C or G

<400> 367

```
ccagctctgt ctcatacttg actctaaagt cttnagcagc aagacgggca ttgnaatct 60
gcagaacgat gggggcattg tccacagtat ttgcgaagat ctgagccctc aggtcctcga 120
tgatcttgaa gtaatgyctc cagtcctctya cctggggctc cttcttctcc aagtgcctcc 180
ggattttctg ctccagcttc cggttctcgg tctccaggct cctcactctg tccaggtaag 240
aggccaggcg gtcgttcagg ctttgcctgg tctcctctc gttctggatg cctcccatc 300
ctgccagacc cccggctatc ccggttg 327
```

<210> 368

<211> 306

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 24

<223> n = A,T,C or G

<400> 368

```
ctggagaagg acttcagcag tttnaagaag tactgccaaag tcatccgtgt cattgcccac 60
acccagatgc gcctgcttcc tctgcgccag aagaaggccc acctgatgga gatccagggtg 120
aacggaggga ctgtggccga gaagctggac tgggcccgcg agaggcttga gcagcaggta 180
cctgtgaacc aagtgtttgg gcaggatgag atgatcgacg tcatcggggt gaccaagggc 240
aaaggctaca aaggggtcac cagtcgttgg cacaccaaga agctgccccg caagaccac 300
cgagga                                           306
```

<210> 369

<211> 394

<212> DNA

<213> Homo sapiens

<400> 369

```
tcgaccacac ccggaacacg gagagctggg ccagcattgg cacttgatag gatttcccg 60
cggctgccac gaaagtgcgt ttctttgtgt tctcgggttg gaacctgat ttccacagac 120
ccttgaaata cactgcgttg acgaggacca gtctgggtgag cacaccatca ataagatctg 180
gggacagcag attgtcaatc atatccctgg ttccattttt aacctatgca ttgatggaat 240
cacaggcaga ggctggatcc tcaaagttca cattccggac ctcacactgg aacacatctt 300
tgttccttgt aacaaaaggc acttcaattt cagaggcatt cttaacaaac acggcggttag 360
ccactgtcac aatgtcttta ttcttcttgg agac                                           394
```

<210> 370

<211> 653

<212> DNA

<213> Homo sapiens

<400> 370

```
ccaccacacc caattccttg ctggtatcat ggcagccgac acgtgccagg attaccggct 60
acatcatcaa gtatgagaag cctgggtctc ctcccagaga agtgggtccct cggccccgcc 120
ctggtgtcac agaggctact attactggcc tggaaaccgg aaccgaatat acaatttatg 180
tcattgccct gaagaataat cagaagagcg agccctgat tggaaaggaaa aagacagacg 240
agcttcccca actggttaacc cttccacacc ccaatcttca tggaccagag atcttggatg 300
ttccttccac agttcaaaag acccctttcg tcaccacacc tgggtatgac actggaaatg 360
gtattcagct tcttggcact tctggtcagc aaccagtggt tgggcaacaa atgatctttg 420
aggaacatgg ttttaggcgg accacaccgc ccacaacggc caccaccata aggcataggc 480
caagaccata cccgccgaat gtaggacaag aagctctctc tcagacaacc atctcatggg 540
ccccattcca ggacacttct gagtacatca ttcatgtca tctgtttggc actgatgaag 600
aaccettaca gttcagggtt cctggaactt ctaccagtc cactctgaca gga                                           653
```

<210> 371

<211> 268

<212> DNA

<213> Homo sapiens

<400> 371

```
ctgcccagcc cccattggcg agtttgagaa ggtgtgcagc aatgacaaca agaccttoga 60
ctcttctctg cacttctttg ccacaaagtg caccctggag ggcaccaaga agggccacaa 120
gtctccacct gactacatcg ggccttgcaa atacatcccc ccttgcctgg actctgagct 180
gaccgaattc ccctgcgca tgcgggactg gctcaagaac gtctgtgtca ccctgtatga 240
gagggatgag gacaacaacc ttctgact                                           268
```

<210> 372

<211> 392

<212> DNA

<213> Homo sapiens

<400> 372

```
gctggtgccc ctggtgaacg tggacctcct ggattggcag gggccccagg acttagaggt 60
ggaactggtc cccttggtcc cgaaggagga aaggggtgct ctggctcctc tgggccacct 120
ggtgctgctg gtactcctgg tctgcaagga atgcctggag aaagaggagg tottggaagt 180
cctggtccaa agggtgacaa ggggtgaacca ggcgggtccag gtgctgatgg tgtcccaggg 240
aaagatggcc caaggggtcc tactggtcct attggtcctc ctggcccagc tggccagcct 300
ggagataagg gtgaagggtg tgcccccgga cttccaggta tagctggacc tcgtggtagc 360
cctggtgaga gaggtgaaac ctgggcgcgc ac 392
```

<210> 373

<211> 388

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 30

<223> n = A,T,C or G

<400> 373

```
ccaagcgctc agatcgccaa ggggcaccan ttttgatctg cccagtgcac agccccacaa 60
ccaggtcagc gatgaaggta tcttcagtct cccccgaacg atgagacacc atgacgcccc 120
aaccattggc ctgggccagc ttgcacgcct gaagagactc ggtcacggag ccaatctggt 180
tgactttgag caggaggcag ttgcaggact tctcgttcac ggccttgagg atcctctttg 240
ggttggtcac tgtgagatca tccccacta cctggattcc tgcactggct gtgaacttct 300
gccaagctcc ccagtcaccc tgggtcaaagg gatcttcgat agacaccact gggtagtcct 360
tgatgaagga cttgtacagg tcagccag 388
```

<210> 374

<211> 393

<212> DNA

<213> Homo sapiens

<400> 374

```
ctgacgaccg cgtgaacccc tgcattgggg gtgtcatcct cttccatgag acactctacc 60
agaaggcgga tgatggcggt cccttcccc cagttatcaa atccaagggc ggtgttgtgg 120
gcatcaaggt agacaagggc gtggtcccc tggcagggac aaatggcgag actaccaccc 180
aagggttgga tgggctgtct gagcgctgtg ccagtagcaa gaaggacgga gctgacttcg 240
ccaagtggcg ttgtgtgctg aagattgggg aacacacccc ctgagccctc gccatcatgg 300
aaaatgccaa tgttctggcc cgttatgcca gtatctgcca gcagaatggc attgtgcccc 360
tcgtggagcc tgagatcctc cctgatgggg anc 393
```

<210> 375

<211> 394

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 30, 33

<223> n = A,T,C or G

<400> 375

```
ccacaaatgg cgtggtccat gtcacacn tntttctgca gcctccagcc aacagacctc 60
aggaaagagg ggatgaactt gcagactctg cgcttgagat cttcaaacia gcatcagcgt 120
```

```

tttccagggc ttcccagagg tctgtgcgac tagccccctgt ctatcaaaag ttattagaga 180
ggatgaagca ttagcttgaa gcactacagg aggaatgcac caccgcagct ctccgccaat 240
ttctctcaga ttcccacaga gactgtttga atgttttcaa aaccaagtat cacacttta 300
tgtacatggg ccgcaccata atgagatgtg agccttgtgc atgtggggga ggagggagag 360
agatgtactt tttaaatacat gttcccccta aaca 394

```

<210> 376
 <211> 392
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 30
 <223> n = A,T,C or G

```

<400> 376
ctgcccagcc cccattggcg agtttgattn ggtgtgcagc aatgacaaca agaccttcca 60
ctcttcctgc cacttctltg ccacaaagtg caccctggag ggcaccaaga agggccacaa 120
gctccacctg gactacatcg ggccttgcaa atacatcccc ccttgcctgg actctgagct 180
gaccgaattc cccctgcgca tgcgggactg gctcaagaac gtctgtgtca cctgtatga 240
gagggatgag gacaacaacc ttctgactga gaagcagaag ctgctgggtga agaagatcca 300
tgagaatgag aagcgccttg aggcaggaga ccacccctg gagctgtctg cccgggactt 360
cgagaagaac tataacatgt acatcttccc tg 392

```

<210> 377
 <211> 292
 <212> DNA
 <213> Homo sapiens

```

<400> 377
caatgtttga tgcttaaccc ccccaatttc tctgagatgg atggccagtg caagcgtgac 60
ttgaagtgtt gcatgggcat gtgtgggaaa tcctgcgttt cccctgtgaa agcttgattc 120
ctgccaatag gaggaggetc tggagtccctg ctctgtgtgg tccaggtcct ttccacctg 180
agacttgget ccaccactga tatctctctt tggggaaagg cttggcacac agcaggcttt 240
caagaagtgc cagttgatca atgaataaat aaacgagcct atttctcttt gc 292

```

<210> 378
 <211> 395
 <212> DNA
 <213> Homo sapiens

```

<400> 378
ctgctgcttc agcgaagggt ttctggcata tccaatgata aggctgccaa agactgttcc 60
aataccagca ccagaaccag ccactcctac tgttgacgca cctgcaccaa taaatttggc 120
agcagtatca atgtctctgc tgattgcact gctctgaaac tcccttttga ttagctgaga 180
cacaccatc tgggccttga ttttcctaag atagaactcc aactctttgc cctctagcac 240
atagccatct gctcggccac actgtcccgg ccttgaagcg atgcacgcaa gaagcttgcc 300
ctgctggaac tgctcttcca ggagactgct gattttggca ttctttttcc ttcatcata 360
tttcttctga atttttttaga tcgttttttg ttttaa 395

```

<210> 379
 <211> 223
 <212> DNA
 <213> Homo sapiens

```

<400> 379
ccagatgaaa tgctgccga atggctgtgg gaaggtgtcc tgtgtcactc ccaatttctg 60

```

agctccagcc accaccaggc tgagcagtga ggagagaaag tttctgcctg gccctgcac 120
tggttccagc ccacctgcc tccccctttt cgggactctg tatccccctt tgggctgacc 180
acagcttctc cctttcccaa ccaataaagt aaccactttc agc 223

<210> 380
<211> 317
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> 30, 32
<223> n = A,T,C or G

<400> 380
tcgaccacag tattccaacc ctccctgtgc tngagaagt atggaggggt ctgacaacca 60
gggtgcagga gaacaaggta gaccagttag gcagaatat tctcggggat atagaccacg 120
attccgcagg ggccctccct gccaaagaca gcttagagag gacggcaatg aagaagataa 180
agaaaalcaa ggagatgaga cccaagggtc gcagccacct caacgtcggg accgcccga 240
cttcaattac cgacgcagac gccagaaaa ccctaaacca caagatggca aagagacaaa 300
agcagccgat ccaccag 317

<210> 381
<211> 392
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> 29, 30, 31
<223> n = A,T,C or G

<400> 381
cctgaaggaa gagctggcct acctgaatnn naaccatgag gaggaaatca gtacgtgag 60
gggccaagtg ggaggccagg tcagtgtgga ggtggattcc gctccgggca ccgatctcgc 120
caagatcctg agtgacatgc gaagccaata tgaggtcatg gccgagcaga accggaagga 180
tgctgaagcc tgyttacca gccggactga agaattgaac cgggaggtcg ctggccacac 240
ggagcagctc cagatgagca ggtccgaggt tactgacctg cggcgacccc ttcagggtct 300
tgagattgag ctgcagtcac agacctcggc cgcgaccacg ctaagccgaa ttccagcaca 360
ctggcggccg ttactagtgg atccgagctc gg 392

<210> 382
<211> 234
<212> DNA
<213> Homo sapiens

<400> 382
cctcgatgtc taaatgagcg tgytaaagga tgggtgcctgc tggggtctcg tagatacctc 60
gggacttcat tccaatgaag cggttctcca cgatgtcaat acggcccacg ccattgttgc 120
ccgcgacttc gttcaggtac atgaagagct ccaaggaggt ctggtgggtg gtgccatcct 180
tgacgttggg caccctcaca gggacccctt ttttgaactc catctccaga atgt 234

<210> 383
<211> 396
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature

<222> 66

<223> n = A,T,C or G

<400> 383

```
ccttgacctt ttcagcaagt gggaagggtgt tttccgtctc cacagacaag gccaggactc 60
gtttgnaccc gttgatgata gaatggggta ctgatgcaac agttgggtag ccaatctgca 120
gacagacact ggcaacattg cggacaccca ggatttcaat ggtgccctg gagatttttag 180
tggtgatacc taaagcctgg aaaaaggagg tcttctcggg cccagagacca gtgttctggg 240
ctggcacagt gacttcacat ggggcaatgg caccagcacg ggcagcagac ctgcccgggc 300
ggccgctcga aagccgaatt ccagcacact ggccggcgtt actagtggat ccgagctcgg 360
taccaagctt ggcgtaatca tggatcatagc tgtttc 396
```

<210> 384

<211> 396

<212> DNA

<213> Homo sapiens

<400> 384

```
gctgaatagg cacagagggc acctgtacac ettcagacca gtctgcaacc tcaggctgag 60
tagcagtga ctcaggagcg ggagcagctcc attcaccctg aaattcctcc ttggtcactg 120
ccttctcagc agcagcctgc tcttcttttt caatctcttc aggatctctg tagaagtaca 180
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cccagccag catccaccac atcaaaccca ctgagtgcgc tccctgtgtg ttgcatggga 300
tggcaatgtc cacatagcgc agaggagaat ctgtgttaca cagcgcaatg gtaggtaggt 360
taacataaga tgcctccgtg agaggctggt ggtcag 396
```

<210> 385

<211> 2943

<212> DNA

<213> Homo sapiens

<400> 385

```
cagccaccgg agtggatgcc atctgcaccc accgccctga cccacaggc cctgggctgg 60
acagagagca gctgtatttg gagctgagcc agctgaccca cagcatcact gagctgggcc 120
cctacacccct ggacaggga agtctctatg tcaatgggtt cacacagcgg agctctgtgc 180
ccaccactag cattcctggg acccccacag tggacctggg aacatctggg actccagttt 240
ctaaacctgg tccctcggct gccagccctc tctgtgtgct attcactctc aacttcacca 300
tcaccaacct gcggtatgag gagaacatgc agcaccctgg ctccaggaa gttcaacacca 360
cggagaggggt ccttcagggc ctggtccctg tcaagagca ccagtgttg cctctgttac 420
tctggctgca gactgacttt gctcaggcct gaaaaggatg ggacagccac tggagtggat 480
gccatctgca cccaccacc tgaacccaaa agccctaggc tggacagaga gcagctgtat 540
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ccaggtctgc ctatcaagca ggtgttccat gagctgagcc agcagaccca tggcatcacc 1440
cggctgggcc cctactctct ggacaaagac agcctctacc ttaacggtta caatgaacct 1500
```



```

gggccagatg agcctcctac aactcccaag ccagccacca cattcctgcc tcctctgtca 1560
gaagccacaa cagccatggg gtaccacctg aagaccctca cactcaactt caccatctcc 1620
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aattaccaga ggaacaaaag gaattattgag gatgcggcac cacaccgggg tggactccct 2460
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aaaccaatatt ggtcggaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2940
aaa

```

<210> 386

<211> 2608

<212> DNA

<213> Homo sapiens

<400> 386

```

gttcaagagc accagtgttg gccctctgta ctctggctgc agactgactt tgctcaggcc 60
tgaaaaggat gggacagcca ctggagtggg tgcctctgca acccaccacc ctgaccccaa 120
aagccctagg ctggacagag agcagctgta ttgggagctg agccagctga cccacaatat 180
cactgagctg gggccctatg ccctggacaa cgacagctc tttgtcaatg gtttcaacta 240
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taagactcca gcctcgatat ttggcccttc agctgccagc catctcctga tactattcac 360
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gttcaacact acagagaggg tccttcaggg cctgctaagg cccttggtca agaaccaccg 480
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ccaactgggc ttctatgtcc tggacaggga tagcctcttc atcaatggct atgcacccca 1560

```

```

gaatttatca atccggggcg agtaccagat aaatttccac attgtcaact ggaacctcag 1620
taatccagac cccacatcct cagagtacat caccctgctg agggacatcc aggacaaggt 1680
caccacactc tacaaaggca gtcaactaca tgacacattc cgcttctgcc tggtcaccaa 1740
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ctggggtgcc tttccccag ccagggtcca aagaagcttg gctggggcag aaataaacca 2580
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2608

```

<210> 387

<211> 1761

<212> DNA

<213> Homo sapiens

<400> 387

```

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aagttaaca tcacagacaa cgtcatgaag caccctgctc gtcctttgtt ccagaggagc 120
agcctgggtg caggttacac aggtctgcag gtcatgcac taaggctctg gaagaacggt 180
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tcacactcaa cttcaccatc tccaatctcc agtattcacc agatattggc aagggctcag 420
ctacattcaa ctcaccgag ggggtccttc agcacctgct cagacccttg ttccagaaga 480
gcagcatggg ccccttctac ttgggttgcc aactgatctc cctcaggcct gagaaggatg 540
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caatccgggg cgagtaccag ataaatttcc acattgtcaa ctggaacctc agtaatccag 780
acccacatc ctcagagtac atcaccctgc tgagggacat ccaggacaag gtcaccacac 840
tctacaaagg cagtcaacta catgacacat tccgcttctg cctggtcacc aacttgacga 900
tggactccgt gttgggtcact gtcaaggcat tgttctcctc caatttgga cccagcctgg 960
tggagcaagt ctttctagat aagaccctga atgcctcatt ccattggctg ggctccacct 1020
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gyacacaaaa aaaaaaaaaa a
1751

```

<210> 388

<211> 772

<212> PRT

<213> Homo sapiens

<400> 388

```

Met Ser Met Val Ser His Ser Gly Ala Leu Cys Pro Pro Leu Ala Phe
 1          5          10          15
Leu Gly Pro Pro Gln Trp Thr Trp Glu His Leu Gly Leu Gln Phe Leu
 20          25          30
Asn Leu Val Pro Arg Leu Pro Ala Leu Ser Trp Cys Tyr Ser Leu Ser
 35          40          45
Thr Ser Pro Ser Pro Thr Cys Gly Met Arg Arg Thr Cys Ser Thr Leu
 50          55          60
Ala Pro Gly Ser Ser Thr Pro Arg Arg Gly Ser Phe Arg Ala Trp Ser
 65          70          75          80
Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu
 85          90          95
Thr Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly Val Asp Ala
100          105          110
Ile Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu
115          120          125
Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu
130          135          140
Gly Pro Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn Gly Phe Thr
145          150          155          160
His Arg Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Pro Thr Val
165          170          175
Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile Phe Gly Pro Ser Ala
180          185          190
Ala Ser His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn
195          200          205
Leu Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys Phe Asn Thr
210          215          220
Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr
225          230          235          240
Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro
245          250          255
Glu Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg
260          265          270
Pro Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu
275          280          285
Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu
290          295          300
Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val
305          310          315          320
Pro Thr Thr Ser Thr Gly Val Val Ser Glu Glu Pro Phe Thr Leu Asn
325          330          335
Phe Thr Ile Asn Asn Leu Arg Tyr Met Ala Asp Met Gly Gln Pro Gly
340          345          350
Ser Leu Lys Phe Asn Ile Thr Asp Asn Val Met Lys His Leu Leu Ser
355          360          365
Pro Leu Phe Gln Arg Ser Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg
370          375          380
Val Ile Ala Leu Arg Ser Val Lys Asn Gly Ala Glu Thr Arg Val Asp
385          390          395          400
Leu Leu Cys Thr Tyr Leu Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile
405          410          415
Lys Gln Val Phe His Glu Leu Ser Gln Gln Thr His Gly Ile Thr Arg
420          425          430

```

Leu Gly Pro Tyr Ser Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr
 435 440 445
 Asn Glu Pro Gly Pro Asp Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr
 450 455 460
 Thr Phe Leu Pro Pro Leu Ser Glu Ala Thr Thr Ala Met Gly Tyr His
 465 470 475 480
 Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn Leu Gln Tyr Ser
 485 490 495
 Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser Thr Glu Gly Val
 500 505 510
 Leu Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser Ser Met Gly Pro
 515 520 525
 Phe Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly
 530 535 540
 Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp Pro Val
 545 550 555 560
 Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu
 565 570 575
 Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser
 580 585 590
 Leu Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu
 595 600 605
 Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp
 610 615 620
 Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys
 625 630 635 640
 Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe
 645 650 655
 Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu Val Thr Val Lys
 660 665 670
 Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val Glu Gln Val Phe
 675 680 685
 Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu Gly Ser Thr Tyr
 690 695 700
 Gln Leu Val Asp Ile His Val Thr Glu Met Glu Ser Ser Val Tyr Gln
 705 710 715 720
 Pro Thr Ser Ser Ser Thr Gln His Phe Tyr Leu Asn Phe Thr Ile
 725 730 735
 Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn
 740 745 750
 Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Ala Pro His Arg Gly
 755 760 765
 Gly Leu Pro Val
 770

<210> 389

<211> 833

<212> PRT

<213> Homo sapiens

<400> 389

Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
 1 5 10 15
 Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly Val Asp Ala Ile
 20 25 30
 Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu Gln
 35 40 45

Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly
 50 55 60
 Pro Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn Gly Phe Thr His
 65 70 75 80
 Arg Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Pro Thr Val Tyr
 85 90 95
 Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile Phe Gly Pro Ser Ala Ala
 100 105 110
 Ser His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu
 115 120 125
 Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys Phe Asn Thr Thr
 130 135 140
 Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser
 145 150 155 160
 Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Arg Pro Glu
 165 170 175
 Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Pro
 180 185 190
 Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu Leu
 195 200 205
 Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
 210 215 220
 Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro
 225 230 235 240
 Thr Thr Ser Thr Gly Val Val Ser Glu Glu Pro Phe Thr Leu Asn Phe
 245 250 255
 Thr Ile Asn Asn Leu Arg Tyr Met Ala Asp Met Gly Gln Pro Gly Ser
 260 265 270
 Leu Lys Phe Asn Ile Thr Asp Asn Val Met Lys His Leu Leu Ser Pro
 275 280 285
 Leu Phe Gln Arg Ser Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg Val
 290 295 300
 Ile Ala Leu Arg Ser Val Lys Asn Gly Ala Glu Thr Arg Val Asp Leu
 305 310 315 320
 Leu Cys Thr Tyr Leu Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile Lys
 325 330 335
 Gln Val Phe His Glu Leu Ser Gln Gln Thr His Gly Ile Thr Arg Leu
 340 345 350
 Gly Pro Tyr Ser Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr Asn
 355 360 365
 Glu Pro Gly Pro Asp Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr Thr
 370 375 380
 Phe Leu Pro Pro Leu Ser Glu Ala Thr Thr Ala Met Gly Tyr His Leu
 385 390 395 400
 Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn Leu Gln Tyr Ser Pro
 405 410 415
 Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser Thr Glu Gly Val Leu
 420 425 430
 Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser Ser Met Gly Pro Phe
 435 440 445
 Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly Ala
 450 455 460
 Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp Pro Val Gly
 465 470 475 480
 Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
 485 490 495
 His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser Leu
 500 505 510

Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu Tyr
 515 520 525
 Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp Pro
 530 535 540
 Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys Val
 545 550 555 560
 Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe Cys
 565 570 575
 Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu Val Thr Val Lys Ala
 580 585 590
 Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val Glu Gln Val Phe Leu
 595 600 605
 Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu Gly Ser Thr Tyr Gln
 610 615 620
 Leu Val Asp Ile His Val Thr Glu Met Glu Ser Ser Val Tyr Gln Pro
 625 630 635 640
 Thr Ser Ser Ser Ser Thr Gln His Phe Tyr Leu Asn Phe Thr Ile Thr
 645 650 655
 Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr
 660 665 670
 Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe Arg
 675 680 685
 Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr Phe
 690 695 700
 Arg Ser Val Pro Asn Arg His His Thr Gly Val Asp Ser Leu Cys Asn
 705 710 715 720
 Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val Ala Ile Tyr Glu Glu
 725 730 735
 Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr Leu
 740 745 750
 Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Phe Pro Asn Arg Asn Glu
 755 760 765
 Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp Ala Val Ile Leu Ile
 770 775 780
 Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly Val
 785 790 795 800
 Leu Val Thr Thr Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val Gln
 805 810 815
 Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp Leu
 820 825 830
 Gln

<210> 390

<211> 438

<212> PRT

<213> Homo sapiens

<400> 390

Met Gly Tyr His Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn
 1 5 10 15
 Leu Gln Tyr Ser Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser
 20 25 30
 Thr Glu Gly Val Leu Gln His Leu Arg Pro Leu Phe Gln Lys Ser
 35 40 45
 Ser Met Gly Pro Phe Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro
 50 55 60

Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His
 65 70 75 80
 Pro Asp Pro Val Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu
 85 90 95
 Leu Ser Gln Leu Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu
 100 105 110
 Asp Arg Asp Ser Leu Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser
 115 120 125
 Ile Arg Gly Glu Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu
 130 135 140
 Ser Asn Pro Asp Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp
 145 150 155 160
 Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp
 165 170 175
 Thr Phe Arg Phe Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu
 180 185 190
 Val Thr Val Lys Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val
 195 200 205
 Glu Gln Val Phe Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu
 210 215 220
 Gly Ser Thr Tyr Gln Leu Val Asp Ile His Val Thr Glu Met Glu Ser
 225 230 235 240
 Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser Thr Gln His Phe Tyr Leu
 245 250 255
 Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro
 260 265 270
 Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu
 275 280 285
 Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys
 290 295 300
 Gln Val Ser Thr Phe Arg Ser Val Pro Asn Arg His His Thr Gly Val
 305 310 315 320
 Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val
 325 330 335
 Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu
 340 345 350
 Gln Asn Phe Thr Leu Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Phe
 355 360 365
 Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp
 370 375 380
 Ala Val Ile Leu Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys
 385 390 395 400
 Leu Ile Cys Gly Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly
 405 410 415
 Glu Tyr Asn Val Gln Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu
 420 425 430
 Asp Leu Glu Asp Leu Gln
 435

<210> 391
 <211> 2627
 <212> DNA
 <213> Homo sapiens

<400> 391
 ccacgcgtcc gccacgcgt ccggaaggca gcggcagctc cactcagcca gtaccagat 60
 acgctgggaa ccttcccag ccattggttc cctggggcag atcctcttct ggagcataat 120

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tagcatcatc attattctgg ctggagcaat tgcactcatc attggctttg gtatttcagg 180
gagacactcc atcacagtca ctactgtcgc ctacagctggg aacattgggg aggatggaat 240
cctgagctgc acttttgaac ctgacatcaa actttctgat atcgtgatac aatggctgaa 300
ggaagggtgt ttaggcttgg tccatgagtt caaagaaggc aaagatgagc tgcgggagca 360
ggatgaaatg ttcagaggcc ggacagcagt gtttctgat caagtgatag ttggcaatgc 420
ctctttgcgg ctgaaaaacg tgcaactcac agatgctggc acctacaaat gttatatcat 480
cacttctaaa gccaaggagg atgctaacct tgagtataaa actggagcct tcagcatgcc 540
ggaagtgaat gtggactata atgccagctc agagaccttg cgggtgtgagg ctccccgatg 600
gttccccag cccacagtgg totgggcatc ccaagttgac cagggagcca acttctcgga 660
agtctccaat accagctttg agctgaactc tgagaatgtg accatgaagg ttgtgtctgt 720
gctctacaat gttacgatca acaacacata ctctgtatg attgaaatg acattgccaa 780
agcaacaggg gatatacaag tgacagaatc ggagatcaaa agggcgagtc acctacagct 840
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atotttggga ggaatgaat tcatatctag aagtctggag tgagcaaaaca agagcaagaa 1080
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aaaggtgcct tggcttctct tcccactga caaatgccaa agttgagaaa aatgatcata 1560
attttagcat aaacagagca gtccggcaga ccgattttat aaataaactg agcaccttct 1620
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caaggacaat gactgcttga attgaggcct tgagggaatga agctttgaag gaaaagaata 2460
ctttgttcc agcccccttc ccacactctt catgtgttaa ccactgcctt cctggacctt 2520
ggagccacgg tgactgtatt acatgttgtt atagaaaact gatttttagg ttctgatcgt 2580
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<210> 392

<211> 309

<212> PRT

<213> Homo sapiens

<400> 392

```

His Ala Ser Ala His Ala Ser Gly Arg Gln Arg Gln Leu His Ser Ala
1           5           10           15
Ser Thr Gln Ile Arg Trp Glu Pro Ser Pro Ala Met Ala Ser Leu Gly
20           25           30
Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile Ile Ile Leu Ala Gly
35           40           45
Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile Ser Gly Arg His Ser Ile
50           55           60
Thr Val Thr Thr Val Ala Ser Ala Gly Asn Ile Gly Glu Asp Gly Ile

```



```

65          70          75          80
Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu Ser Asp Ile Val Ile
      85          90          95
Gln Trp Leu Lys Glu Gly Val Leu Gly Leu Val His Glu Phe Lys Glu
      100         105         110
Gly Lys Asp Glu Leu Ser Glu Gln Asp Glu Met Phe Arg Gly Arg Thr
      115         120         125
Ala Val Phe Ala Asp Gln Val Ile Val Gly Asn Ala Ser Leu Arg Leu
      130         135         140
Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr Lys Cys Tyr Ile Ile
145      150         155         160
Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu Tyr Lys Thr Gly Ala
      165         170         175
Phe Ser Met Pro Glu Val Asn Val Asp Tyr Asn Ala Ser Ser Glu Thr
      180         185         190
Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln Pro Thr Val Val Trp
      195         200         205
Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser Glu Val Ser Asn Thr
      210         215         220
Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met Lys Val Val Ser Val
225      230         235         240
Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser Cys Met Ile Glu Asn
      245         250         255
Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val Thr Glu Ser Glu Ile
      260         265         270
Lys Arg Arg Ser His Leu Gln Leu Leu Asn Ser Lys Ala Ser Leu Cys
      275         280         285
Val Ser Ser Phe Phe Ala Ile Ser Trp Ala Leu Leu Pro Leu Ser Pro
290      295         300
Tyr Leu Met Leu Lys
305

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<210> 393
 <211> 282
 <212> PRT
 <213> Homo sapiens

```

<400> 393
Met Ala Ser Leu Gly Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile Ile
 1      5      10      15
Ile Ile Leu Ala Gly Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile Ser
      20      25      30
Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala Gly Asn Ile
      35      40      45
Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu
      50      55      60
Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly Val Leu Gly Leu Val
65      70      75      80
His Glu Phe Lys Glu Gly Lys Asp Glu Leu Ser Glu Gln Asp Glu Met
      85      90      95
Phe Arg Gly Arg Thr Ala Val Phe Ala Asp Gln Val Ile Val Gly Asn
      100     105     110
Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr
      115     120     125
Lys Cys Tyr Ile Ile Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu
      130     135     140
Tyr Lys Thr Gly Ala Phe Ser Met Pro Glu Val Asn Val Asp Tyr Asn

```

```

145          150          155          160
Ala Ser Ser Glu Thr Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln
165          170          175
Pro Thr Val Val Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser
180          185          190
Glu Val Ser Asn Thr Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met
195          200          205
Lys Val Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser
210          215          220
Cys Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val
225          230          235
Thr Glu Ser Glu Ile Lys Arg Arg Ser His Leu Gln Leu Leu Asn Ser
245          250          255
Lys Ala Ser Leu Cys Val Ser Ser Phe Phe Ala Ile Ser Trp Ala Leu
260          265          270
Leu Pro Leu Ser Pro Tyr Leu Met Leu Lys
275          280

```

```

<210> 394
<211> 20
<212> PRT
<213> Homo sapiens

```

```

<400> 394
Met Ala Ser Leu Gly Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile Ile
1          5          10          15
Ile Ile Leu Ala
20

```

```

<210> 395
<211> 20
<212> PRT
<213> Homo sapiens

```

```

<400> 395
Ile Ile Ile Leu Ala Gly Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile
1          5          10          15
Ser Gly Arg His
20

```

```

<210> 396
<211> 20
<212> PRT
<213> Homo sapiens

```

```

<400> 396
Ile Ser Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala Gly
1          5          10          15
Asn Ile Gly Glu
20

```

```

<210> 397
<211> 20
<212> PRT

```

<213> Homo sapiens

<400> 397

Gly Asn Ile Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro Asp
1 5 10 15
Ile Lys Leu Ser
20

<210> 398

<211> 20

<212> PRT

<213> Homo sapiens

<400> 398

Asp Ile Lys Leu Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly Val
1 5 10 15
Leu Gly Leu Val
20

<210> 399

<211> 20

<212> PRT

<213> Homo sapiens

<400> 399

Val Leu Gly Leu Val His Glu Phe Lys Glu Gly Lys Asp Glu Leu Ser
1 5 10 15
Glu Gln Asp Glu
20

<210> 400

<211> 20

<212> PRT

<213> Homo sapiens

<400> 400

Ser Glu Gln Asp Glu Met Phe Arg Gly Arg Thr Ala Val Phe Ala Asp
1 5 10 15
Gln Val Ile Val
20

<210> 401

<211> 20

<212> PRT

<213> Homo sapiens

<400> 401

Asp Gln Val Ile Val Gly Asn Ala Ser Leu Arg Leu Lys Asn Val Gln
1 5 10 15
Leu Thr Asp Ala
20

<210> 402

<211> 21
<212> PRT
<213> Homo sapiens

<400> 402
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Lys	Asp	Gly	Thr	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys	Thr	His	His	Pro		
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Asp	Pro	Lys	Ser	Pro	Arg	Leu	Asp	Arg	Glu	Gln	Leu	Tyr	Trp	Glu	Leu		
		355					360					365					
Ser	Gln	Leu	Thr	His	Asn	Ile	Thr	Glu	Leu	Gly	His	Tyr	Ala	Leu	Asp		
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Thr	Thr	Ser	Thr	Pro	Gly	Thr	Pro	Thr	Val	Tyr	Leu	Gly	Ala	Ser	Lys		
				405					410						415		
Thr	Pro	Ala	Ser	Ile	Phe	Gly	Pro	Ser	Ala	Ala	Ser	His	Leu	Leu	Ile		
			420					425					430				
Leu	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Arg	Tyr	Glu	Glu	Asn		
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Met	Trp	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln		
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Ser	Gly	Ser	Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys	Asp	Gly	Glu	Ala		
				485				490					495				
Thr	Gly	Val	Asp	Ala	Ile	Cys	Thr	His	Arg	Pro	Asp	Pro	Thr	Gly	Pro		
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Gly	Leu	Asp	Arg	Glu	Gln	Leu	Tyr	Leu	Glu	Leu	Ser	Gln	Leu	Thr	His		
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Ser	Ile	Thr	Glu	Leu	Gly	Pro	Tyr	Thr	Leu	Asp	Arg	Asp	Ser	Leu	Tyr		
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Val	Val	Ser	Glu	Glu	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Asn	Asn	Leu		
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Thr	Asp	Asn	Val	Met	Lys	His	Leu	Leu	Ser	Pro	Leu	Phe	Gln	Arg	Ser		
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Ser	Leu	Gly	Ala	Arg	Tyr	Thr	Gly	Cys	Arg	Val	Ile	Ala	Leu	Arg	Ser		
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Val	Lys	Asn	Gly	Ala	Glu	Thr	Arg	Val	Asp	Leu	Leu	Cys	Thr	Tyr	Leu		
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 Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Val Thr Gln
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 Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys
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 Gly Ser Gln Leu His Asp Thr Phe Arg Phe Cys Leu Val Thr Asn Leu
 885 890 895
 Thr Met Asp Ser Val Leu Val Thr Val Lys Ala Leu Phe Ser Ser Asn
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 Leu Asp Pro Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn
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 Ala Ser Phe His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His
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 945 950 955 960
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 965 970 975
 Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg
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 Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys
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 Ser Asp Leu Pro Phe Trp Ala Val Ile Phe Ile Gly Leu Ala Gly Leu
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<211> 1156

<212> PRT

<213> Homo sapiens

<400> 459

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 Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Lys Leu
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 Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
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 Arg His Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser Ser Met Thr
 85 90 95
 Thr Thr Arg Thr Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg
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 Thr Pro Ala Ser Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu Val
 115 120 125
 Leu Phe Thr Ile Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn
 130 135 140
 Met His His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
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 Gln Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser Val Gly Pro Leu
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 Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala
 180 185 190
 Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser
 195 200 205
 Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
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 His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu
 225 230 235 240
 Tyr Val Asn Gly Phe Thr Gln Arg Ser Ser Val Pro Thr Thr Ser Ile
 245 250 255
 Pro Gly Thr Pro Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Val Ser
 260 265 270
 Lys Pro Gly Pro Ser Ala Ala Ser Pro Leu Leu Val Leu Phe Thr Leu
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 Asp Ala Ile Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp
 355 360 365
 Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr
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 Glu Leu Gly His Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn Gly
 385 390 395 400
 Phe Thr His Arg Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Pro
 405 410 415
 Thr Val Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile Phe Gly Pro
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 His Arg Pro Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu Tyr
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 545 550 555 560
 Ser Val Pro Thr Thr Ser Thr Gly Val Val Ser Glu Glu Pro Phe Thr
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 Leu Asn Phe Thr Ile Asn Asn Leu Arg Tyr Met Ala Asp Met Gly Gln
 580 585 590
 Pro Gly Ser Leu Lys Phe Asn Ile Thr Asp Asn Val Met Lys His Leu
 595 600 605
 Leu Ser Pro Leu Phe Gln Arg Ser Ser Leu Gly Ala Arg Tyr Thr Gly
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 Cys Arg Val Ile Ala Leu Arg Ser Val Lys Asn Gly Ala Glu Thr Arg
 625 630 635 640
 Val Asp Leu Leu Cys Thr Tyr Leu Gln Pro Leu Ser Gly Pro Gly Leu
 645 650 655
 Pro Ile Lys Gln Val Phe His Glu Leu Ser Gln Gln Thr His Gly Ile
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 Thr Arg Leu Gly Pro Tyr Ser Leu Asp Lys Asp Ser Leu Tyr Leu Asn
 675 680 685
 Gly Tyr Asn Glu Pro Gly Leu Asp Glu Pro Pro Thr Thr Pro Lys Pro
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 Tyr Ser Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser Thr Glu
 740 745 750
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 Gly Glu Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu Ser Asn
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 Val Lys Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val Glu Gln
 915 920 925
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945 950 955 960
 Tyr Gln Pro Thr Ser Ser Ser Ser Thr Gln His Phe Tyr Pro Asn Phe
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 Thr Ile Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr
 980 985 990
 Thr Asn Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu Asn Gln
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 1090 1095 1100
 Ile Phe Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys Leu Ile
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 Cys Gly Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly Glu Tyr
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 <212> PRT
 <213> Homo sapiens

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35 40 45
 Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu Thr His Gly Ile Thr
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 Glu Leu Gly Pro Tyr Thr Leu Asp Arg His Ser Leu Tyr Val Asn Gly
 65 70 75 80
 Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr Ser
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 115 120 125
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 130 135 140
 Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe
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 260 265 270
 Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Arg
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<211> 2996

<212> DNA

<213> Homo sapiens

<400> 462

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<211> 3557

<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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<211> 1175

<212> DNA

<213> Homo sapiens

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<211> 1959

<212> DNA

<213> Homo sapiens

<400> 466

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<211> 1636

<212> DNA

<213> Homo sapiens

<400> 467

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<211> 231

<212> DNA

<213> Homo sapiens

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<210> 469

<211> 607

<212> DNA

<213> Homo sapiens

<400> 469

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<211> 981

<212> DNA

<213> Homo sapiens

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<211> 959

<212> DNA

<213> Homo sapiens

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<211> 1315

<212> DNA

<213> Homo sapiens

<400> 472

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<210> 473

<211> 689

<212> DNA

<213> Homo sapiens

<400> 473

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<211> 495

<212> DNA

<213> Homo sapiens

<400> 474

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aggccaggca gggagtgtga cctctagtta gagattagag gctgccagc aagggggaag 360
agatttcaac cacatcacag ccactcacca ttgacataga gactgttctt gtcagggtg 420
taggggccca gctcttcaat gtcattggtc agtttgctta gctccagta cagctgctcc 480
ctgttgagtc caggg 495

<210> 475

<211> 192

<212> DNA

<213> Homo sapiens

<400> 475

agtggccagg ctactaccag tcacacctag acctggagga tctgcaatga ctggaacttg 60
ccggtgcctg gggatagcct cttcatcaat ggtatgcac ccagaattt atcaatccg 120

ggcgagtagc agataaattt ccacattgtc aactggaacc tcagtaatcc agacccaca 180
tcctcagagt ac 192

<210> 476
<211> 500
<212> DNA
<213> Homo sapiens

<400> 476
ccggtggctg cccacggtt ttcaggcctg agcaaggta gctcgcagcc agagtacaga 60
gggccaacac tgggtgctctt gaacaagggc ttgagcagac cctgcaggac tctctccgtg 120
gtgttgaaact tcctggaacc agggtagcgc atgtcctcct catactgcag gttgggtgata 180
gtgaagttga gggtagaatgg caccaggaga gggccagggc tgtgtggcca gggagggagg 240
ctggagtcctc agaggtttcc aggtgcactg cagaggtccc aggaatactg gtggttggca 300
cagagctccg atgggtgaag ccattgacat agagactgtc cctgtccagg tgtaggggcc 360
cagctctgta acgctgttgg tcagctggct cagctcccag tatagccgct ctctgtccag 420
tccaggacca gtgggatcaa ggcggagggt gcagatggcg tccactccag tggctgcccc 480
atgtttctca ggtctgagca 500

<210> 477
<211> 191
<212> DNA
<213> Homo sapiens

<400> 477
gaggtatgct aactactact attatitagt aggccttgggt agaaacttct gttgttatag 60
tcaagggacg catggaaact ttttatatta ttctctcttt aaatcctggt gcatatgttt 120
agaagtaggc cttttgaaa tatataaagt tctccacttt tgaacatggt gtttctttcc 180
cacctccacg a 191

<210> 478
<211> 914
<212> PRT
<213> Homo sapiens

<400> 478
Met Ser Met Val Ser His Ser Gly Ala Leu Cys Pro Pro Leu Ala Phe
1 5 10 15
Leu Gly Pro Pro Gln Trp Thr Trp Glu His Leu Gly Leu Gln Phe Leu
20 25 30
Asn Leu Val Pro Arg Leu Pro Ala Leu Ser Trp Cys Tyr Ser Leu Ser
35 40 45
Thr Ser Pro Ser Pro Thr Cys Gly Met Arg Arg Thr Cys Ser Thr Leu
50 55 60
Ala Pro Gly Ser Ser Thr Pro Arg Arg Gly Ser Phe Arg Ala Trp Ser
65 70 75 80
Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu
85 90 95
Thr Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly Val Asp Ala
100 105 110
Ile Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu
115 120 125
Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu
130 135 140
Gly Pro Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn Gly Phe Thr
145 150 155 160
His Arg Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Pro Thr Val
165 170 175

Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile Phe Gly Pro Ser Ala
180 185 190
Ala Ser His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn
195 200 205
Leu Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys Phe Asn Thr
210 215 220
Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr
225 230 235 240
Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro
245 250 255
Glu Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg
260 265 270
Pro Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu
275 280 285
Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu
290 295 300
Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val
305 310 315 320
Pro Thr Thr Ser Thr Gly Val Val Ser Glu Glu Pro Phe Thr Leu Asn
325 330 335
Phe Thr Ile Asn Asn Leu Arg Tyr Met Ala Asp Met Gly Gln Pro Gly
340 345 350
Ser Leu Lys Phe Asn Ile Thr Asp Asn Val Met Lys His Leu Leu Ser
355 360 365
Pro Leu Phe Gln Arg Ser Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg
370 375 380
Val Ile Ala Leu Arg Ser Val Lys Asn Gly Ala Glu Thr Arg Val Asp
385 390 395 400
Leu Leu Cys Thr Tyr Leu Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile
405 410 415
Lys Gln Val Phe His Glu Leu Ser Gln Gln Thr His Gly Ile Thr Arg
420 425 430
Leu Gly Pro Tyr Ser Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr
435 440 445
Asn Glu Pro Gly Pro Asp Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr
450 455 460
Thr Phe Leu Pro Pro Leu Ser Glu Ala Thr Thr Ala Met Gly Tyr His
465 470 475 480
Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn Leu Gln Tyr Ser
485 490 495
Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser Thr Glu Gly Val
500 505 510
Leu Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser Ser Met Gly Pro
515 520 525
Phe Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly
530 535 540
Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp Pro Val
545 550 555 560
Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu
565 570 575
Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser
580 585 590
Leu Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu
595 600 605
Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp
610 615 620
Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys
625 630 635 640

Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe
 645 650 655
 Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu Val Thr Val Lys
 660 665 670
 Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val Glu Gln Val Phe
 675 680 685
 Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu Gly Ser Thr Tyr
 690 695 700
 Gln Leu Val Asp Ile His Val Thr Glu Met Glu Ser Ser Val Tyr Gln
 705 710 715 720
 Pro Thr Ser Ser Ser Thr Gln His Phe Tyr Leu Asn Phe Thr Ile
 725 730 735
 Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn
 740 745 750
 Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe
 755 760 765
 Arg Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr
 770 775 780
 Phe Arg Ser Val Pro Asn Arg His His Thr Gly Val Asp Ser Leu Cys
 785 790 795 800
 Asn Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val Ala Ile Tyr Glu
 805 810 815
 Glu Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr
 820 825 830
 Leu Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Phe Pro Asn Arg Asn
 835 840 845
 Glu Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp Ala Val Ile Leu
 850 855 860
 Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly
 865 870 875 880
 Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val
 885 890 895
 Gln Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp
 900 905 910
 Leu Gln

<210> 479

<211> 1148

<212> PRT

<213> Homo sapiens

<400> 479

Met Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly Cys
 1 5 10 15
 Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val
 20 25 30
 Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp
 35 40 45
 Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu Thr His Gly Ile Thr
 50 55 60
 Glu Leu Gly Pro Tyr Thr Leu Asp Arg His Ser Leu Tyr Val Asn Gly
 65 70 75 80
 Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr Ser
 85 90 95
 Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly Pro
 100 105 110

Thr Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn Phe Thr Ile
 115 120 125
 Thr Asn Leu Arg Tyr Glu Glu Asn Met His His Pro Gly Ser Arg Lys
 130 135 140
 Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe
 145 150 155 160
 Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu
 165 170 175
 Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys
 180 185 190
 Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu
 195 200 205
 Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro
 210 215 220
 Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg
 225 230 235 240
 Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Pro Thr Val Asp Leu
 245 250 255
 Gly Thr Ser Gly Thr Pro Val Ser Lys Pro Gly Pro Ser Ala Ala Ser
 260 265 270
 Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Arg
 275 280 285
 Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr
 290 295 300
 Glu Arg Val Leu Gln Gly Leu Leu Arg Ser Leu Phe Lys Ser Thr Ser
 305 310 315 320
 Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 325 330 335
 Lys Asp Gly Thr Ala Thr Gly Val Asp Ala Ile Cys Thr His His Pro
 340 345 350
 Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
 355 360 365
 Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly His Tyr Ala Leu Asp
 370 375 380
 Asn Asp Ser Leu Phe Val Asn Gly Phe Thr His Arg Ser Ser Val Ser
 385 390 395 400
 Thr Thr Ser Thr Pro Gly Thr Pro Thr Val Tyr Leu Gly Ala Ser Lys
 405 410 415
 Thr Pro Ala Ser Ile Phe Gly Pro Ser Ala Ala Ser His Leu Leu Ile
 420 425 430
 Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn
 435 440 445
 Met Trp Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln
 450 455 460
 Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr
 465 470 475 480
 Ser Gly Ser Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Glu Ala
 485 490 495
 Thr Gly Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro Thr Gly Pro
 500 505 510
 Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu Leu Ser Gln Leu Thr His
 515 520 525
 Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr
 530 535 540
 Val Asn Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Thr Gly
 545 550 555 560
 Val Val Ser Glu Glu Pro Phe Thr Leu Asn Phe Thr Ile Asn Asn Leu
 565 570 575

Arg Tyr Met Ala Asp Met Gly Gln Pro Gly Ser Leu Lys Phe Asn Ile
 580 585 590
 Thr Asp Asn Val Met Lys His Leu Leu Ser Pro Leu Phe Gln Arg Ser
 595 600 605
 Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg Val Ile Ala Leu Arg Ser
 610 615 620
 Val Lys Asn Gly Ala Glu Thr Arg Val Asp Leu Leu Cys Thr Tyr Leu
 625 630 635 640
 Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile Lys Gln Val Phe His Glu
 645 650 655
 Leu Ser Gln Gln Thr His Gly Ile Thr Arg Leu Gly Pro Tyr Ser Leu
 660 665 670
 Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr Asn Glu Pro Gly Leu Asp
 675 680 685
 Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr Thr Phe Leu Pro Pro Leu
 690 695 700
 Ser Glu Ala Thr Thr Ala Met Gly Tyr His Leu Lys Thr Leu Thr Leu
 705 710 715 720
 Asn Phe Thr Ile Ser Asn Leu Gln Tyr Ser Pro Asp Met Gly Lys Gly
 725 730 735
 Ser Ala Thr Phe Asn Ser Thr Glu Gly Val Leu Gln His Leu Leu Arg
 740 745 750
 Pro Leu Phe Gln Lys Ser Ser Met Gly Pro Phe Tyr Leu Gly Cys Gln
 755 760 765
 Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Val Asp
 770 775 780
 Thr Thr Cys Thr Tyr His Pro Asp Pro Val Gly Pro Gly Leu Asp Ile
 785 790 795 800
 Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Val Thr Gln
 805 810 815
 Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser Leu Phe Ile Asn Gly Tyr
 820 825 830
 Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu Tyr Gln Ile Asn Phe His
 835 840 845
 Ile Val Asn Trp Asn Leu Ser Asn Pro Asp Pro Thr Ser Ser Glu Tyr
 850 855 860
 Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys
 865 870 875 880
 Gly Ser Gln Leu His Asp Thr Phe Arg Phe Cys Leu Val Thr Asn Leu
 885 890 895
 Thr Met Asp Ser Val Leu Val Thr Val Lys Ala Leu Phe Ser Ser Asn
 900 905 910
 Leu Asp Pro Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn
 915 920 925
 Ala Ser Phe His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His
 930 935 940
 Val Thr Glu Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser
 945 950 955 960
 Thr Gln His Phe Tyr Pro Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser
 965 970 975
 Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg
 980 985 990
 Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys
 995 1000 1005
 Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val Pro Asn
 1010 1015 1020
 Arg His His Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala
 1025 1030 1035 1040

Arg Arg Val Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr
 1045 1050 1055
 Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr Leu Asp Arg Ser Ser Val
 1060 1065 1070
 Leu Val Asp Gly Tyr Ser Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn
 1075 1080 1085
 Ser Asp Leu Pro Phe Trp Ala Val Ile Phe Ile Gly Leu Ala Gly Leu
 1090 1095 1100
 Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly Val Leu Val Thr Thr Arg
 1105 1110 1115 1120
 Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val Gln Gln Gln Cys Pro Gly
 1125 1130 1135
 Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp Leu Gln
 1140 1145

<210> 480
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 480
 Met His Arg Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 1 5 10 15
 Gln Thr Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu
 20 25 30
 Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala
 35 40 45
 Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser
 50 55 60
 Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
 65 70 75 80
 Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
 85 90 95
 Tyr Val Asn Gly Phe Thr His Trp Ile Pro Val Pro Thr Ser Ser Thr
 100 105 110
 Pro Gly Thr Ser Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Ser Leu
 115 120 125
 Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn
 130 135 140
 Phe Thr Ile Thr Asn Leu Lys Tyr Glu Glu Asp Met His Cys Pro Gly
 145 150 155 160
 Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Ser Leu Leu Gly
 165 170 175
 Pro Met Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
 180 185 190
 Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp
 195 200 205
 Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Leu Glu Trp Thr Gly
 210 215 220
 Ser Ser Tyr Thr Gly Ser
 225 230

<210> 481
 <211> 210
 <212> PRT
 <213> Homo sapiens

<400> 481

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Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 1          5          10          15
Gln Gly Leu Leu Arg Ser Leu Phe Lys Ser Thr Ser Val Gly Pro Leu
          20          25          30
Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Thr
          35          40          45
Ala Thr Gly Val Asp Ala Ile Cys Thr His His Pro Asp Pro Lys Ser
          50          55          60
Pro Arg Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
          65          70          75          80
His Asn Ile Thr Glu Leu Gly Pro Tyr Ala Leu Asp Asn Asp Ser Leu
          85          90          95
Phe Val Asn Gly Phe Thr His Arg Ser Ser Val Ser Thr Thr Ser Thr
          100          105          110
Pro Gly Thr Pro Thr Val Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser
          115          120          125
Ile Phe Gly Pro Ser Ala Ala Ser His Leu Leu Ile Leu Phe Thr Leu
          130          135          140
Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met Trp Pro Gly
          145          150          155          160
Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg
          165          170          175
Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
          180          185          190
Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Glu Ala Thr Gly Val Asp
          195          200          205
Ala Ile
          210

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<210> 482

<211> 97

<212> PRT

<213> Homo sapiens

<400> 482

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Met Ser Met Val Ser His Ser Gly Ala Leu Cys Pro Pro Leu Ala Phe
 1          5          10          15
Leu Gly Pro Pro Gln Trp Thr Trp Glu His Leu Gly Leu Gln Phe Leu
          20          25          30
Asn Leu Val Pro Arg Leu Pro Ala Leu Ser Trp Cys Tyr Ser Leu Ser
          35          40          45
Thr Ser Pro Ser Pro Thr Cys Gly Met Arg Arg Thr Cys Ser Thr Leu
          50          55          60
Ala Pro Gly Ser Ser Thr Pro Arg Arg Gly Ser Phe Arg Ala Cys Ser
          65          70          75          80
Gly Pro Cys Ser Arg Ala Pro Val Leu Ala Leu Cys Thr Leu Ala Ala
          85          90          95
Asp

```

<210> 483

<211> 438

<212> PRT

<213> Homo sapiens

<400> 483
 Met Gly Tyr His Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn
 1 5 10 15
 Leu Gln Tyr Ser Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser
 20 25 30
 Thr Glu Gly Val Leu Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser
 35 40 45
 Ser Met Gly Pro Phe Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro
 50 55 60
 Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His
 65 70 75 80
 Pro Asp Pro Val Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu
 85 90 95
 Leu Ser Gln Leu Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu
 100 105 110
 Asp Arg Asp Ser Leu Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser
 115 120 125
 Ile Arg Gly Glu Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu
 130 135 140
 Ser Asn Pro Asp Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp
 145 150 155 160
 Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp
 165 170 175
 Thr Phe Arg Phe Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu
 180 185 190
 Val Thr Val Lys Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val
 195 200 205
 Glu Gln Val Phe Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu
 210 215 220
 Gly Ser Thr Tyr Gln Leu Val Asp Ile His Val Thr Glu Met Glu Ser
 225 230 235 240
 Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser Thr Gln His Phe Tyr Leu
 245 250 255
 Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro
 260 265 270
 Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu
 275 280 285
 Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys
 290 295 300
 Gln Val Ser Thr Phe Arg Ser Val Pro Asn Arg His His Thr Gly Val
 305 310 315 320
 Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val
 325 330 335
 Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu
 340 345 350
 Gln Asn Phe Thr Leu Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Ser
 355 360 365
 Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp
 370 375 380
 Ala Val Ile Leu Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys
 385 390 395 400
 Leu Ile Cys Gly Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly
 405 410 415
 Glu Tyr Asn Val Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu
 420 425 430
 Asp Leu Glu Asp Leu Gln
 435

<210> 484
 <211> 216
 <212> PRT
 <213> Homo sapiens

<400> 484
 Met Thr Leu Lys Ser Trp Ala Pro Thr Pro Trp Thr Gly Thr Val Ser
 1 5 10 15
 Met Ser Met Val Ser Pro Ile Arg Ala Leu Cys Pro Pro Pro Ala Leu
 20 25 30
 Leu Gly Pro Pro Gln Trp Ile Ser Glu Pro Gln Trp Thr Pro Ser Ser
 35 40 45
 Leu Ser Ser Pro Thr Ile Met Ala Ala Gly Pro Leu Leu Val Pro Phe
 50 55 60
 Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Gly Glu Asp Met Gly
 65 70 75 80
 His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
 85 90 95
 Leu Leu Gly Pro Ile Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser
 100 105 110
 Gly Cys Arg Leu Thr Ser Leu Arg Ser Lys Lys Asp Gly Ala Ala Thr
 115 120 125
 Gly Val Asp Ala Ile Cys Ile His His Leu Asp Pro Lys Ser Pro Gly
 130 135 140
 Leu Asn Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly
 145 150 155 160
 Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val
 165 170 175
 Asn Gly Phe Thr His Arg Thr Ser Val Pro Thr Thr Ser Thr Pro Gly
 180 185 190
 Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Leu Pro
 195 200 205
 Ala Thr Gln Ser Leu Ala Leu Ser
 210 215

<210> 485
 <211> 268
 <212> PRT
 <213> Homo sapiens

<400> 485
 Met Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val Gly Thr
 1 5 10 15
 Ser Gly Thr Pro Ser Ser Ser Pro Ser Pro Thr Thr Ala Gly Pro Leu
 20 25 30
 Leu Met Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu
 35 40 45
 Glu Asp Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu Ser
 50 55 60
 Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly
 65 70 75 80
 Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp
 85 90 95
 Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro
 100 105 110

Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys
 115 120 125
 Leu Thr Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn
 130 135 140
 Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser Ser Val Ser Thr Thr
 145 150 155 160
 Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Arg Thr Ser Val Asp Ser
 165 170 175
 Ile Leu Pro Leu Gln Pro His Asn Tyr Gly Cys Trp Pro Ser Pro Gly
 180 185 190
 Thr Ile His Pro Gln Leu His His His Gln Pro Ala Val Trp Gly Gly
 195 200 205
 His Gly Ser Pro Trp Leu Gln Glu Val Gln His His Arg Glu Gly Pro
 210 215 220
 Ala Gly Ser Ala Trp Ser His Ile Gln Glu His Gln Cys Trp Pro Ser
 225 230 235 240
 Val Leu Trp Leu Gln Thr Asp Leu Ser Gln Val Gln Glu Gly Trp Ser
 245 250 255
 Ser His Trp Ser Gly Cys His Leu His Pro Ser Ser
 260 265

<210> 486

<211> 304

<212> PRT

<213> Homo sapiens

<400> 486

Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 1 5 10 15
 Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu
 20 25 30
 Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Glu
 35 40 45
 Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro Thr Gly
 50 55 60
 Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu Leu Ser Gln Leu Thr
 65 70 75 80
 His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu
 85 90 95
 Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Thr
 100 105 110
 Gly Val Val Ser Glu Glu Pro Phe Thr Leu Asn Phe Thr Ile Asn Asn
 115 120 125
 Leu Arg Tyr Met Ala Asp Met Gly Gln Pro Gly Ser Leu Lys Phe Asn
 130 135 140
 Ile Thr Asp Asn Val Met Lys His Leu Leu Ser Pro Leu Phe Gln Arg
 145 150 155 160
 Ser Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg Val Ile Ala Leu Arg
 165 170 175
 Ser Val Lys Asn Gly Ala Glu Thr Arg Val Asp Leu Leu Cys Thr Tyr
 180 185 190
 Leu Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile Lys Gln Val Phe His
 195 200 205
 Glu Leu Ser Gln Gln Thr His Gly Ile Thr Arg Leu Gly Pro Tyr Ser
 210 215 220
 Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr Asn Glu Pro Gly Pro
 225 230 235 240

Asp Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr Thr Phe Leu Pro Pro
 245 250 255
 Leu Ser Glu Ala Thr Thr Ala Met Gly Tyr His Leu Lys Thr Leu Thr
 260 265 270
 Leu Asn Ser His Leu Gln Ser Pro Val Phe Thr Arg Tyr Gly Gln Gly
 275 280 285
 Leu Lys Val His Ser Ile His Arg Gly Gly Ser Phe Ser Asn Trp Ser
 290 295 300

<210> 487
 <211> 294
 <212> PRT
 <213> Homo sapiens

<400> 487
 Met Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn
 1 5 10 15
 Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Gly Leu Thr Thr
 20 25 30
 Ser Thr Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro
 35 40 45
 Ser Pro Val Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Val Pro Phe
 50 55 60
 Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His
 65 70 75 80
 Arg Pro Gly Ser Arg Lys Phe Asn Ala Thr Glu Arg Val Leu Gln Gly
 85 90 95
 Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser
 100 105 110
 Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr
 115 120 125
 Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg Pro Gly
 130 135 140
 Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn
 145 150 155 160
 Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu Tyr Val
 165 170 175
 Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser Thr Pro Gly
 180 185 190
 Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Phe Pro
 195 200 205
 Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe
 210 215 220
 Thr Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser
 225 230 235 240
 Arg Lys Phe Asn Ala Thr Glu Arg Val Leu Gln Gly Leu Leu Ser Pro
 245 250 255
 Ile Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu
 260 265 270
 Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Met Asp Ala
 275 280 285
 Val Cys Leu Tyr Arg Pro
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<210> 488
 <211> 233

<212> PRT

<213> Homo sapiens

<400> 488

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Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn Ala Ser Phe
 1          5          10          15
His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His Val Thr Glu
          20          25          30
Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser Thr Gln His
          35          40          45
Phe Tyr Leu Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser Gln Asp Lys
          50          55          60
Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg Asn Ile Glu
65          70          75          80
Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys Ser Tyr Phe
          85          90          95
Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val Pro Asn Arg His His
          100          105          110
Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala Arg Arg Val
          115          120          125
Asp Arg Val Ala Ile Tyr Glu Phe Leu Arg Met Thr Arg Asn Gly
130          135          140
Thr Gln Leu Gln Asn Phe Thr Leu Asp Arg Ser Ser Val Leu Val Asp
145          150          155          160
Gly Tyr Phe Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn Ser Asp Leu
          165          170          175
Pro Phe Trp Ala Val Ile Leu Ile Gly Leu Ala Gly Leu Leu Gly Leu
          180          185          190
Ile Thr Cys Leu Ile Cys Gly Val Leu Val Thr Thr Arg Arg Arg Lys
195          200          205
Lys Glu Gly Glu Tyr Asn Val Gln Gln Gln Cys Pro Gly Tyr Tyr Gln
210          215          220
Ser His Leu Asp Leu Glu Asp Leu Gln
225          230

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<210> 489

<211> 178

<212> PRT

<213> Homo sapiens

<400> 489

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Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn Ala Ser Phe
 1          5          10          15
His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His Val Thr Glu
          20          25          30
Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser Thr Gln His
          35          40          45
Phe Tyr Leu Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser Gln Asp Lys
          50          55          60
Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg Asn Ile Glu
65          70          75          80
Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys Ser Tyr Phe
          85          90          95
Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val Pro Asn Arg His His
          100          105          110
Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala Arg Arg Val
          115          120          125

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Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr Arg Asn Gly
 130 135 140
 Thr Gln Leu Gln Asn Phe Thr Leu Asp Arg Ser Ser Val Leu Val Asp
 145 150 155 160
 Gly Tyr Phe Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn Ser Asp Leu
 165 170 175
 Pro Phe

<210> 490
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 490
 Thr Cys Gly Met Arg Arg Thr Cys Ser Thr Leu Ala Pro Gly Ser
 1 5 10 15

<210> 491
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 491
 Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr
 1 5 10 15

<210> 492
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 492
 Asp Gly Thr Ala Thr Gly Val Asp Ala Ile Cys Thr His His Pro
 1 5 10 15

<210> 493
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 <212> PRT
 <213> Homo sapiens

<400> 493
 Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu
 1 5 10 15

<210> 494
 <211> 15
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<400> 494
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<210> 495
<211> 15
<212> PRT
<213> Homo sapiens

<400> 495
Leu Gly Pro Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn Gly
1 5 10 15

<210> 496
<211> 15
<212> PRT
<213> Homo sapiens

<400> 496
Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Pro Thr Tyr Val Leu
1 5 10 15

<210> 497
<211> 15
<212> PRT
<213> Homo sapiens

<400> 497
Leu Arg Pro Glu Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile
1 5 10 15

<210> 498
<211> 15
<212> PRT
<213> Homo sapiens

<400> 498
Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu
1 5 10 15

<210> 499
<211> 15
<212> PRT
<213> Homo sapiens

<400> 499
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1 5 10 15

<210> 500
<211> 15
<212> PRT
<213> Homo sapiens

<400> 500

Gly Pro Tyr Ser Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr
1 5 10 15

<210> 501

<211> 15

<212> PRT

<213> Homo sapiens

<400> 501

Tyr Leu Asn Gly Tyr Asn Glu Pro Gly Pro Asp Glu Pro Pro Thr
1 5 10 15

<210> 502

<211> 15

<212> PRT

<213> Homo sapiens

<400> 502

Ala Thr Phe Asn Ser Thr Glu Gly Val Leu Gln His Leu Leu Arg
1 5 10 15

<210> 503

<211> 15

<212> PRT

<213> Homo sapiens

<400> 503

Gln Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly
1 5 10 15

<210> 504

<211> 15

<212> PRT

<213> Homo sapiens

<400> 504

Gly Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp
1 5 10 15

<210> 505

<211> 15

<212> PRT

<213> Homo sapiens

<400> 505

Thr Tyr His Pro Asp Pro Val Gly Pro Gly Leu Asp Ile Gln Gln
1 5 10 15

<210> 506

<211> 15

<212> PRT

<213> Homo sapiens

<400> 506

Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His
1 5 10 15

<210> 507

<211> 15

<212> PRT

<213> Homo sapiens

<400> 507

His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp Pro Thr Ser Ser
1 5 10 15

<210> 508

<211> 15

<212> PRT

<213> Homo sapiens

<400> 508

Asp Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln
1 5 10 15

<210> 509

<211> 15

<212> PRT

<213> Homo sapiens

<400> 509

Leu Arg Asp Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys Gly Ser
1 5 10 15

<210> 510

<211> 15

<212> PRT

<213> Homo sapiens

<400> 510

Leu Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe Cys Leu
1 5 10 15

<210> 511

<211> 15

<212> PRT

<213> Homo sapiens

<400> 511

Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg
1 5 10 15

<210> 512

<211> 450

<212> DNA

<213> Homo sapiens

<400> 512

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acttcacccat ctccaatctc cagtattcac cagatatggg caagggctca gctacattca 180
actccaccga ggggggtcctt cagcacctgc tcagaccctt gttccagaag agcagcatgg 240
gccccttcta cttgggttgc caactgatct ccctcaggcc tgagaaggat ggggcagcca 300
ctgggtggtga caccacctgc acctaccacc ctgaccctgt gggccccggg ctggacatac 360
agcagcttta ctgggagctg agtcagctga cccatggtgt cacccaactg ggcttctatg 420
tcctggacag ggatagcctc ttcattcaatg 450
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<210> 513

<211> 402

<212> DNA

<213> Homo sapiens

<400> 513

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tcacactgaa cttcaccatc aacaacctgc gctacatggc ggacatgggc caaccggct 120
ccctcaagtt caacatcaca gacaacgtca tgaagcacct gctcagtcct ttgttccaga 180
ggagcagcct ggggtgcacgg tacacaggct gcagggtcat cgcactaagg tctgtgaaga 240
acgggtgctga gacacgggtg gacctcctct gcacctacct gcagccctc agcggcccg 300
gtctgectat caagcagggtg ttccatgagc tgagccagca gacctatggc atcaccggc 360
tggggcccta ctctctggac aaagacagcc telaccttaa cg 402
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<210> 514

<211> 465

<212> DNA

<213> Homo sapiens

<400> 514

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tactattcac cctcaacttc accatcacta acctgcggta tgaggagaac atgtggcctg 180
gctccaggaa gttcaacact acagagaggg tccttcaggg cctgctaagg cccttgttca 240
agaacaccag tgttggccct ctgtactctg gctgcaggct gacctgtctc aggccagaga 300
aagatgggga agccaccgga gtggatgcca tctgcaccca ccgccctgac cccacaggcc 360
ctgggctgga cagagagcag ctgtatttgg agctgagcca gctgacccac agcatcactg 420
agctgggccc ctacacactg gacagggaca gtctctatgt caatg 465
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<210> 515

<211> 463

<212> DNA

<213> Homo sapiens

<400> 515

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tgctattcac tctcaacttc accatcacca acctgcggta tgaggagaac atgcagcacc 180
ctggctccag gaagttcaac accacggaga gggtccttca gggcctggtc cctgttcaag 240
agcaccagtg ttggccctct gtactctggc tgcagactga ctttgtctag gcctgaaaag 300
gatgggacag ccaactggagt ggatgccatc tgcacccacc acctgacccc caaaaagccct 360
aggctggaca gagagcagct gtattgggag ctgagccagc tgacccacaa tatcactgag 420
ctggggccct atgccctgga caacgacagc ctctttgtca atg 463
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<210> 516

<211> 156
<212> DNA
<213> Homo sapiens

<400> 516
cagccaccgg agtggatgcc atctgcaccc accgcectga cccacagge cctgggctgg 60
acagagagca gctgtatttg gagctgagcc agctgaccga cagcatcact gagctgggcc 120
cctacacctt ggacaggagc agtctctatg tcaatg 156

<210> 517
<211> 450
<212> DNA
<213> Homo sapiens

<400> 517
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tgctctctct gtcagaagcc acaacagcca tggggtagcca cctgaagacc ctcacactca 120
acttcacctt ctccaatctc cagtattcac cagatatggg caagggctca gctacattca 180
actccaccga gggggtcctt cagcaccctg tcagaccctt gttecagaag agcagcatgg 240
gcccttctta ctgtgggttg caactgatct ccctcaggcc tgagaaggat ggggcagcca 300
ctggtgtgga caccacctgc acctaccacc ctgaccctgt gggccccggg ctggacatac 360
agcagcttta ctgggagctg agtcagctga cccatggtgt caccacaactg ggcttctatg 420
tcctggagag ggatagcctc ttcatcaatg 450

<210> 518
<211> 402
<212> DNA
<213> Homo sapiens

<400> 518
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lcacactgaa cttcaccatc aacaacctgc gctacatggc ggacatgggc caaccggct 120
ccctcaagtt caacatcaca gacaacgtca tgaagcact gctcagtcct ttgttcaga 180
ggagcagcct ggggtgcagg tacacaggct gcagggtcat cgcactaagg tctgtgaaga 240
acggtgctga gacacgggtg gacctcctct gcacctacct gcagccctc agcggcccag 300
gtctgcctat caagcagggt ttccatgagc tgagccagca gacctatggc atcaccggcg 360
tgggccccca ctctctggac aaagacagcc tctaccttaa cg 402

<210> 519
<211> 465
<212> DNA
<213> Homo sapiens

<400> 519
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tgggagcacc taagactcca gcctcgatat ttggcccttc agctgccagc catctcctga 120
tactattcac cctcaacttc accatcacta acctgcggta tgaggagaac atgtggcctg 180
gctccaggaa gttcaacact acagagaggg tccttcaggg cctgctaagg cccttgttca 240
agaacaccag tgttgccctt ctgtactctg gctccaggct gaccttgctc aggccagaga 300
aagatgggga agccaccgga gtggatgcca tctgcacca ccgccctgac cccacaggcc 360
ctgggctgga cagagagcag ctgtatttgg agctgagcca gctgacccac agcatcactg 420
agctggggcc ctacacactg gacagggaca gtctctatgt caatg 465

<210> 520
<211> 468
<212> DNA
<213> Homo sapiens

<400> 520
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tgctattcac tctcaacttc accatcacca acctgcggta tgaggagaac atgcagcacc 180
ctggctccag gaagtccaac accacggaga gggctcctca gggcctgctc aggtccctgt 240
tcaagagcac cagtgttggc cctctgtact ctggctgcag actgactttg ctgagcctg 300
aaaaggatgg gacagccact ggagtggatg ccatctgcac ccaccacct gaccccaaaa 360
gccctaggct ggacagagag cagctgtatt gggagctgag ccagctgacc cacaatatca 420
ctgagctggg ccactatgcc ctggacaacg acagcctctt tgtcaatg 468

<210> 521
<211> 468
<212> DNA
<213> Homo sapiens

<400> 521
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tggcaacctc gagaactcca gcctccctgt ctggacctac gaccgccagc cctctcctgg 120
tgctattcac aattaacttc accatcacta acctgcggta tgaggagaac atgcatcacc 180
ctggctctag aaagtccaac accacggaga gagtccctca gggctgctc aggcctgtgt 240
tcaagaacac cagtgttggc cctctgtact ctggctgcag actgaccttg ctgagcccca 300
agaaggatgg ggcagccacc aaagtggatg ccatctgcac ctaccgccct gatcccaaaa 360
gccctggact ggacagagag cagctatact gggagctgag ccagctaacc cacagcatca 420
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<210> 522
<211> 262
<212> DNA
<213> Homo sapiens

<400> 522
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tactctggtt gcagactgac cttgctcagg cctgagaagg atggggcagc caccagagt 120
gatgctgtct gaccccatcg tctgacccc aaaagccctg gactggacag agagcggctg 180
tactggaagc tgagccagct gaccacggc atcactgagc tgggcccta caccctggac 240
aggcacagtc tctatgtcaa tg 262

<210> 523
<211> 302
<212> DNA
<213> Homo sapiens

<400> 523
aggacatgcg tcacctggc tccaggaagt tcaacaccac agagagggtc ctgcagggtc 60
tgcttggtcc ettgttcaag aactccagtg tcggccctct gtactctggc tgcagactga 120
tctctctcag gtctgagaag gatggggcag ccactggagt ggatgccatc tgcacccacc 180
accttaacct tcaaagcctg gactggacag ggagcagctg tactggcagc tgagccagat 240
gaccaatggc atcaaagagc tgggcccta caccctggac cggaacagtc tctacgtcaa 300
tg 302

<210> 524
<211> 468
<212> DNA
<213> Homo sapiens

<400> 524
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ttggaacctc agggactcca tccccgtcc ccagcccccac aactgctggc cctctcctgg 120


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tgccattcac cctaaacttc accatcacca acctgcagta tgaggaggac atgcatcgcc 180
ctggatctag gaagttcaac gccacagaga gggtcctgca gggctctgctt agtcccatat 240
tcaagaactc cagtgttggc cctctgtact ctggctgcag actgacctct ctcaggcccg 300
agaaggatgg ggcagcaact ggaatggatg ctgtctgcct ctaccaccct aatcccaaaa 360
gacctgggct ggacagagag cagctgtact gggagctaag ccagctgacc cacaacatca 420
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<210> 525

<211> 470

<212> DNA

<213> Homo sapiens

<400> 525

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taccattcac attcaacttt accatcacca acctgcatta tgaggaaaac atgcaacacc 180
ctggttccag gaagttcaac gccacagaga gggtcctgca gggctctgctt agtcccatat 240
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agaaggatgg ggcagcaact ggaatggatg ctgtctgtct ctaccgacct taatcccatc 360
ggacctgggc tggacagaga gcagctgtac tgggagctga gccagctgac ccacgacatc 420
actgagctgg gcccctacag ccctggacag ggacagctct tatgtcaatg 470

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<210> 526

<211> 467

<212> DNA

<213> Homo sapiens

<400> 526

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taccattcac tttcaacttt accatcacca acctgcatta tgaggaaaac atgcaacacc 180
tggttccagg aagttcaaca ccacggagag ggttctgcag ggtctgtctc cggccttggt 240
caagaacacc agtggttgcc ctctgtactc tggctgcaga ctgaccttgc tcagacctga 300
gaagcaggag gcagccactg gagtggacac catctgcact caccgccttg accctctaaa 360
ccctggactg gacagagagc agctatactg ggagctgagc aaactgacct gtggcatcat 420
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<210> 527

<211> 468

<212> DNA

<213> Homo sapiens

<400> 527

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tgccattcac cctcaacttc accatcacca acctgcagta tgaggaggcc atgcgacacc 180
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tcaagaatac cagtatcggc cctctgtact ccagctgcag actgaccttg ctcaggccag 300
agaaggacaa ggcagccacc agagtggatg ccactctgtac ccaccaccct gaccctcaaa 360
gccttgactg gaacagagag cagctgtact gggagctgag ccagctgacc caccggcatca 420
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<210> 528

<211> 537

<212> DNA

<213> Homo sapiens

<400> 528

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tgggaacctc gagaactcca gcctccctgt ctggacctac gaccgccagc cctctcctgg 120
tgctattcac aattaacttc accatcacta acctgcggta tgaggagaac atgcatcacc 180
gctggctcta gaaagtttaa caccacggag agagtccttc agggctctgt caggcctgtg 240
ttcaaagaac accagtgttg gccctctgta ctctggctgc agactgacct tgctcaggcc 300
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aaagccctgg actggacaga gacgagctat actgggagct gagccagggt gatgcatgtt 420
ctcctcatat cgcaggttag tgatggtgaa gttaattgtg aatagcacca ggagaggggt 480
ggcggtcatg ggtccagaca gggagcctgg agttctcgag gttgccaggt gcatgtc 537

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<210> 529

<211> 231

<212> DNA

<213> Homo sapiens

<400> 529

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tgttccagag gaggagcctg ggtgcacggt acacaggctg cagggtcatc gcactaaggt 60
ctgtgaagaa cgggtgctgag acacgggtgg acctcctctg cactacactg cagccctca 120
ggggccagg tctgcctatc aagcaggtgt tccatgagct gagccagcag acccatggca 180
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<210> 530

<211> 376

<212> DNA

<213> Homo sapiens

<400> 530

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tgctcctctc gtcagaagcc acaacagcca tgggtacca cctgaagacc ctcacactca 120
acttcaccaat ctccaatctc cagtattcac cagatatggg caaggggtca gctacattca 180
actccaccga ggggtcctt cagcacctgg cctgagaagg atggggcagc cactggtgtg 240
gacaccacct gcacctacca cctgaacct gtgggcccgg ggcctggacat acagcagctt 300
tactgggagc tgagttagct gacctatggt gtcacccaac tgggcttcta tgccttgga 360
agcgatagct cttcat 376

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<210> 531

<211> 75

<212> DNA

<213> Homo sapiens

<400> 531

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gtctctatgt caatg 75

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<210> 532

<211> 906

<212> DNA

<213> Homo sapiens

<400> 532

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tgccgttcac cctcaacttt accatcacca atctgcagta tggggaggac atgctcacc 180
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gccctggact ggacagggag cagctgtact ggcagctgag ccagagacca caacctcatt 420
tatacctat tctgagacac acacaagttc agccattcca actctcctg tctcccttg 480

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gtgcatcaaa gatgctgacc tcaactggta tcagttctgg gacagacagc actacaactt 540
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acaccacact cccagtagcc atcaccagtc ctggggccaga agccagtcca gctgtttcaa 720
cgacaactat ctcaactgat atgtcagatc tgggtgacctc actgggtccct agttctggga 780
cagacaccag tacaaccttc ccaacattga gtgagacccc atatgaacca gagactacag 840
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tttccc                                     906

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<210> 533
 <211> 404
 <212> DNA
 <213> Homo sapiens

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<400> 533
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tcaagaactc cagtgtcggc cctctgtact ctggctgcag actgatctct ctccaggtctg 300
agaaggatgg ggcagccact ggagtggatg ccactctgcac ccaccacctt aaccctcaaa 360
gcctctggact ggacaggagg cagctgtact ggcagctgag ccag                                     404

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<210> 534
 <211> 157
 <212> DNA
 <213> Homo sapiens

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<400> 534
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gacagagagc agctatactg ggagctgagc cagctaacc acagcatcac tgagctgggc 120
ccctacaccc tggacaggga cagtctctat gtcaatg                                     157

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<210> 535
 <211> 468
 <212> DNA
 <213> Homo sapiens

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<400> 535
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tgctattcac tctcaacttc accatcacca acctgcggtg tgaggagaac atgcagcacc 180
ctggctccag gaagttcaac accacggaga gggctcctca gggcctgctc aggtccctgt 240
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gccttaggct ggacagagag cagctgtatt gggagctgag ccagctgacc cacaatatca 420
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<210> 536
 <211> 334
 <212> DNA
 <213> Homo sapiens

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<400> 536
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tactattcac cctcaacttc accatcacta acctgcggtg tgaggagaac atgtggcctg 180
gctccaggaa gttcaacact acagagaggg tccttcaggg cctgctaagg cccttgttca 240

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agaacaccag tgttgccct ctgtactctg gctgcaggct gacettgtctc aggccagaga 300
aagatgggga agccaccgga gtggatgcca tctg 334

<210> 537
<211> 127
<212> DNA
<213> Homo sapiens

<400> 537
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gtcaatg 127

<210> 538
<211> 468
<212> DNA
<213> Homo sapiens

<400> 538
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<210> 539
<211> 465
<212> DNA
<213> Homo sapiens

<400> 539
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aggatggagc agccactgga gtggatgcca tctgcaccca ccgtcttgac cccaaaagcc 360
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gctgggtccc tacaccctgg acagcaacag tcttctatgt caatg 465

<210> 540
<211> 255
<212> DNA
<213> Homo sapiens

<400> 540
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tgccattcac cctcaacttc accatcacca acctgcagta cgaggaggac atgcatcacc 180
caggctccag gaagttcaac accacggagc gggctcctgca gggctctgctt ggtcccatgt 240
tcaagaacac tacga 255

<210> 541
<211> 390
<212> DNA

<213> Homo sapiens

<400> 541

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catccccagc tcgaacagca gccacagtcc cattcatggt gccattcacc ctcaacttca 60
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gcgcacagag agagaactgc agggctcgtgc tcaaaccccta gatcaggaat agcagtctgg 180
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cggcagtggg tggcatctgc acacatcgcc ctgacctga agacctcgga ctggacagag 300
agcgactgta ctgggagctg agcaatctga caaatggcat ccaggagctg ggccctaca 360
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<210> 542

<211> 468

<212> DNA

<213> Homo sapiens

<400> 542

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gccctggact caacagggag cagctgtact gggagctaag caaactgacc aatgacattg 420
aagagctggg cccctacacc ctggacagga acagtctcta tgtcaatg 468
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<210> 543

<211> 475

<212> DNA

<213> Homo sapiens

<400> 543

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aggccaaga aggatggagc agccactgga gtggatgcca tctgcatcca tcatcttgac 360
cccaaaagcc ctggactcaa cagagagcgg ctgtactggg agctgagcca actgaccaat 420
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<210> 544

<211> 485

<212> DNA

<213> Homo sapiens

<400> 544

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<210> 545

<211> 141

<212> DNA

<213> Homo sapiens

<400> 545

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<210> 546

<211> 142

<212> DNA

<213> Homo sapiens

<400> 546

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aaagacagcc tctaccttaa cy 142

<210> 547

<211> 185

<212> DNA

<213> Homo sapiens

<400> 547

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tcgccctgac cctgaagacc tcggactgga cagagagcga ctgtactggg agctgagcaa 120
tctgacaaat ggcatccagg agctggggcc ctacaccctg gaccggaaca gtctctatgt 180
caatg 185

<210> 548

<211> 462

<212> DNA

<213> Homo sapiens

<400> 548

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gactcaacag ggagcagctg tactgggagc taagcaaaact gaccaatgac attgaagagc 420
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<210> 549

<211> 400

<212> DNA

<213> Homo sapiens

<400> 549

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ggccctaca ccctggacag gaacagtctc tatgtcaatg 400

<210> 550
<211> 468
<212> DNA
<213> Homo sapiens

<400> 550
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<210> 551
<211> 366
<212> DNA
<213> Homo sapiens

<400> 551
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<210> 552
<211> 465
<212> DNA
<213> Homo sapiens

<400> 552
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agctggggcc ctacaccctg gacaggcaca gtctctatgt caatg 465

<210> 553
<211> 401
<212> DNA
<213> Homo sapiens

<400> 553
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ggatgccatc tgacccacc gtcttgaccc caaaagccct ggagtggaca gggagcagct 360
atactgggag ctgagccagc tgaccaatgg catcaaagaa a 401

<210> 554
<211> 385
<212> DNA
<213> Homo sapiens

<400> 554
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gcaggggtctg cttgggtccca tgttcaagaa caccagtgtc ggccttctgt actctggctg 240
cagactgacc ttgctcaggc ctgagaagaa tggggcagcc actggaatgg atgccatctg 300
cagccaccgt cttgacccca aaagccctgg actcaacaga gacgagctgt actgggagct 360
gagccagctg acccatggca tcaaa 385

<210> 555
<211> 173
<212> DNA
<213> Homo sapiens

<400> 555
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catcaaagag ctgggcccct acaccctgga ccggaacagt ctctacgtca atg 173

<210> 556
<211> 468
<212> DNA
<213> Homo sapiens

<400> 556
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gacctgggct ggacagagag cagctgtact gggagctaag ccagctgacc cacaacatca 420
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<210> 557
<211> 468
<212> DNA
<213> Homo sapiens

<400> 557
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<210> 558
<211> 468
<212> DNA

<213> Homo sapiens

<400> 558

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gtcctggact ggacagagag cggctatact gggagctgag ccagctgacc aacagcgta 420
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<210> 559

<211> 468

<212> DNA

<213> Homo sapiens

<400> 559

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<210> 560

<211> 468

<212> DNA

<213> Homo sapiens

<400> 560

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<210> 561

<211> 468

<212> DNA

<213> Homo sapiens

<400> 561

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tgccattcac actcaacttc accatcacta acctacagta tgaggagAAC atgggtcacc 180
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ctgagctggg accctacacc ctggataggg acagtctcta tgtcaatg 468
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<210> 562

<211> 407
<212> DNA
<213> Homo sapiens

<400> 562
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ccaggaagtt caacaccacg gagagggtcc ttcagggtct gcttatgccc ttgttcaaga 180
acaccagtgt cagctctctg tactctggtt gcagactgac cttgctcagg cctgagaagg 240
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gactggacag agagcggctg tactggaagc tgagccagct gaccacggc atcactgagc 360
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<210> 563
<211> 468
<212> DNA
<213> Homo sapiens

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accaccaatt accagaggaa caaaagggaat attgaggatg cgctcaacca actcttccga 10080
aacagcagca tcaagagtta ttttctgac tgtcaagttt caacattcag gtctgtcccc 10140
aecaggcacc acaccggggt ggactccctg tgtaacttct cgccactggc tcggagagta 10200
gacagagttg ccatctatga ggaatttctg cggatgaccc ggaatggtac ccagctgcag 10260
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cccttaactg ggaattctga ccttcccttc tgggtgttca tcytcacgg cttggcagga 10380
ctctctggac tcatcacatg cctgatctgc ggtgtcctgg tgaccaccg ccggcggaag 10440
aagggaaggag aatacaacgt ccagcaacag tgcccaggct actaccagtc acacctagac 10500
ctggaggatc tgcaatgact ggaacttgcc ggtgcctggg gtgcctttcc cccagccagg 10560
gtccaaagaa gcttggctgg ggcagaaata aaccatattg gtcggacaca aaaaaaaaaa 10620
aa

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<210> 570

<211> 469

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 71,92,93,120,124,168,178,218,230,300,
321,350,387,412,414,415,422,423,451

<223> n = A,T,C or G

<400> 570

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gtttcaccca tcggagctct gtgcccacca ccagcaactcc tgggacctcc acagtggacc 60
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tgeyattcac cctcaacttc accatcacca acctgcagta tgaggagrac atgcatercc 180
ctggctccag gaagtcaac accacggaga ggtcctkca gggctgtgty aggtcccttg 240
ttcaagaaca ccagtgttgg cctctgttac tetggtgca gactgacct gctcaggccy 300
gagaaggatg gggcagccac yggagtggat gccatctgca cccaccgccc tgaccccaaa 360
agccctggac tggacagaga gcagctrtac tgggagctga gccagctgac cmayrgcatc 420
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```

<210> 571

<211> 130

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> 69,107,110

<223> Xaa = Any amino acid

<400> 571

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His Pro Gln Leu Glu Gln Gln Pro Gln Ser His Ser Trp Cys His Ser
          5                      10                      15

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Pro Ser Thr Ser Thr His His Gln Pro Ala Val Arg Gly Gly His Ala
          20                      25                      30

```

Ala Pro Gly Ser Arg Lys Phe Asn Ala His Arg Glu Arg Thr Ala Gly
 35 40 45
 Ser Cys Ser Asn Pro Arg Ser Gly Ile Ala Val Trp Asn Thr Ser Ile
 50 55 60
 Gln Ala Ala Asp Xaa Pro His Ser Gly Gln Arg Arg Ile Ala Gln Pro
 65 70 75 80
 Arg Gln Trp Met Pro Ser Ala His Ile Ala Leu Thr Leu Lys Thr Ser
 85 90 95
 Asp Trp Thr Glu Ser Asp Cys Thr Gly Ser Xaa Ala Ile Xaa Gln Met
 100 105 110
 Ala Ser Arg Ser Trp Ala Pro Thr Pro Trp Thr Gly Thr Val Ser Met
 115 120 125
 Ser Met
 130

<210> 572
 <211> 130
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> 1,58,78,92,94
 <223> Xaa = Any amino acid

<400> 572
 Xaa Ile Pro Ser Ser Asn Ser Ser His Ser Pro Ile His Gly Ala Ile
 5 10 15
 His Pro Gln Leu Gln Leu Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met
 20 25 30
 Arg His Leu Val Pro Gly Ser Ser Thr Arg Thr Glu Arg Glu Leu Gln
 35 40 45
 Gly Arg Ala Gln Thr Leu Asp Gln Glu Xaa Gln Ser Gly Ile Pro Leu
 50 55 60
 Phe Arg Leu Gln Thr Ser Leu Thr Gln Ala Arg Glu Gly Xaa Leu Ser
 65 70 75 80
 His Gly Ser Gly Cys His Leu His Thr Ser Pro Xaa Pro Xaa Arg Pro
 85 90 95
 Arg Thr Gly Gln Arg Ala Thr Val Leu Gly Ala Glu Gln Ser Asp Lys
 100 105 110
 Trp His Pro Gly Ala Gly Pro Leu His Pro Gly Pro Glu Gln Ser Leu
 115 120 125
 Cys Gln

130

<210> 573

<211> 130

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> 1,54

<223> Xaa = Any amino acid

<400> 573

Xaa Ser Pro Ala Arg Thr Ala Ala Thr Val Pro Phe Met Val Pro Phe
5 10 15

Thr Leu Asn Phe Asn Ser Ser Pro Thr Cys Ser Thr Arg Arg Thr Cys
20 25 30

Gly Thr Trp Phe Gln Glu Val Gln Arg Ala Gln Arg Glu Asn Cys Arg
35 40 45

Val Val Leu Lys Pro Xaa Ile Arg Asn Ser Ser Leu Glu Tyr Leu Tyr
50 55 60

Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu Lys Asp Ser Ser Ala
65 70 75 80

Thr Ala Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro Glu Asp Leu
85 90 95

Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Asn Leu Thr Asn
100 105 110

Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr
115 120 125

Val Asn

130

<210> 574

<211> 156

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> 101

<223> Xaa = Any amino acid

<400> 574

Gly Phe Thr His Arg Ser Ser Met Pro Thr Thr Ser Thr Pro Gly Thr
5 10 15

Ser Thr Val Asp Val Gly Thr Ser Gly Thr Pro Ser Ser Ser Pro Ser
20 25 30

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<210> 575
<211> 158
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> 103
<223> Xaa = Any amino acid
```

<400> 575

Gly Phe Thr His Gln Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr
5 10 15

Ser Thr Val Asp Leu Arg Thr Ser Val Thr Pro Ser Ser Leu Ser Ser
20 25 30

Pro Thr Ile Met Ala Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn
35 40 45

Phe Thr Ile Thr Asn Leu Gln Tyr Gly Glu Asp Met Gly His Pro Gly
50 55 60

Ser Arg Lys Phe Asn Thr Thr Gln Arg Val Leu Gln Gly Leu Leu Gly
65 70 75 80

Pro Ile Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
85 90 95

Leu Thr Ser Leu Arg Ser Xaa Lys Asp Gly Ala Ala Thr Gly Val Asp
100 105 110

Ala Ile Cys Ile His His Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg
115 120 125

Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu
130 135 140

Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn
145 150 155

<210> 576

<211> 122

<212> PRT

<213> Homo sapiens

<400> 576

Ala Ala Gly Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr Ile Thr
5 10 15

Asn Leu Lys Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Thr Leu Arg Gly Pro Met Phe Lys
35 40 45

Asn Thr Ser Gly Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
50 55 60

Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr
65 70 75 80

His Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr
85 90 95

Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr
100 105 110

Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn
115 120

<210> 577

<211> 156

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> 11,106,151

<223> Xaa = Any amino acid

<400> 577

Gly Phe Thr His Arg Thr Ser Val Pro Thr Xaa Ser Thr Pro Gly Thr
5 10 15

Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Phe Ser Leu Pro Ser
20 25 30

Pro Ala Thr Ala Gly Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr
 35 40 45
 Ile Thr Asn Leu Lys Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg
 50 55 60
 Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Thr Leu Leu Gly Pro Met
 65 70 75 80
 Phe Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr
 85 90 95
 Leu Leu Arg Ser Glu Lys Asp Gly Ala Xaa Thr Gly Val Asp Ala Ile
 100 105 110
 Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln
 115 120 125
 Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly
 130 135 140
 Pro Tyr Thr Leu Asp Arg Xaa Ser Leu Tyr Val Asn
 145 150 155

<210> 578

<211> 155

<212> PRT

<213> Homo sapiens

<400> 578

Gly Phe Thr His Trp Ile Pro Val Pro Thr Ser Ser Thr Pro Gly Thr
 5 10 15
 Ser Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro
 20 25 30
 Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile
 35 40 45
 Thr Asn Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys
 50 55 60
 Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe
 65 70 75 80
 Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu
 85 90 95
 Leu Arg Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp Ala Ile Cys
 100 105 110
 Ser His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu
 115 120 125
 Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Ile Lys Glu Leu Gly Pro
 130 135 140

Tyr Thr Leu Asp Arg His Ser Leu Tyr Val Asn
 145 150 155

<210> 579
 <211> 155
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> 52,138
 <223> Xaa = Any amino acid

<400> 579
 Gly Phe Thr His Trp Ile Pro Val Pro Thr Ser Ser Thr Pro Gly Thr
 5 10 15
 Ser Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro
 20 25 30
 Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile
 35 40 45
 Thr Asn Leu Xaa Tyr Glu Glu Asp Met His Cys Pro Gly Ser Arg Lys
 50 55 60
 Phe Asn Thr Thr Glu Arg Val Leu Gln Ser Leu Leu Gly Pro Met Phe
 65 70 75 80
 Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu
 85 90 95
 Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys
 100 105 110
 Thr His Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu
 115 120 125
 Tyr Trp Glu Leu Ser Gln Leu Thr Asn Xaa Ile Lys Glu Leu Gly Pro
 130 135 140
 Tyr Thr Leu Asp Ser Asn Ser Leu Tyr Val Asn
 145 150 155

<210> 580
 <211> 156
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> 23
 <223> Xaa = Any amino acid

<400> 580
 Gly Phe Thr His Gln Thr Ser Ala Pro Asn Thr Ser Thr Pro Gly Thr

5 10 15
 Ser Thr Val Asp Leu Gly Xaa Ser Gly Thr Pro Ser Ser Leu Pro Ser
 20 25 30
 Pro Thr Ser Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr
 35 40 45
 Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg
 50 55 60
 Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met
 65 70 75 80
 Phe Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr
 85 90 95
 Leu Leu Arg Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp Ala Ile
 100 105 110
 Cys Ser His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln
 115 120 125
 Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Ile Lys Glu Leu Gly
 130 135 140
 Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn
 145 150 155

<210> 581
 <211> 156
 <212> PRT
 <213> Homo sapiens

<400> 581
 Gly Phe Thr His Arg Ser Ser Val Ala Pro Thr Ser Thr Pro Gly Thr
 5 10 15
 Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser
 20 25 30
 Pro Thr Thr Ala Val Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr
 35 40 45
 Ile Thr Asn Leu Gln Tyr Gly Glu Asp Met Arg His Pro Gly Ser Arg
 50 55 60
 Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Leu
 65 70 75 80
 Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Ile
 85 90 95
 Ser Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile
 100 105 110
 Cys Thr His His Leu Asn Pro Gln Ser Pro Gly Leu Asp Arg Glu Gln

<220>
<221> variant

<400> 583

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<210> 584
<211> 156
<212> ?RT
<213> Homo sapiens
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<400> 584

Gly Phe Asn Pro Trp Ser Ser Val Pro Thr Thr Ser Thr Pro Gly Thr
5 10 15
Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu Pro Gly
20 25 30
His Thr Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr
35 40 45
Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg
50 55 60
Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu
65 70 75 80
Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
85 90 95

Leu Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile
100 105 110
Cys Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Arg
115 120 125
Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Val Thr Glu Leu Gly
130 135 140
Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn
145 150 155

<210> 585
<211> 156
<212> PRT
<213> Homo sapiens

<400> 585
Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr
5 10 15
Ser Ala Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly
20 25 30
His Thr Ala Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr
35 40 45
Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg
50 55 60
Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu
65 70 75 80
Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
85 90 95
Leu Leu Arg Pro Glu Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile
100 105 110
Cys Thr His Arg Leu Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln
115 120 125
Leu Tyr Trp Glu Leu Ser Lys Leu Thr Cys Gly Ile Ile Glu Leu Gly
130 135 140
Pro Tyr Leu Leu Asp Arg Gly Ser Leu Tyr Val Asn
145 150 155

<210> 586
<211> 156
<212> PRT
<213> Homo sapiens

<220>
<221> variant

<400> 586

Pro Tyr Thr Leu Asp Arg Xaa Ser Leu Tyr Val Xaa
145 150 155

<213> Homo sapiens

Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
85 90 95

Leu Leu Arg Pro Glu Lys Asp Gly Val Ala Thr Arg Val Asp Ala Ile
 100 105 110

Cys Thr His Arg Pro Asp Pro Lys Ile Pro Gly Leu Asp Arg Gln Gln
 115 120 125

Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly
 130 135 140

Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn
 145 150 155

<210> 588

<211> 156

<212> PRT

<213> Homo sapiens

<400> 588

Gly Phe Thr Gln Arg Ser Ser Val Pro Thr Thr Ser Thr Pro Gly Thr
 5 10 15

Phe Thr Val Gln Pro Glu Thr Ser Glu Thr Pro Ser Ser Leu Pro Gly
 20 25 30

Pro Thr Ala Thr Gly Pro Val Leu Leu Pro Phe Thr Leu Asn Phe Thr
 35 40 45

Ile Ile Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg
 50 55 60

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Met Pro Leu
 65 70 75 80

Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly Cys Arg Leu Thr
 85 90 95

Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val Asp Ala Val
 100 105 110

Cys Thr His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Arg
 115 120 125

Leu Tyr Trp Lys Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly
 130 135 140

Pro Tyr Thr Leu Asp Arg His Ser Leu Tyr Val Asn
 145 150 155

<210> 589

<211> 156

<212> PRT

<213> Homo sapiens

<400> 589

Gly Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr

5 10 15
 Ser Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly
 20 25 30
 Pro Thr Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn Phe Thr
 35 40 45
 Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met His His Pro Gly Ser Arg
 50 55 60
 Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Val
 65 70 75 80
 Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
 85 90 95
 Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile
 100 105 110
 Cys Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln
 115 120 125
 Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly
 130 135 140
 Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn
 145 150 155

<210> 590
 <211> 156
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> variant
 <222> 145
 <223> Xaa = Any amino acid

<400> 590
 Gly Phe Thr Gln Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr
 5 10 15
 Pro Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Val Ser Lys Pro Gly
 20 25 30
 Pro Ser Ala Ala Ser Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr
 35 40 45
 Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg
 50 55 60
 Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Ser Leu
 65 70 75 80
 Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
 85 90 95

Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly Val Asp Ala Ile
 100 105 110
 Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu Gln
 115 120 125
 Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly
 130 135 140
 Xaa Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn
 145 150 155

<210> 591
 <211> 155
 <212> PRT
 <213> Homo sapiens

<400> 591
 Gly Phe Thr His Arg Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr
 5 10 15
 Pro Thr Val Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile Phe Gly
 20 25 30
 Pro Ser Ala Ala Ser His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr
 35 40 45
 Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys
 50 55 60
 Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe
 65 70 75 80
 Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu
 85 90 95
 Leu Arg Pro Glu Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile Cys
 100 105 110
 Thr His Arg Pro Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu
 115 120 125
 Tyr Leu Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro
 130 135 140
 Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn
 145 150 155

<210> 592
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 592
 Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Thr Gly Val Val

5 10 15
 Ser Glu Glu Pro Phe Thr Leu Asn Phe Thr Ile Asn Asn Leu Arg Tyr
 20 25 30
 Met Ala Asp Met Gly Gln Pro Gly Ser Leu Lys Phe Asn Ile Thr Asp
 35 40 45
 Asn Val Met Lys His Leu Leu Ser Pro Leu Phe Gln Arg Ser Ser Leu
 50 55 60
 Gly Ala Arg Tyr Thr Gly Cys Arg Val Ile Ala Leu Arg Ser Val Lys
 65 70 75 80
 Asn Gly Ala Glu Thr Arg Val Asp Leu Leu Cys Thr Tyr Leu Gln Pro
 85 90 95
 Leu Ser Gly Pro Gly Leu Pro Ile Lys Gln Val Phe His Glu Leu Ser
 100 105 110
 Gln Gln Thr His Gly Ile Thr Arg Leu Gly Pro Tyr Ser Leu Asp Lys
 115 120 125
 Asp Ser Leu Tyr Leu Asn
 130

 <210> 593
 <211> 150
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> variant
 <222> 7
 <223> Xaa = Any amino acid

 <400> 593
 Gly Tyr Asn Glu Pro Gly Xaa Asp Glu Pro Pro Thr Thr Pro Lys Pro
 5 10 15
 Ala Thr Thr Phe Leu Pro Pro Leu Ser Glu Ala Thr Thr Ala Met Gly
 20 25 30
 Tyr His Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn Leu Gln
 35 40 45
 Tyr Ser Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser Thr Glu
 50 55 60
 Gly Val Leu Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser Ser Met
 65 70 75 80
 Gly Pro Phe Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro Glu Lys
 85 90 95
 Asp Gly Ala Ala Thr Gly Val Asp Thr Cys Thr Tyr His Pro Asp
 100 105 110

Pro Val Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser
115 120 125

Gln Leu Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp Arg
130 135 140

Asp Ser Leu Phe Ile Asn
145 150

<210> 594

<211> 318

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> 136,248,268

<223> Xaa = Any amino acid

<400> 594

Gly Tyr Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu Tyr Gln Ile Asn
5 10 15

Phe His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp Pro Thr Ser Ser
20 25 30

Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys Val Thr Thr Leu
35 40 45

Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe Cys Leu Val Thr
50 55 60

Asn Leu Thr Met Asp Ser Val Leu Val Thr Val Lys Ala Leu Phe Ser
65 70 75 80

Ser Asn Leu Asp Pro Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr
85 90 95

Leu Asn Ala Ser Phe His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp
100 105 110

Ile His Val Thr Glu Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser
115 120 125

Ser Ser Thr Gln His Phe Tyr Xaa Asn Phe Thr Ile Thr Asn Leu Pro
130 135 140

Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn
145 150 155 160

Lys Arg Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser
165 170 175

Ile Lys Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val
180 185 190

Pro Asn Arg His His Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro
 195 200 205
 Leu Ala Arg Arg Val Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu Arg
 210 215 220
 Met Thr Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr Leu Asp Arg Ser
 225 230 235 240
 Ser Val Leu Val Asp Gly Tyr Xaa Pro Asn Arg Asn Glu Pro Leu Thr
 245 250 255
 Gly Asn Ser Asp Leu Pro Phe Trp Ala Val Ile Xaa Ile Gly Leu Ala
 260 265 270
 Gly Leu Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly Val Leu Val Thr
 275 280 285
 Thr Arg Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val Gln Gln Gln Cys
 290 295 300
 Pro Gly Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp Leu Gln
 305 310 315

<210> 595
 <211> 3451
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> 177, 335, 523, 618, 663, 875, 961, 1001, 1441, 1555, 1560,
 1563, 1574, 1585, 2065, 2070, 2683, 2990, 3269, 3381, 3401
 <223> Xaa = Any Amino Acid

<400> 595
 Ile Arg Asn Ser Ser Leu Glu Tyr Leu Tyr Ser Gly Cys Arg Leu Ala
 1 5 10 15
 Ser Leu Arg Pro Glu Lys Asp Ser Ser Ala Thr Ala Val Asp Ala Ile
 20 25 30
 Cys Thr His Arg Pro Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg
 35 40 45
 Leu Tyr Trp Glu Leu Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly
 50 55 60
 Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His
 65 70 75 80
 Arg Ser Ser Met Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp
 85 90 95
 Val Gly Thr Ser Gly Thr Pro Ser Ser Ser Pro Ser Pro Thr Thr Ala
 100 105 110
 Gly Pro Leu Leu Met Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu
 115 120 125
 Gln Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr
 130 135 140
 Met Glu Ser Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr
 145 150 155 160
 Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro

165										170					175				
Xaa	Lys	Asp	Gly	Ala	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys	Thr	His	Arg				
			180				185						190						
Leu	Asp	Pro	Lys	Ser	Pro	Gly	Leu	Asn	Arg	Glu	Gln	Leu	Tyr	Trp	Glu				
			195				200						205						
Leu	Ser	Lys	Leu	Thr	Asn	Asp	Ile	Glu	Glu	Leu	Gly	Pro	Tyr	Thr	Leu				
			210				215						220						
Asp	Arg	Asn	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr	His	Gln	Ser	Ser	Val				
			225				230						235						
Ser	Thr	Thr	Ser	Thr	Pro	Gly	Thr	Ser	Thr	Val	Asp	Leu	Arg	Thr	Ser				
			245				250						255						
Val	Thr	Pro	Ser	Ser	Leu	Ser	Ser	Pro	Thr	Ile	Met	Ala	Ala	Gly	Pro				
			260				265						270						
Leu	Leu	Val	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Gln	Tyr				
			275				280						285						
Gly	Glu	Asp	Met	Gly	His	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu				
			290				295						300						
Arg	Val	Leu	Gln	Gly	Leu	Leu	Gly	Pro	Ile	Phe	Lys	Asn	Thr	Ser	Val				
			305				310						315						
Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Ser	Leu	Arg	Ser	Xaa	Lys				
			325				330						335						
Asp	Gly	Ala	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys	Ile	His	His	Leu	Asp				
			340				345						350						
Pro	Lys	Ser	Pro	Gly	Leu	Asn	Arg	Glu	Arg	Leu	Tyr	Trp	Glu	Leu	Ser				
			355				360						365						
Gln	Leu	Thr	Asn	Gly	Ile	Lys	Glu	Leu	Gly	Pro	Tyr	Thr	Leu	Asp	Arg				
			370				375						380						
Asn	Ser	Leu	Tyr	Val	Asn	Ala	Ala	Gly	Pro	Leu	Leu	Val	Leu	Phe	Thr				
			385				390						395						
Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Lys	Tyr	Glu	Glu	Asp	Met	His	Arg				
			405				410						415						
Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Thr	Leu				
			420				425						430						
Arg	Gly	Pro	Met	Phe	Lys	Asn	Thr	Ser	Gly	Gly	Leu	Leu	Tyr	Ser	Gly				
			435				440						445						
Cys	Arg	Leu	Thr	Leu	Leu	Arg	Ser	Glu	Lys	Asp	Gly	Ala	Ala	Thr	Gly				
			450				455						460						
Val	Asp	Ala	Ile	Cys	Thr	His	Arg	Leu	Asp	Pro	Lys	Ser	Pro	Gly	Val				
			465				470						475						
Asp	Arg	Glu	Gln	Leu	Tyr	Trp	Glu	Leu	Ser	Gln	Leu	Thr	Asn	Gly	Ile				
			485				490						495						
Lys	Glu	Leu	Gly	Pro	Tyr	Thr	Leu	Asp	Arg	Asn	Ser	Leu	Tyr	Val	Asn				
			500				505						510						
Gly	Phe	Thr	His	Arg	Thr	Ser	Val	Pro	Thr	Xaa	Ser	Thr	Pro	Gly	Thr				
			515				520						525						
Ser	Thr	Val	Asp	Leu	Gly	Thr	Ser	Gly	Thr	Pro	Phe	Ser	Leu	Pro	Ser				
			530				535						540						
Pro	Ala	Thr	Ala	Gly	Pro	Leu	Leu	Val	Leu	Phe	Thr								

625 630 635 640
Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly
645 650 655
Pro Tyr Thr Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Thr His
660 665 670
Trp Ile Pro Val Pro Thr Ser Ser Thr Pro Gly Thr Ser Thr Val Asp
675 680 685
Leu Gly Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Thr Ala Gly
690 695 700
Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln
705 710 715 720
Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys Phe Asn Thr Thr
725 730 735
Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe Lys Asn Thr Ser
740 745 750
Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
755 760 765
Lys Asn Gly Ala Ala Thr Gly Met Asp Ala Ile Cys Ser His Arg Leu
770 775 780
Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu
785 790 795 800
Ser Gln Leu Thr His Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp
805 810 815
Arg His Ser Leu Tyr Val Asn Gly Phe Thr His Trp Ile Pro Val Pro
820 825 830
Thr Ser Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Ser Gly Thr
835 840 845
Pro Ser Ser Leu Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Val Pro
850 855 860
Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Asp Met
865 870 875 880
His Cys Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln
885 890 895
Ser Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr
900 905 910
Ser Gly Cys Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala Ala
915 920 925
Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro
930 935 940
Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn
945 950 955 960
Xaa Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Ser Asn Ser Leu Tyr
965 970 975
Val Asn Gly Phe Thr His Gln Thr Ser Ala Pro Asn Thr Ser Thr Pro
980 985 990
Gly Thr Ser Thr Val Asp Leu Gly Xaa Ser Gly Thr Pro Ser Ser Leu
995 1000 1005
Pro Ser Pro Thr Ser Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn
1010 1015 1020
Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His His Pro Gly
1025 1030 1035 1040
Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly
1045 1050 1055
Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg
1060 1065 1070
Leu Thr Leu Leu Arg Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp
1075 1080 1085
Ala Ile Cys Ser His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg

1090 1095 1100
 Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Ile Lys Glu
 1105 1110 1115 1120
 Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe
 1125 1130 1135
 Thr His Arg Ser Ser Val Ala Pro Thr Ser Thr Pro Gly Thr Ser Thr
 1140 1145 1150
 Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr
 1155 1160 1165
 Thr Ala Val Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
 1170 1175 1180
 Asn Leu Gln Tyr Gly Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe
 1185 1190 1195 1200
 Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Leu Phe Lys
 1205 1210 1215
 Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Ile Ser Leu
 1220 1225 1230
 Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr
 1235 1240 1245
 His His Leu Asn Pro Gln Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr
 1250 1255 1260
 Trp Gln Leu Ser Gln Met Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr
 1265 1270 1275 1280
 Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser
 1285 1290 1295
 Ser Gly Leu Thr Thr Ser Thr Pro Trp Thr Ser Thr Val Asp Leu Gly
 1300 1305 1310
 Thr Ser Gly Thr Pro Ser Pro Val Pro Ser Pro Thr Thr Ala Gly Pro
 1315 1320 1325
 Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr
 1330 1335 1340
 Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe Asn Ala Thr Glu
 1345 1350 1355 1360
 Arg Val Leu Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser Val
 1365 1370 1375
 Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys
 1380 1385 1390
 Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn
 1395 1400 1405
 Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser
 1410 1415 1420
 Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg
 1425 1430 1435 1440
 Xaa Ser Leu Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr
 1445 1450 1455
 Thr Ser Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr
 1460 1465 1470
 Pro Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro
 1475 1480 1485
 Phe Thr Phe Asn Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn Met
 1490 1495 1500
 Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln
 1505 1510 1515 1520
 Gly Leu Leu Thr Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr
 1525 1530 1535
 Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Gln Glu Ala Ala
 1540 1545 1550
 Thr Gly Xaa Asp Thr Ile Cys Xaa His Arg Xaa Asp Pro Ile Gly Pro

1555 1560 1565
 Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Gln Leu Thr His
 1570 1575 1580
 Xaa Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr
 1585 1590 1595 1600
 Val Asn Gly Phe Asn Pro Trp Ser Ser Val Pro Thr Thr Ser Thr Pro
 1605 1610 1615
 Gly Thr Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu
 1620 1625 1630
 Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu Asn
 1635 1640 1645
 Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly
 1650 1655 1660
 Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys
 1665 1670 1675 1680
 Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
 1685 1690 1695
 Leu Thr Leu Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp
 1700 1705 1710
 Ala Ile Cys Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg
 1715 1720 1725
 Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Val Thr Glu
 1730 1735 1740
 Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe
 1745 1750 1755 1760
 Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala
 1765 1770 1775
 Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly His Thr
 1780 1785 1790
 Ala Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
 1795 1800 1805
 Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe
 1810 1815 1820
 Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys
 1825 1830 1835 1840
 Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
 1845 1850 1855
 Arg Pro Glu Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr
 1860 1865 1870
 His Arg Leu Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr
 1875 1880 1885
 Trp Glu Leu Ser Lys Leu Thr Cys Gly Ile Ile Glu Leu Gly Pro Tyr
 1890 1895 1900
 Leu Leu Asp Arg Gly Ser Leu Tyr Val Asn Gly Phe Thr His Arg Asn
 1905 1910 1915 1920
 Phe Val Pro Ile Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Gly
 1925 1930 1935
 Thr Ser Glu Thr Pro Ser Ser Leu Pro Arg Pro Ile Val Pro Gly Pro
 1940 1945 1950
 Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr
 1955 1960 1965
 Glu Glu Ala Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu
 1970 1975 1980
 Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser Ile
 1985 1990 1995 2000
 Gly Pro Leu Tyr Ser Ser Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys
 2005 2010 2015
 Asp Lys Ala Ala Thr Arg Val Asp Ala Ile Cys Thr His His Pro Asp

2020	2025	2030
Pro Gln Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu Ser		
2035	2040	2045
Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg		
2050	2055	2060
Xaa Ser Leu Tyr Val Xaa Gly Phe Thr His Trp Ser Pro Ile Pro Thr		
2065	2070	2075
Thr Ser Thr Pro Gly Thr Ser Ile Val Asn Leu Gly Thr Ser Gly Ile		
2085	2090	2095
Pro Pro Ser Leu Pro Glu Thr Thr Ala Thr Gly Pro Leu Leu Val Pro		
2100	2105	2110
Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn Met		
2115	2120	2125
Gly His Pro Gly Ser Arg Lys Phe Asn Ile Thr Glu Ser Val Leu Gln		
2130	2135	2140
Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr		
2145	2150	2155
Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Val Ala		
2165	2170	2175
Thr Arg Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro Lys Ile Pro		
2180	2185	2190
Gly Leu Asp Arg Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His		
2195	2200	2205
Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr		
2210	2215	2220
Val Asn Gly Phe Thr Gln Arg Ser Ser Val Pro Thr Thr Ser Thr Pro		
2225	2230	2235
Gly Thr Phe Thr Val Gln Pro Glu Thr Ser Glu Thr Pro Ser Ser Leu		
2245	2250	2255
Pro Gly Pro Thr Ala Thr Gly Pro Val Leu Leu Pro Phe Thr Leu Asn		
2260	2265	2270
Phe Thr Ile Ile Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly		
2275	2280	2285
Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Met		
2290	2295	2300
Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly Cys Arg		
2305	2310	2315
Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val Asp		
2325	2330	2335
Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg		
2340	2345	2350
Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu Thr His Gly Ile Thr Glu		
2355	2360	2365
Leu Gly Pro Tyr Thr Leu Asp Arg His Ser Leu Tyr Val Asn Gly Phe		
2370	2375	2380
Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr Ser Thr		
2385	2390	2395
Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly Pro Thr		
2405	2410	2415
Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn Phe Thr Ile Thr		
2420	2425	2430
Asn Leu Arg Tyr Glu Glu Asn Met His His Pro Gly Ser Arg Lys Phe		
2435	2440	2445
Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe Lys		
2450	2455	2460
Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu		
2465	2470	2475
Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr		

2485 2490 2495
Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr
2500 2505 2510
Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr
2515 2520 2525
Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg Ser
2530 2535 2540
Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Pro Thr Val Asp Leu Gly
2545 2550 2555 2560
Thr Ser Gly Thr Pro Val Ser Lys Pro Gly Pro Ser Ala Ala Ser Pro
2565 2570 2575
Leu Leu Val Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Arg Tyr
2580 2585 2590
Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu
2595 2600 2605
Arg Val Leu Gln Gly Leu Leu Arg Ser Leu Phe Lys Ser Thr Ser Val
2610 2615 2620
Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys
2625 2630 2635 2640
Asp Gly Thr Ala Thr Gly Val Asp Ala Ile Cys Thr His His Pro Asp
2645 2650 2655
Pro Lys Ser Pro Arg Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser
2660 2665 2670
Gln Leu Thr His Asn Ile Thr Glu Leu Gly Xaa Tyr Ala Leu Asp Asn
2675 2680 2685
Asp Ser Leu Phe Val Asn Gly Phe Thr His Arg Ser Ser Val Ser Thr
2690 2695 2700
Thr Ser Thr Pro Gly Thr Pro Thr Val Tyr Leu Gly Ala Ser Lys Thr
2705 2710 2715 2720
Pro Ala Ser Ile Phe Gly Pro Ser Ala Ala Ser His Leu Leu Ile Leu
2725 2730 2735
Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met
2740 2745 2750
Trp Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
2755 2760 2765
Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser
2770 2775 2780
Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Glu Ala Thr
2785 2790 2795 2800
Gly Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro Thr Gly Pro Gly
2805 2810 2815
Leu Asp Arg Glu Gln Leu Tyr Leu Glu Leu Ser Gln Leu Thr His Ser
2820 2825 2830
Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val
2835 2840 2845
Asn Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Thr Gly Val
2850 2855 2860
Val Ser Glu Glu Pro Phe Thr Leu Asn Phe Thr Ile Asn Asn Leu Arg
2865 2870 2875 2880
Tyr Met Ala Asp Met Gly Gln Pro Gly Ser Leu Lys Phe Asn Ile Thr
2885 2890 2895
Asp Asn Val Met Lys His Leu Leu Ser Pro Leu Phe Gln Arg Ser Ser
2900 2905 2910
Leu Gly Ala Arg Tyr Thr Gly Cys Arg Val Ile Ala Leu Arg Ser Val
2915 2920 2925
Lys Asn Gly Ala Glu Thr Arg Val Asp Leu Leu Cys Thr Tyr Leu Gln
2930 2935 2940
Pro Leu Ser Gly Pro Gly Leu Pro Ile Lys Gln Val Phe His Glu Leu

2945 2950 2955 2960
 Ser Gln Gln Thr His Gly Ile Thr Arg Leu Gly Pro Tyr Ser Leu Asp
 2965 2970 2975
 Lys Asp Ser Leu Tyr Leu Asn Gly Tyr Asn Glu Pro Gly Xaa Asp Glu
 2980 2985 2990
 Pro Pro Thr Thr Pro Lys Pro Ala Thr Thr Phe Leu Pro Pro Leu Ser
 2995 3000 3005
 Glu Ala Thr Thr Ala Met Gly Tyr His Leu Lys Thr Leu Thr Leu Asn
 3010 3015 3020
 Phe Thr Ile Ser Asn Leu Gln Tyr Ser Pro Asp Met Gly Lys Gly Ser
 3025 3030 3035 3040
 Ala Thr Phe Asn Ser Thr Glu Gly Val Leu Gln His Leu Leu Arg Pro
 3045 3050 3055
 Leu Phe Gln Lys Ser Ser Met Gly Pro Phe Tyr Leu Gly Cys Gln Leu
 3060 3065 3070
 Ile Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Thr
 3075 3080 3085
 Thr Cys Thr Tyr His Pro Asp Pro Val Gly Pro Gly Leu Asp Ile Gln
 3090 3095 3100
 Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Val Thr Gln Leu
 3105 3110 3115 3120
 Gly Phe Tyr Val Leu Asp Arg Asp Ser Leu Phe Ile Asn Gly Tyr Ala
 3125 3130 3135
 Pro Gln Asn Leu Ser Ile Arg Gly Glu Tyr Gln Ile Asn Phe His Ile
 3140 3145 3150
 Val Asn Trp Asn Leu Ser Asn Pro Asp Pro Thr Ser Ser Glu Tyr Ile
 3155 3160 3165
 Thr Leu Leu Arg Asp Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys Gly
 3170 3175 3180
 Ser Gln Leu His Asp Thr Phe Arg Phe Cys Leu Val Thr Asn Leu Thr
 3185 3190 3195 3200
 Met Asp Ser Val Leu Val Thr Val Lys Ala Leu Phe Ser Ser Asn Leu
 3205 3210 3215
 Asp Pro Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn Ala
 3220 3225 3230
 Ser Phe His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His Val
 3235 3240 3245
 Thr Glu Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser Thr
 3250 3255 3260
 Gln His Phe Tyr Xaa Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser Gln
 3265 3270 3275 3280
 Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg Asn
 3285 3290 3295
 Ile Glu Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys Ser
 3300 3305 3310
 Tyr Phe Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val Pro Asn Arg
 3315 3320 3325
 His His Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala Arg
 3330 3335 3340
 Arg Val Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr Arg
 3345 3350 3355 3360
 Asn Gly Thr Gln Leu Gln Asn Phe Thr Leu Asp Arg Ser Ser Val Leu
 3365 3370 3375
 Val Asp Gly Tyr Xaa Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn Ser
 3380 3385 3390
 Asp Leu Pro Phe Trp Ala Val Ile Xaa Ile Gly Leu Ala Gly Leu Leu
 3395 3400 3405
 Gly Leu Ile Thr Cys Leu Ile Cys Gly Val Leu Val Thr Thr Arg Arg

